GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run on January 31, 2002, 13:20:11; Search time 78.64 Seconds (without alignments)
13.561 Million cell updates/sec

Perfect score: Sequence: US-08-957-709-74 14

Scoring table: 1 AGWIDAGFKGKITL 14

Gapop 60.0 , Gapext 60.0 OLIGO

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_68:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT F64353

dCTP deaminase (EC 3.5.4.13) MJ0430 [similarity] - Methanococcus jannaschii C;Species: Methanococcus jannaschii

C; Date:

C; Accession: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
sion: F64353

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fletschmann, R.D.; Sutton, G.G.; Blak R;Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Reference number: A64300; MUID:96337999 A; Reference number: A; Accession: F64353

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;MoLecule type: DNA
A;MoLecule type: DNA
A;Residues: 1-204 CBUL>
A;Cross-references: GB:U67494; GB:L77117; NID:g1591120; PIDN:AAB98415.1; PID:g1591133

Genetics:

A; Map position: REV386963-386349 C; Superfamily: dCTP deaminase

C; Superfamily: dCTP d
C; Keywords: hydrolase

Ov 1 AGWIDAGFKGKITI	Matches 14; Conservative	Best Local Similarity	Query Match	
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	0;			

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thioredoxin reductase (NADPH) (EC 1.6.4.5) - Eubacterium acidaminophilum N;Alternate names: dihydrolipoamide dehydrogenase [misidentification]

C;Species: Eubacterium acidaminophilum C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998

Accession: S38988; D35156 #text_change 04-Feb-2000

J.R.

R;Luebbers, M.; Andreesen, J.K. Eur. J. Biochem. 217, 791-798,

Eur. J. Blochem. 217, 791-795, 1935 A;Title: Components of glycine reductase from Eubacterium acidaminophilum. Cloning, s A;Reference number: S38988; MUID:94039119

A;Molecule type: DNA A;Residues: 1-315 <LUE>

A;Cross-references: GB:L04500; NID:g2708733 R;Dietrichs, D.; Meyer, M.; Schmidt, B.; An J. Bacteriol. 172, 2088-2095, 1990 B.; Andreesen, J.R.

A;Title: Purification of NADPH-dependent electron-transferring flavoproteins and N-te A;Reference number: A35156; MUID:90202731

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(c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

A;Cross-references: GB:U67553; GB:L77117; NID:g1591744; PIDN:AAB99105.1; PID:g1591747 C;Genetics: probable dCTP deaminase (EC 3.5.4.13) MJ1102 [similarity] - Methanococcus jannaschi1 ;Species: Methanococcus jannaschii ;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, Science 273, 1058-1073, 1996 R; Bult, C.J.; White, Accession: E64437 Reich, C.I.; Overbeek, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blaek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, M.D.; Roberts, K.M.; Hurst, M.A. Blak

A;Reference number: A64300; A;Accession: E64437 A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; A; Title: Complete genome sequence of the methanogenic sequence of the 1 0; MUID:96337999 methanogenic Fraser, archaeon, Methanococcus jannasc C.M.; Smith, H.O.; Woese

A; Molecule type: DNA A; Residues: 1-161 <BUL> A; Status: preliminary; nucleic acid sequence not shown; translation not

Shown

C; Superramı. A; Map position: FOR1043233-1043718 C; Superfamily: dCTP deaminase

hydrolase

100.0%; Score 14; Pred. No. 4e-09; DB 2:

밁 20 Query Match
Best Local Similarity
Matches 14; Conserv 110 SAVHDPGYEGRPEY 1 SAVHDPGYEGRPEY Conservative 123 14 0; Mismatches 0; Length 161; Indels 0, Gaps

0

DNA-binding protein - human herpesvirus Species:

A; Note: host Homo sapiens (man) C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 31-May-1996 human herpesvirus 2 st Homo sapiens (man)

R; Toh, C; Accession: A48350

R;Toh, Y; Liu, Y; Tanaka, S; Mori, R. Arch. Virol. 129, 183-196, 1993
A;Title: Nucleotide sequence of the major A;Reference number: A48350; MUID:93228441
A;Accession: A48350 DNA-binding protein gene of herpes simplex

A; Molecule type: DNA A; Residues: 1-1197 < AHOH>

A; Note: sequence extracted C; Genetics: Genetics: from NCBI backbone (NCBIN:129069, NCBIP:129070)

A; Map position: 0.375-0.405 C; Superfamily: herpesvirus DNA-binding C; Keywords: DNA binding; zinc finger

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Nature 407:81-86(2000).
-!- CATALYTIC ACTIVITY: DC.
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Shigenobu S., Watanabe H., Hattori
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Hydrolase; Complete proteome.
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NCBI_TaxID=118099;
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Bacteria; Proteobacteria; gamma subdivision: Buchnera
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(Rel. 40,
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P44534;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEDXYCTTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Haemophilus influenzae. Bacteria; Proteobacteria; Haemophilus. EMBL; AE006134; AAK03035.1; -... InterPro; IPR003232; dCTP_deaminse. InterPro; IPR001428; dUTPase. Pfam; PF00692; dUTPase; 1. MAY B. J. Zhang Q., Li L.L. Paustian M.L. Whittam T.S "Complete genomic sequence of Pasteurella multocida Pm7 Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

1- CATALYTIC ACTIVITY: DCTP + H(2)O - DUTP + NH(3).

1- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY. MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paust 20-AUG-2001 (Rel. 40, Last 20-AUG-2001 (Rel. 40, Last DEOXYCYTIDINE TRIPHOSPHATE Bacteria; Proteobacteria; 57.1%; larity 100.0% Conservative dCTP_deaminse; 1. te proteome. ; 21467 MW; AC76D219F5258F94 CRC64; Created) 0; gamma subdivision; Pasteurellaceae gamma sequence update)
annotation update)
DEAMINASE (EC 3.5.4.13) (DCTP DEAMINASE). Score 8; DB 1; Pred. No. 0.0 0; Mismatches PRT; PRT; subdivision; Fields C.A., (195 194 DB 1; I Clayton R.A., Kirkness E.F., Dougherty B.A., Merrick J.M., Ą 8 Pasteurellaceae; Length 194; 0 Indels Pm70. Kapur V.; a collaboration 0, Gaps 0

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Result
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Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                           Word size :
                                                                            Pred. No. is the numbe score greater than or and is derived by anal
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Query
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ber of results predicted by chance to have a	RN	[P]
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	Q45920 coxiella bu	DUT_COXBU	ب	152	71.4	Ļ	
	P57914 pasteurella	DUT_PASMU	<u>_</u>	151	71.4	1 1	
	haemophi	DUT_HAEIN	H	TCT	/ L . 4	, L	
ř	P57623 buchnera ap	DUT_BUCAI	<u>_</u>	154	T00.0	14	
	P06968 escherichia	DUT_ECOLI	<u>,</u>	151	100.0	14	
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FABH_RICPR	RLAO_PLAF8	HFLC_BUCAI	SP2G_BACSU	Y117_HELPY	Y117_HELPJ	DHYS_METTH	SCRK_ZYMMO	Y4OV_RHISN	GLK2_XENLA	TFXG_RHILT	YSC1_STRGC	
Q9zch1	294660	P57630	P13801	P56080	92mv6	026230	203417	P55607	Q91755	P42729	P42360	
rickettsia	plasmodium	buchnera ap	bacillus su	helicobacte	helicobacte	methanobact	zymomonas m	rhizobium s	xenopus lae	rhizobium l	streptococc	

ALIGNMENTS

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RESULT
DUT_BUCAI
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Best Local S
Matches 14
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EMBL; V01578; CAA24897.1; --
EMBL; L01328; AAA61993.1; --
EMBL; AE000441; AAC76664.1; --
PIX; Q00497; WPECDU;
PDB; LDUP; 01-SEP-95
PDB; 1DUD; 08-NOV-96
PDB; 1DUD; 08-NOV-96
PDB; 1DUD; 03-MAY-00.
SWISS-DDPAGE; P06968; COLI.
ECO2DBASE; C017.2; 6TH EDITION.
MEDLINE-20445173; pubmed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.;
Nature 407:81-86(2000).
-1-FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT
PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYNIDIME NUCLEOTIDES
AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
URACIL CANNOT BE INCORPORATED INTO DNA (BY SIMILARITY).
- "ATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.
- "ATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.
                                                                                                                                                                                                                                                                                                            P57623;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last anotation update)
20-AUG-2001 (Rel. 40, Last anotation update)
neoxyuridine 5'-Triphosphare nucleotidohydrolase
                                                                                                                                                                                                                                          Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).

Bacteria; gamma subdivision; Buchnera.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      DEOXYURIDINE 5'-TRIPHOSPHATE NUCL: (DUTPASE) (DUTP PYROPHOSPHATASE).
DUT OR BU560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; pf006
Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      NCBI_TaxID=118099;
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InterPro; IPR001428; dU7
Pfam; PF00692; duringer
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; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide metabolism; 3D-structure; Complete proteome 151 AA; 16155 MW; 98FA3DE0BC70FFB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                  154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
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i de

EMBL; U32776; AAC22615.1;

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RESULT 3
DUT_HAEIN
ID T_HAIN
AC P4379
DT 01-NO
DT 01-NO
DT 20-AU
DE DEOXY
DE (DUTP
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-9535630; PubMed-7547800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields A., Kelley J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields A., Kelley J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen J.L., Geoghagen N.S.M.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Fenser C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUT_HARIN STANDARD; PRT; 151 AA.

P43792;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
DUT OR HI0954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-RD / KW20 /
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InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism; Complete proteome.
SEQUENCE 154 AA; 16936 MW; E5B5FDEBFB09E920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Pred. No.
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1.3e-08;
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Title:
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Maximum DB seq
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                                            \sigma
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14
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EV3L_MOUSE
EV3L_TREPA
LARP_ORYSA
ATPE_VIBAL
AMPM_MYCGA
ATPE_ONCYO
DUT_AQUAE
SODC_ONCYO
DUT_CANAL
Y269_AQUAE
SODC_ONCYO
RYNP7_YEAST
RIMM_PSEAE
RIMM_RIMM_PSEAE
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TRPE_NEIMO
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10.973 Million cell updates/sec
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P24706
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8 candida alb
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                  pseudomonas
cyanophora
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neisseria r
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vicia faba
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vibrio algi
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	INCEPTIC) 1FXUUL428; GUTFASE. Pfam; PF00692; dUTPASE; 1. Hydrolase; Nucleotide metabolism.	Z36121; CAA85215.1;	L20296;		to license@isb-sib.ch).	requires a license agreement (See http://www.is	ified and this statement is not removed. Usage by and for	its content is in no	ween the Swiss Institute of Bioinformatics and the EMBL outstation	uced through a	: SIMILARILI: DEHONGS TO INE DOITAGE FAMILUI.	!- PATHWAY: DE NOVO SYNTHESIS	!- CATALYTIC ACTIVITY: DUTP +	CIL CANNOT BE INCORPORATED INTO DNA.	AND IT DECREASES THE INTRACESTALILLAR CONCENTRATION OF DITTO SO THAT	~	Yeast 9:1131-1137(1993).	se in a yeast.";	s cerevisiae. Finding of a putati	"The complete sequence of a 6794 by segment located on the right arm	٠.	STRAIN-S288C;	SEQUENCE FROM N.A.		EMBO J. 12:4425-4431(1993).	"dUTP pyrophosphatase is an essential enzyme in Saccharomyces	en M.H., McIntosh E.M., Game J.C., Wilson P	MEDLINE-94038925; PubMed-8223452;	SEQUENCE FROM N.A.	NCBI_TaxID=4932;	s; Saccharomycetaceae; Saccharon	Saccharomyces cerevisiae (Baker's Yeast), Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	DUT1 OR YBR252W OR YBR1705.		E 5'-TRIPHO	(ACL	1994 (Rel. 28, Creat	P33317;	DUT_YEAST STANDARD; PRT; 147 AA.	DUT_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iv
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E.,
Trust T.J.;
                                                                                                                                                               InterPro; IPR001469; ATP-synt_DE.
pfam; PF00401; ATP-synt_DE; 1.
probom; PD000944; ATP-synt_DE; 1.
Hydrolase; ATP_synthesis; CF(1); Hydrogen ion transport;
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Q0-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34).
                                                                                                                                         Complete proteome SEQUENCE 123 AA.
                                                                                                                                                                                                                                    EMBL; AE001533; AAD06638.1; -. HSSP; P00832; 1BSH.
                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.

1. SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1)...CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

1. SIMILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated isolates of gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter
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larity 100.0%;
Conservative
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01-NOV-1997
20-AUG-2001
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000619; AAD08173.1; ALT_INIT.
HSSP; P00832; 1AQT.
TIGR; HP1131; -
TIGR; HP1131; -
TIGR; HP131; -
TIGR; HP131; -
TIGR; HP1001469; ATP-synt_DE; 1
Pfam; PF00401; ATP-synt_DE; 1
Probom; PD000944; ATP-synt_DE; 1
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
Complete proteome.
Complete proteome.
Complete proteome.
T23 AA; 13357 MW; 19EDDA4D2B3A5461 CRC64;
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MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.
Welson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Velson K., Guackenbush J., Dodson R., Khalak H.G., Glodek A.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.
Cotton M.D., Weidman J.M., Fujli C., Bowman C., Watthey L., Wallin
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
Venter J.C.,
                                                   MERR BACSR STANDARD; PRT; 192853; O1-AUG-1991 (Rel. 19, Created) O1-AUG-1991 (Rel. 19, Last anotation O1-OCT-1993 (Rel. 27, Last anotation MERCURIC RESISTANCE OPERON REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.cr or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- FUNCTION: PRODUCES ATD FROM ADD IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE:
-I- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(COMPASS THE MAIN SUBUNITS: A, B AND C.
-I- SIMILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.
Bacillus sp. (strain RC607).
Bacteria; Firmicutes; Bacillus/Clostridium group;
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-210;
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(Rel. 40, Last sequence up
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(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                           .0%;
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ID OT-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 37, Last annotation update)
DT 01-APR-1990 (Rel. 37, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DECXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC (DUTPASE) (DUTP PYROPHOSPHATASE).
OX (RUB_1000 (Rel. 37, Last annotation update)
DE DECXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC (DUTPASE))
OC (PATADOTATION (STANK)

ROW (RUB_1000 (Rel. 37, Last annotation)
RAM MERCET A.A., FRASET K.M., Stockwell P.A., Robinson A RAT (Rel. 31, Rel. 31)
RAM MERCET A.A., FRASET K.M., Stockwell P.A., Robinson A A homologue of retroviral pseudoproteases in the pa RT virus."
RAM METCH A.A., FRASET K.M., Stockwell P.A., Robinson A A homologue of retroviral pseudoproteases in the pa RT virus."
RAM METCH A.A., FRASET K.M., Stockwell P.A., Robinson A A NOTION (REL. CANNOT BE INCORPACE IS INVOLVED IN NUCLEOTIDE CO. AND IT DECREASES THE INTRACELLULAR CONCENTRATION (URACIL CANNOT BE INCORPORATED INTO DATA (URACIL CANNOT BE INCORPORATED INTO DATA (URACIL CANNOT BE INCORPORATED INTO DATA (PSEUDOPROTEASE))
CC -1- CAUTLON: WAS ORIGINALLY THOUGHT TO BE A PROTEASE (PSEUDOPROTEASE).
CC -1- CAUTLON: WAS ORIGINALLY THOUGHT TO BE A PROTEASE (PSEUDOPROTEASE).
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                                                                                                                                                                                                                                                                                     InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism.
SEQUENCE 159 AA; 16893 MW; 08CD852D47AE17AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIINE-90021200; PubMed-2678731;
Mercer A.A., Fraser K.M., Stockwell P.A., Robinson A.J.;
"A homologue of retroviral pseudoproteases in the parapoxvirus,"
                                                                                         81
                                                                                                                                    μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRODUCES DUMP, THE INVOLVED IN NUCLEOTIDE METABOLISM: IT PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT URACIL CANNOT BE INCORPORATED INTO DNA.

CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

SIMILARITY: BELONGS TO THE DUTPASE FAMILY.

CAUTION: WAS ORIGINALLY THOUGHT TO BE A PROTEASE-LIKE PROTEIN
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                                                                                                                                                                           Similarity 100 14; Conservative
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YFB2_YEAST
YFT6_YEAST
YHT6_YEAST
UL51_HCMVA
CRGF_MOUSE
DUT_CANAL
DUT_ADEG8
FLAV_HELPJ
FLAV_HELPJ
DUT_LYCES
CRGD_BOVIN
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Pred. No. 2.9e-08;
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DUT_ADEGI
IM23_SCHMA
DAFB_MYCBO
YHDE_BACSU
SERA_ARATH
RRP1_IAFOM
EYA_DICAI
YAKI_SCHPO
N157_YEAST
VA19_VARV
COAB_BPF1
RLAO_PIG
CHA3_BOMMO
VP16_NPVOP
YS88_CAEEL
UNR_CAVPO
Y1FY_ECOLI
CHA1_BOMMO
VP12_SCHPO
CHA2_BOMMO
VP12_SCHPO
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summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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hits satisfying chosen parameters:

100059

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60

100059 segs, 36664827 residues

Title: Perfect score:

US-08-957-709-80 14

AGVIDEDYRGNVGV

14

Sequence

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protein search,

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31,

2002,

13:39:24

Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec

Copyright

GenCore version 4.5 (c) 1993 - 2000 Comp

Compugen Ltd

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REVISIONS.

REVISIONS.

RA CHU R Y., LIN Y.L., RAO M.S., REDGY J.K.;

RA CHU R Y., LIN Y.L., RAO M.S., REDGY J.K.;

RA CHU R Y., LIN Y.L., RAO M.S., REDGY J.K.;

RA CHU R Y., LIN Y.L., RAO M.S., REDGY J.K.;

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REVISIONS.

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DUT_HUMAN
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Best Loc
Matches
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P33316; Q16860; Q16

Q1-FEB-1994 (Rel. 2

Q1-FEB-1998 (Rel. 3

Q1-AUG-2001 (Rel. 4

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20-ANG-2001 (Rel. 40, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
20-XNGTIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.
(DUTPASE) (DUTP PYROPHOSPHATASE) (PPAR-INTERACTING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIR-SPRAGUE-DAWLEY; TISSUE-Liver;
STRAIR-SPRAGUE-DAWLEY; TISSUE-Liver;
MEDLINE-97066956; PubMed-8910358;
Chu R.Y., Lin Y.L., Rao M.S., Reddy J.K.;
"Cloning and identification of rat deoxyuridine triphosphatase as inhibitor of peroxisome proliferator-activated receptor alpha.";
J. Biol. Chem. 271:27670-27676(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by another the statement is not removed. Usage by another than the statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor.send an email to licenseeisb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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pfam; PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism; Magnesium.
SEQUENCE 205 AA; 22003 MW; A9D54EBF5ED015C4 CRC64;
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14; Conservative
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1. 28, Created)
21. 36, Last sequence update)
21. 36, Last annotation update)
21. 40, Last annotation update
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Pred. No. 3.6e-08;
Mismatches 0;
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REDITINE—19381691; PubMed-8389461;

WEDLINE—93881691; PubMed-8389461;

WEDLINE—93881691; PubMed-8389461;

RA Strahler J.R., Zhu X.-X., Wang Y.K., Hora N., Andrews P.C.,

RA Strahler J.R., Zhu X.-X., Wang Y.K., Hanash S.M.;

RA Roseman N.A., Neel J.V., Turka L., Hanash S.M.;

RA Roseman N.A., Neel J.V., Turka L., Hanash S.M.;

RA ROSEMAN TEAGE AND PROLIFERATION—0ependent expression of dUTPase

RI PHOC. Natl. Acad. Sci. U.S.A. 90:4991-4995(1993).

RL PTOC. NATL. CANNOT BE INVENCE PROCURSOR OF THYMIDIE MUCLEOTIDES

C. I- FUNCTION: THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT

C. INTRACTIC CACTIVITY: DITTOP HOLD OF DUTP SO THAT

C. I- CATALYTIC ACTIVITY: DITTOP HOLD OF DUTP SO THAT

C. I- CATALYTIC ACTIVITY: DITTOP HOLD OF DUTP NEW ACTIVITY.

CC. I- PANTHWAY: DE MOYO SYNTHESIS OF THYMIDYLATE.

C. I- PANTHWAY: DE MOYO SYNTHESIS OF THYMIDYLATE.

CC. I- PANTHWAY: DE MOYO SYNTHESIS OF THY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 112-252 FROM N.A.
MEDILINE-92390380; PubMed=1325640;
MCINTOSh E.M., Ager D.D., Gadsden
"Human dUTP pyrophosphatase: CDNA
importance of the enzyme.";
Proc. Natl. Acad. Sci. U.S.A. 89:8
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Hadher R.D., McNulty D.E., Carr S.A., Roberts G.D., Caradonna "Characterization of distinct nuclear and mitochondrial forms human deoxyuridine triphosphate nucleotidohydrolase.";
J. Biol. Chem. 271:7745-7751(1996).
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Cohen D., Heng H.H.Q., Shi X.M., McIntosh E.M., Tsui L.

Pearlman R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
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Submitted (JAN-1998) to
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Eutheria;
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Acad. Sci. U.S.A. 90:4328-4328(1993).
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etazoa; Chordata;
theria; Primates;
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DUT_HSVSA
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DE DEDXYURIDINE
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OR EDES:
OS Herpesvirus s.
OS VITUS-92333
RA ALDIGENT J.
OX NEBLINE-92333
RA HONES R.W.;
RT SEQUENCE FROM
RX MEDLINE-92333
RA HONES R.W.;
RT SEQUENCE FROM
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RA HONES S.W.;
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01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE
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MEDLINE-92333688; PubMed-1321287;
MEDLINE-92333688, PubMed-1321287;
MEDLINE-92333688, PubMed-1321287;
MEDLINE-1321287;
MEDL
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NCBI_TaxID=10383;
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Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anhounce/
                                                                                                              PIK; G36811; WZBEP1.
InterPro; IPRO01428; dUTPase.
Pfam; PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism.
SEQUENCE 287 AA; 32507 MW; 598D495D74274A11 CRC64;
                                                                                                                                                                                                                 EMBL; X64346; CAA45677.1; -. EMBL; M86409; AAA46131.1; -. PIR; G36811; WZBEP1.
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           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure of the herpesvirus saimiri genome.";
66:5047-5058(1992).
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A., Coleman F
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oleman H., Fleckenstein
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18 19 20 21 21 22 23 23 24 24 25 27 28 28 30 31 31

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Matches
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Eukaryota; Fungi; Ascomycota
Eurotiales; Trichocomaceae;
NCBI_TaxID=5060;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
RIBONUCLEASE ALPHA-SARCIN PRECURSOR (EC 3.1.27.10).
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P00655;
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STRAIN-MDH 18894;
Wnendt S., Felske H.,
Submitted (JUN-1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90245591; PubMed-2336369;
Oka T., Natori Y., Tanaka S., Tsurugi
"Complete nucleotide sequence of cDNA
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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PIR; S21866; S21866.
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SIGNAL
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                                                                                                                                              e; Protein : 27
177
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                                                                                                                      123
19724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Henze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.F., Ulbrich N.,
EMBL/GenBank/DDBJ
                                                         0;
                                                         Score 6; DB : Pred. No. 7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                               synthesis inhibitor; Signal.
                                                                                                                                                                        RIBONUCLEASE ALPHA-SARCIN.
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                                                                                                                      6C711D9482DC9DD1 CRC64;
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                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the cytotoxin alpha
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databases
                                                          0,
                                                                                  Length 177
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                                                            Indels
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                                                    RESULT
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Best Local S
Matches 6
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P45799;
01-NOV-1995
01-NOV-1995
01-NOV-1995
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; FubMed-9278503;
MEDLINE-97426617; FubMedt G. III, Bloch C.A., Perna N.T., Burland V.
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Mau B., Shao Y.;
The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'Handley S.F., Frick D.N., Dunn C.A., Bessman M.J.;
O'Handley S.F., Frick D.N., Dunn C.A., Bessman M.J.;
"Orfil86 represents a new member of the nudix hydrolases, active on adenosine(5) triphospho(5') adenosine, ADP-ribose, and NADH.";
J. Biol. Chem. 273:3192-3197(1998).
J. BIOL. Chem. 273:3192-3197(1998).
J. PORCTION: ACTIVE ON ADENOSINE(5') TRIPHOSPHO(5') ADENOSINE (AP3A).
ADP-RIBOSE, MADH, ADENOSINE(5') DIPHOSPHO(5') ADENOSINE (AP2A).
ADP-RIBOSE ACTIVITY: ADP-RIBOSE + H(2)O. - AMP + D-RIBOSE 5-
DIROCHARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE-98123081; PubMed-9452430;
O'Handley S.F., Frick D.N., Dunn
O'Handley S.F. a new member o
                                                                                                                                                                                                                                                                                                                                                                                                                                                 - PHOSERALE.
- COFACTOR: MAGNESIUM OR OTHER DIVALENT CATIONS.
- SUBUNIT: HOMODIMER (PROBABLE).
- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 QGELKL 174
                                                                                                                                                                                                                                          EcoGene; EG12926; nudE.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF00293; mutT; 1.
PRINTS; PR00502; MUTTDOMAIN.
PROSITE; PS00893; NUDIX; 1.
                                                                                                                                                                                                                                                                                                          EMBL; U18997; AAA58194.1; -.
EMBL; AE000415; AAC76422.1; -.
                                                                                                                                                                                                       Hydrolase; Magnesium; Complet
DOMAIN 80 101
SEQUENCE 186 AA; 21153 MW;
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                                                                                          80 GLIDPG
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                                                                                                                  GLIDPG
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6; Conser
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
SHYDROLASE NUDE (EC 3.6.1.~)
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                                                                                          85
                                                                                                                                           Conservative
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NUDIX BOX.

1 NUDIX BOX.

1153 MW; D959AD8ECF73FCC4 CRC64;
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                                                                                                                                              Score 6; DB
Pred. No. 7.
D; Mismatches
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1271

Length 186;

0;

Indels

0;

Gaps

0;

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A; Cross references: EMBL:Z31376; NID:g449379; PIDN:CAA83249.1; PID:g499382
A; Cross references: EMBL:Z31376; NID:g449379; PIDN:CAA83249.1; PID:g499382
C; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
B; Authors: Toshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
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Best Local Similarity
Thes 8; Conserv
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A;Title: The Bacillus subtilis sigma D-dependent operon A;Reference number: 140396; MUID:94252974
A;Accession: 140398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: I40398; E69625
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C;Keywords: acyltransferase; coenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-420 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A84930; A; Accession: D84965
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Nature 407, 81-86, 2000
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C;Date: 02-Mar-2001 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) [imported] - Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-133 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Chen, L.; Helmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flagellar protein fliS – Bacillus subtilis
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100.08; Pr
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100.0%;
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A;Title: Nucleotide sequence of the Yersinia enterocolitica Ail gene and characteriza A;Reference number: A35123; MUID:90130261 A;Accession: A35123
                                                                                                                                                                                                             C;Species: Yersinia enterocolitica
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 02-Sep-2000
C;Accession: A35123
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A;Cross-references: GB:M29945; NID:g155437; PIDN:AAA88694.1; PID:g155438 C;Superfamily: phage lambda membrane protein lom
                                          A; Molecule type: DNA
A; Residues: 1-178 <MIL>
                                                                              A; Status: preliminary
                                                                                                                                                                     R; Miller, V.L.; Bliska, J.B.; Falkow, J. Bacteriol. 172, 1062-1069, 1990
                                                                                                                                                                                                                                                                            ail protein
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C; Superfamily: flagellar protein flis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sas
Nuclelc Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic
A;Reference number: A83650; MUID:20263314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: E84101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flagellar protein flis [imported] - Bacillus halodurans (strain C-125).
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: flagellar protein flis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-133 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A69580; MUID:98044033
A; Accession: E69625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-133 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                               102 LTLMLYN 108
                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LTLMLYN 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flis
                                                                                                                                                                                                                                                                                                                                                                                       LTLMLYN 29
                                                                                                                                                                                                                                                                              precursor - Yersinia enterocolitica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.; Sasaki, R.; Masui, N.; Fuji, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterium Bacillus halodurans
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Query Match
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Thes 7; Conserve

Conservative

0;

Mismatches

0;

Indels

<u>,,</u>

Gaps

0;

4.5%;

Score 7; ; Pred. No.

DB 2;

Length 178;

밁 Š

65 98

GVIGSFA 92 GVIGSFA 71

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N;Alternate names: protein c0215
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
C;Accession: S74033
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, & Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: A;Accession: S73076; MUID:97055432
A;Accession: S74033
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-215 <SEN>
A;Cross-references: Para-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Y08256; NID:g1707679; PIDN:CAA69447.1; PID:g1707727
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references:
C;Genetics:
A;Map position: FOR1
C;Superfamily: N-(5'
conserved hypothetical protein MTH1 - Wethanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: A69000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, I.; Fleischmann, R.D.; Sutton, G.G.; Blake, ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1956
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Methagococcus jannaschii
C;Species: Nethagococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: C64491
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, O
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                                                                                                                 A69000
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A; Residues: 1-237 <BUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A64300; MUID:96337999
A;Accession: C64491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase - Methanococcus
                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map position: FOR1508884-1509597
Superfamily: N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                              131 KEGKVVI 137
                                                                                                                                                                                                                                                           46 KEGKVVI 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 RIKLPDD 71
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:U67594; GB:L77117; NID:g1592160;
                                                                                                                                                                                                                                                                                                                                                                   4.5%;
                                                                                                                                                                                                                                                                                                                                                                   Score 7; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 2; ; Pred. No. 18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                         red. No. 20;
Mismatches
                                                                                Methanobacterium thermoautotrophicum (strain Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                2
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                                                                                                                                                                                                                                                                                                                                                                                             Length 237;
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C;Genetics:
A;Gene: MTH1
C;Superfamily: conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                         R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, kl. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete, genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A;Reference number: A69000; MUID:98037514

A;Accession. A69000
QΥ
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-268 <MTH>
                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                    Cross-references: GB:AE000795; GB:AE000666;
Experimental source: strain Delta H
                                                 Similarity 7; Conserv
                                                 Conservative
                                                                           100.0%;
                                                       0;
                                                       Score 7; DB 1;
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                              NID: 92621036; PIDN: AAB84510.1;
                                                                                                   Length 268;
                                                       0;
                                                    0,
                                                    Gaps
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hypothetical protein HI0345 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C;Accession: A64149
C;Accession: A64149
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
C;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.L.; Glodek, A.; Kelley, J.M.; Weldman
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm; C.L.; McDonald, L.A.; Smith, H.O.; Vente
A;Authors:
                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U32719; GB:L42023; NID:g1573310; PIDN:AAC22006.1; PID:g1573315 A;NOte: best homolog was a hypothetical protein from Escherichia coli C;Superfamily: conserved hypothetical protein H10345; ferredoxin 2[4Fe-4S] homology F;65-130/Domain: ferredoxin 2[4Fe-4S] homology <FER6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A64149
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       Similarity
7; Conser
4.5%; Score 7; 1 ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                      Mismatches
                                                                          DB 2;
                                                                                                                                      Length 279;
              0,
              Gaps
                      0,
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cysteine synthase (EC 4.2.99.8) cysM [similarity] - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aguifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Jun-2000 C;Accession: A70435

В δÃ

48

81 SLAREGY SLAREGY

87 54

A;Title: The complete genome of A;Title: The complete genome of A;Reference number: A70300; MUI A;Accession: A70435 A;Status: preliminary; nucleic

acid

sequence

not shown;

translation

not

shown

e of the hyperthermophilic bacterium MUID:98196666

Aquifex aeolicus

Nature 392, 353-358, 1998

R; Deckert, G.; Warren, P.V.; Gaasterland,

T.; Young, W.G.; Lenox, A:L.; Graham,

D.E.;

A; Molecule type: DNA A; Residues: 1-327 < A

us-08-957-709-19.rspt

Thu Jan

31 13:32:13 2002

Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.

Rhabditida; Rhabditoidea;

K08C9.6 PROTEIN 01-NOV-1999 (TrEMBLrel.

12,

Last annotation update)

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RESULT
Q9R1A1
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Granton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson B., Weinston 
                                                                                                                                                                                              MGD; MGI:1349482; Slc9a3r1.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
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Q9R1A1;
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EMBL; Z81567; CAB04589.1;
SEQUENCE 127 AA; 14638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TremBirel 13, Created)
01-MAY-2000 (TremBirel 13, Last sequence update)
01-JUN-2001 (TremBirel 17, Last annotation update)
SODIUM-HYDROGEN EXCHANGER REGULATORY FACTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 0:0-0(1999).
EMBL; AF154912; AAD49224.1; -.
HSSP; Q12923; 3PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weinman E.J., Steplock D.A., Zhang X., Akhter S., Shenolikar S.; "Molecular cloning of the cDNA and promoter sequences for the mouse sodium-hydrogen exchanger regulatory factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLC9A3R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-129/SVJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 FRIRKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 FRIRKIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
8; Conserve
                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                         142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255
                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%; SU
100.0%; PY
0;
                                                                                                                                        15376 MW;
2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8;
Pred. No
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B169A1E75006C2CE CRC64;
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                                                                                                                                            A8994D6A865B283A CRC64;
       . 8;
No.
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       DB 11;
). 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coulson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 102 SWIN NO. 10 PT 10 P
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ZSW7 PRELIMINARY; PRT; 169 AA.
Q9ZSW7;
Q9ZSW7;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-FRUCTOFURANOSIDASE (EC 3.2.1.26) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spermatophyta; Magnoliophyta;
saxifragales; Hamamelidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamamelis virginiana.
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (1998), Pennsylvania State University.
Thesis (1998), Pennsylvania State University.
-i- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING
-i- FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
-i- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virginiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Szpara M.L.T
                                                                                                                                                                                                                                                                                                                                               HMG-1
                                                                                                                                                                                                                                                                                                                                                                                            Q91596;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                      HIGH MOBILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       091596
                   and H1 in organizing chromatin.";
EMBO J. 15:548-561(1996)
EMBL; U21933; AAC59859.1; -.
HSSP; P07155; 1AAB
                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation of invertase gene sequences from
                                                                                                           Knightingale K., Dimitrov S., Reeves R., "Evidence for a shared structural role i
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                           MEDLINE=96174815; PubMed=8599938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LPTGNPVI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 LPTGNPVI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERLKKLGV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERLKKLGV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
IPR000135; Highmoblty_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magnoliophyta; eudicotyledons; core
Hamamelidaceae; Hamamelis
                                                                                                                                                                                                                                                                                                                                                                           GROUP PROTEIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%;
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                                                                                                                                                                                                                                                                                   Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                       role for HMG1 and linker histones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta;
                                                                                                                                          Wolffe A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Tracheophyta; eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Best Local S
Matches 8
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                         P70441;
P70441;
01-FEB-1997
01-FEB-1997
01-JUN-2001
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Q9CKU9;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR000910; HMG_12_box.

Pfam; PF00505; HMG_box; 2.

PRINTS; PR00806; HIGHMOBLITY12.

SMART; SM00398; HMG; 2.

PROSITE; PS00353; HMG1_2; 1.

Chromosomal protein; DNA-binding; Nuclear protein.

Chromosomal protein; DNA-binding; Nuclear Protein.
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SEQUENCE FROM N.A.
STRAIN=C57 BLACK/6; TISSUE=KIDNEY;
Weinman E.J., Steplock D.A., Shenolikar S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
EMBL; U74079; AAB17569.1;
                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006187; AAK03590.1; -
EMBL; AE006187; DR001345; PG_mutase.
Pfam; PF00300; PGAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                              PROTEIN CO-FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-PM70;
                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 SDFRPKIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GKRVLVTA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 SDFRPKIK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKRVLVTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n 2.0%;
Similarity 100.0%;
8; Conservative
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ilarity 100.0%;
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Pred. No.
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Pred. No. 17
); Mismatches
                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
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c. 16;
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5. 17;
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                                       databases.
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; Murinae; Mus
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 Query Match
Best Local Similarity
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MGD; MGI:1349482; Slc9a3rl.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ; 2.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
SEQUENCE 355 AA; 38600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   O9X885; PRELIMINARY; PRT; 396 AA.
O9X885; O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE ASPARTATE AMINOTRANSFERASE.
SCHIO.36.
SCHIO.36.
SCHIO.36.
SCHIO.36.
ACTIOOMYCES coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID-1902;
                                                     MEDITINE-9700/351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol 21:77-96 (1996).
EMBL; AL049754; CAB42045.1; -
HSSP; O56232; 1BKG.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminottan_1.
                                                                                                                                                                                                                                           James K.D., Parkhill Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                Murphy L., Harris D.,
"A set of ordered cosmids and
the 8 Mb Streptomyces coelicol
Submitted (MAY-1999) to the EN
Transferase; Aminotransferase. SEQUENCE 396 AA; 42785 MW;
                                                                                                                                                                                                                                                                         STRAIN=A3(2);
James K.D., F
                            Pfam; PF00155; aminotran_1; 1. PRINTS; PR00753; ACCSYNTHASE.
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STRAIN=A3(2);
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                                                                                                                                                                                                                                                         to 1
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s coelicolor A3(2) chromosome.";
to the EMBL/GenBank/DDBJ databases.
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Pred. No. 27;
0; Mismatches
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 727DBF14C347EBDE CRC64;
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QY

197

VLVTAGAT 204 VLVTAGAT

Query Match 2.0
Best Local Similarity 100
Matches 8; Conservative

2.0%;

Score 8; Pred. No.

0;

Mismatches DB 2

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Indels

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Length 396;

Б

99

106

A;Title: The Bacillus subtilis sigma D-dependent operon A;Reference number: I40396; MUID:94252974
A;Accession: I40398 Ď A;Gene: sucB; BU303 C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding C;Keywords: acyltransferase; coenzyme A A;Residues: 1-420 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144 A; Title: Genome sequence of A; Reference number: A84930; A; Accession: D84965 C; Accession: D84965 dihydrolipoamide S-succinyltransferase R;Chen, L.; Helmann, 밁 A; Experimental source: strain APS A; Molecule type: DNA A; Status: preliminary Nature 407, 81-86, 2000 Ş C; Keywords: hydrolase 밁 flagellar protein flis - Bacillus subtilis Query Match Best Local S Matches 8 ;Species: Bacillus subtilis
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
;Accession: I40398; E69625 Shigenobu, Date: 02-Mar-2001 #sequence_revision Species: Genetics: Query Match Matches Bacteriol. 62 Local Similarity nes 8; Conser 45 89 GSFAWVDPGWDGNLTLMLYNAS 110 Local 89 EKEGKVVI 52 GSFAWVDPGWDGNLTLMLYNAS 110 Buchnera sp. 22; Similarity Conservative Watanabe, H.; Conservative 3093-3101, 1994 69 5.1%; 100.0%; the endocellular bacterial symbiont of aphids Buchnera MUID: 20445173 Hattor1, M.; 0; Score 8; 1 Pred. No. 0 Score 22; Pred. No. Mismatches Mismatches (EC 2.3.1.61) [imported] - Buchnera sp. 02-Mar-2001 . 3; Sakaki, DB 2; 3/4e-15 2; #text_change 0; Length 420 #text_change 23-Mar-2001 0 Y.; Ishikawa, Length 154; Indels Indels encoding 21-Jul-2000 the flagellar proteins 0; 0; Gaps Gaps homology 0 0 (strain A;Molecule type: DNA
A;Residues: 1-178 <MIL>
A;Cross-references: GB:M29945; NID:g155437; PIDN:AAA88694.1;
C;Superfamily: phage lambda membrane protein lom RESULT A35123 ail protein precursor - Yersinia enterocolitica C;Species: Yersinia enterocolitica C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 02-Sep-2000 8 밁 δÃ A; Title: Nucleotide sequence of the Yersinia A; Reference number: A35123; MUID:90130261 A; Accession: A35123 R;Miller, V.L.; Bliska, J.B.; Falkow, S. J. Bacteriol. 172, 1062-1069, 1990 밁 A;Status: preliminary C; Accession: A35123 Query Match
Best Local Similarity

Matches

Conservative

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100.0%;

4.5%; Score 7; 100.0%; Pred. No.

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Length 178 Indels

PID:g155438

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A; Gene: flis
C; Superfamily: flagellar protein flis
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20263314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: flis
C;Superfamily: flagellar protein flis
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                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: E84101
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R; Takami, H.; Nakas
                                                                                                                                                                                                                                                                                                                                                                                                                                           flagellar protein fl1S [imported] - Bacillus halodurans (strain C-125).
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
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A; Residues: 1-133 < KUN>
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A; Residues: 1-133 <STO>
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                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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Best Local
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100.0%;
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                                                                                         Score 7; I
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Pred. No.
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                                                                                           DB 2;
5. 12;
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65 GVIGSFA 86 GVIGSFA 92

71

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N; Alternate | C; Species: SIC; Date: 09-0
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A;Title: Organizational characteristics and information content of A;Reference number: $73076; MUID:97055432
A;Accession: $74033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Y08256; NID:g1707679; PIDN:CAA69447.1; PID:g1707727
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase C2
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, (A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi. A;Reference number: A64300; MUID:96337999
C; Date:
C; Acc
                                                                                             A69000
                                                                   conserved hypothetical protein MTH1 -
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Matches 7
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Alternate names: protein c0215
Species: Sulfolobus solfataricus
Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase - Methanococcus species: Methanococcus jannaschii
Date: 13-58p-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Accession: C64491
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                                             Species:
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Superfamily: N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imida;
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Residues: 1-215 <SEN>
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Residues: 1-237 <B
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larity 100.0%; Pred. No. 18;
Conservative 0; Mismatches
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                      #sequence_revision
                                                                                                                                                                                                                                                                                                                 4.5%;
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                                                                   Methanobacterium thermoautotrophicum (strain Delta
                         Sep-1999
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                   #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chan, C.C.Y.; Liu, Q.Y.;
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A; Molecule type: DNA
A; Residues: 1-268 < MTH>
A; Cross-references: GB:Al
A; Experimental source: st
C; Genetics:
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                                                                                                                                         A; Gene: MTH1
C; Superfamily:
                                                                                                                                                                                                                                                                                           J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H:
A;Reference number: A69000; MUID:98037514

A;Accession: A69000
                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence
                                        Query Match
Best Local S
Matches 7
10 KEILIEP 16
                                                                                                                                                                                                                                                                                                                                                                    D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. iriol 179, 7135-7155, 1997
                                        Similarity 7; Conser
                                                                                                                                                                                                       nces: GB:AE000795; GB:AE000666; NID:g2621036;
source: strain Delta H
                                                                                                                                              conserved
                                        4.5%;
larity 100.0%;
Conservative
                                                                                                                                            hypothetical protein MTH1
                                             0
                                                             Score 7;
Pred. No.
                                                             DB 1;
                                                                              Length 268
                                             0
                                                                                                                                                                                                                               PIDN: AAB84510.1; PID: g262
                                          0,
                                          Gaps
                                             0,
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149 KEILIEP
155
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hypothetical protein H10345 - Haemophilus influenzae (strain Rd KW20)
c;Species: Haemophilus influenzae
c;Date: 18-Aug-1955 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
c;Accession: A64149
c;Accession: A64149
R;Fielschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
c;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Hitle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64010; MUID:95350830
A;Accession: A64149 A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues; 1-279 <TICR>
A;Residues; 1-279 <TICR>
A;Cross-references: GB:U32719; GB:L42023; NID:g1573310; PIDN:AAC22006.1; PID:g1573315
A;Note: best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: conserved hypothetical protein HI0345; ferredoxin 2[4Fe-4S] homology
F;65-130/Domain: ferredoxin 2[4Fe-4S] homology <FER6> 10

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ρy
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Best Local Similarity
Matches 7; Conserv
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             81 SLAREGV 87
SLAREGV
                               Conservative
54
                             4.5%; out
100.0%; Pr
                               Score 7; DB 2
Pred. No. 23;
0; Mismatches
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                                0,
                                             Length 279;
                                Indels
                               0,
                                Gaps
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A70435
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Recession: A70435
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                        cysteine synthase (EC 4.2.99.8) cysM [similarity] - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08.May-1998 *sequence_revision 08-May-1998 *text_change 20-Jun-2000 C;Accession: A70435 C;Accession: A70435 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gral
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type: [: 1-327

Last annotation update)

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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropera A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, K08C9.6 PROTEIN.
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01-MAY-2000
01-JUN-2001
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Q9R1A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
SODIUM-HYDROGEN EXCHANGER REGULATORY FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans.
                    Pfam: PF00595; PDZ; 1.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
NON_TER 142 142
                                                                                                                                                                                                   EMBL;
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*Molecular cloning of the cDNA and p;
sodium-hydrogen exchanger regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLC9A3R1.
                                                                                                                                                                                                                                                                                                                                  STRAIN-129/SVJ;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                               Biochim.
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                                                                                                                            [nterPro;
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                                                                                                                     MGI:1349482; Slc9a3r1.
rPro; IPR001478; PDZ.
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                                                                                                                                                                              Q12923; 3PDZ.
                                                                                                                                                                                                     AF154912;
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  142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                        AAD49224.1;
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inae; Caenorhabditis.
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Rodentia;
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     15376 MW;
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Pred. No.
                                                                                                                                                                                                                                                         Zhang X., Akhter S., Shenolikar S.;
NA and promoter sequences for the mouse
gulatory factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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     A8994D6A865B283A CRC64;
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01-MAY-1999 (TrEMBLIEL 10,
01-JUN-2001 (TrEMBLIEL 17,
BETA-FRUCTOFURANOSIDASE (EC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
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SEQUENCE
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mendel; 36382; Hamvi1002; 36382.
InterPro, 1FR001362; Glyco_hydro_32.

Pfam; PF00251; Glyco_hydro_32; 1.
Glycoprotein; Glycosidase; Hydrolase.
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Saxifragales; Hamamelidaceae;
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                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TIEMBLIE1. 01, Created)
01-NOV-1996 (TIEMBLIE1. 01, Last sequence update)
01-UNV-1091 (TIEMBLIE1. 17, Last annotation update)
HIGH MOBILITY GROUP PROTEIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91596
                  and H1 in organizing chromatin.";
EMBO J. 15:548-561(1996).
EMBL; U21933; AAC59859.1; -.
HSSP; P07155; 1AAB.
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                                                                                                            SEQUENCE FROM N.A.
MEDLINE-96174815; PubMed-8599938;
Knightingale K., Dimitrov S., Reeves R., Wo
"Evidence for a shared structural role for
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; vei
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                          xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                   HMG-1.
                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LPTGNPVI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 LPTGNPVI
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IPR000135; Highmoblty_12
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169 z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamamelidaceae; Hamamelis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invertase gene sequences from witch hazel (Hamamelis
                                                                                                                                                                                                                                             Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA,
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19268 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO FAMILY 32 OF GLYCOSYL
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Last annotation update)
3.2.1.26) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
la; Pipoidea; Pipidae;
                                                                                                                     Wolffe A.P
or HMG1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                       linker histones
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InterPro; IPRO Pfam; PF00505;

IPR000910; HMG_12_box | 505; HMG_box; 2.

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P70441
ID P7
AC P7
DT 011
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Best Local Similarity
"hes 8; Conser
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Best Local Similarity 100.0%;
Matches 8; Conservative
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SMART; SM00398; HMG; 2.
PROSITE; PS00353; HMG1_2; 1.
Chromosomal protein; DNA-binding; Nuclear protein.
SEQUENCE 210 AA; 24442 MW; 192CD46D694FF447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 P70441
P70441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         May B.J., Zhang Q., Li L.L., Paustian M.L., whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL, AE006187; AAK03590.1; -. InterPro. IPR001345; PG_mutase. PF0030; PGAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPMA OR PM1506.
Pasteurella multocida.
Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9CKU9;
Q9CKU9;
Q1-JUN-2001 (TIEMBLITEL:
01-JUN-2001 (TIEMBLITEL:
01-JUN-2001 (TIEMBLITEL:
                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JUN-2001 (TrEMBLrel. 17,
PROTEIN CO-FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 227 AA;
SEQUENCE FROM N.A.
STRAIN-C57 BLACK/6; TISSUE-KIDNEY;
Weinman E.J., Steplock D.A., Shenolikar S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
EMBL; U74079; AAB17569.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21145866; PubMed=11248100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 GKRVLVTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 GKRVLVTA 201
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                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25954 MW;
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Last sequence up
Last annotation
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Last annotation update)
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Pred. No. 17
0; Mismatches
                                                                                                                                                                     Craniata; Vertebrata; I Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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No.
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o. 17;
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o. 16;
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on update)
                            databases.
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                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Best Local S
Matches 8
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Best Local S
Matches 8
                                                                                                                                                                                                              Interpro; IPR001176; ACC_synthase.
Interpro; IPR001176; ACC_synthase.
Interpro; IPR00151; Aminotran_1.
Pfam; PF00155; Aminotran_1 1.
PRINTS; PR00753; ACCSYNTHASE.
Transferase; Aminotraneff
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O9X8S5;

O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE ASPARTATE AMINOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00595; PDZ; 2.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
SEQUENCE 355 AA; 38600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q12923; 3PDZ. "MGD; MGI:1349482; Slc9a3r1. InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2);
Murphy L., Harris D.;
Murphy L., Harris D.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    James K.D.
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-A3(2);
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                                               197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
7 VLVTAGAT 204
|||||||
9 VLVTAGAT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERLKKLGV 104
                                                                                          Similarity
8; Conser
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Similarity 100.0%;
8; Conservative
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(MAY-1999)
                                                                                       2.0%; S. llarity 100.0%; Conservative 0;
                                                                                                                                                                                                         Aminotransferase.
96 AA; 42785 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ţ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Barrell B.G., Rajandream M.A.; the EMBL/GenBank/DDBJ databases
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                                                                                            Score 8; DB
Pred. No. 30
0; Mismatches
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Pred. No.
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                                                                                                    DB .
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o. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                     genetic and physical map hromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eichner A.,
                                                                                                                                       2;
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                                                                                                                                       Length 396;
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                                                                                            Gaps
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    January 31, 2002, 13:37:35 ; Search time 130.99 Seconds (without alignments) 174.200 Million cell updates/sec
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156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
sp_phage:*
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sp_mhc:*
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sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_virus:*
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                                                                                                                  Q9CVR9
Q9PIM7
Q94671
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Q9UQN9
Q9XQQ5
Q9FLH6
P87708
O30218
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Q9N682
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                                                                                            Q9KEQ7
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                                                                                                                                                                                                                                                                                                                                                                       Q9FCY3
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                                                                                                                                                                                                                                                                                                                              O9njc8 mesobuthus
O9n682 mesobuthus
O9k6w1 bacillus ha
O9fcy3 yersinia en
O9uht7 homo sapien
                         Q9cvr9 mus musculu
Q9pin7 campylobact
O94671 schizosacch
O9keq7 bacillus ha
Q9flh6 arabidopsis
P87708 fowlpox vir
                                                                                                                                                                                                        Q9vii0 drosophila
Q9fmx7 arabidopsis
Q9ck17 pasteurella
Q26109 methanobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9uqn9 homo sapien
Q9xqq5 toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q26001 plasmodium
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	08637	086310	.086302	086306	086300	014861	Q997e5	Q9pbp2	P91000	Q9k797	051017	Q9bm32	Q9bm33	050845	Q57485	Q9vfh5	Q9v7c9	001349	Q9j599	Q9h0b0	Q9hch6	Q9vam3	Q9zw97	Q9pmt3	Q9hec3	Q9kkr7
	5	10 microcystis	_	_		51 homo sapien	7e5 human immun	2 xylella)O caenorhabdi)7 bacillus	l7 borrelia	32 themiste	3 themiste	15 borrelia				a	i99 fowlpox vir	homo	າ6 homo sapien	า3 drosophila	/97 arabidopsis	:3 campylobact	:3 neurospora	7 vibrio chol

ALIGNMENTS

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RESULT
Q26001
                                                   Q9UQN9
                                                                 RESULT
                                                                                                                                                                           Query Match 5...
Best Local Similarity 100
Matches 8; Conservative
Q9UQN9 PRELIMINARY; PRT;
Q9UQN9;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q26001;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                        InterPro; IPR002005; Rab_GDI_REP.
pfam; pF00996; GDI; 1.
prinvs; pR00891; RABGDIREP.
sEQUENCE 459 AA; 52311 MW; DEICCA47B124D8EA CRC64;
                                                                                                                                                                                                                                                                                                                       inhibitor.";
Mol. Biochem. Parasitol. 79:91-96(1996).
EMBL; X93166; CAA63653.1;
HSSP; P21856; IGND.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97001683; PubMed=8844675; Attal G., Langsley G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q26001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RABGDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RABGDI PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-3D7
                                                                                                                                                                                                                                                                                                                                                                                  *A Plasmodium falciparum homologue of a rab specific GDP dissociation
                                                                                                               212 LTLERIKL 219
                                                                                                                                  61 LTLERIKL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                       5.1%; >--
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (isolate 3D7).
Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                           Score 8; DB 5; Pred. No. 11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                   DB
11;
                                    34
                                    AA.
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                                                                                                                                                                                                          Length 459,
                                                                                                                                                                              0;
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A COMPLY

NCBI_TaxID=9606;

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

01-MAY-2000 (TIEMBLIEL 13, 01-MAY-2000 (TIEMBLIEL 13, LSFR3A PROTEIN (FRAGMENT). LSFR3A.

Last Last

sequence update)
annotation update)

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0,
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RESULT
Q9N682
ID Q9N682
OC DT O1
DT O1
DT O1
OC 
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Best Local S
Matches 7
                                             TOXICON 38:1653-1661(2000).
EMBL; AF114025; AAF34872.1; -.
EMBL; AF156169; AAF29462.1; -.
EMBL; AF156599; AAK06897.1; -.
InterPro; IPR003614; Knot1.
InterPro; IPR003614; Scorpion_tc
InterPro; IPR001219; ToXin.
Pfam; PF00537; toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUE-VENOM GLAND CYTOPLASM;
Zeng X.-C., Zhu S.-Y., Li W.-X., Jiang D.-H.;
Zeng X.-C., Zhu S.-Y., Li W.-X., Jiang D.-H.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9N682 PRELIMINARY; PRT; 84 AA.
O9N682;
O1-OCT 2000 (TrEMBLrel. 15, Created)
O1-OCT 2000 (TrEMBLrel. 15, Last sequence update)
O1-UCT 2000 (TrEMBLrel. 17, Last annotation update)
O1-JUN 2001 (TrEMBLrel. 17, Last annotation update)
NEUROTOXIN BMX11 PRECURSOR (TOXIN ALPHATXI4) (ALPHA-NEUROTOXIN TX14).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.

11]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1999) to the EMBL/Gen
EMBL; AF155363; AAF31477.1; -.
Interpro; IPR0033614; Knot1.
Interpro; IPR002361; Scorpion_toxin.
Interpro; IPR001219; Toxin.
Interpro; IPR001219; Toxin.
Pfam; PF00537; toxin_3; 1.
                                                                                                                                                                                                                                       MEDLINE-20317244; pubMed=10858508; Zhu S.Y., Li W.X., Zeng X.C., Liu H., Jiang "Nihe novel precursors of Buthus martensii shomologues.";
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=VENOM GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00284; TOXIN.
ProDom; PD000908; Scorpion_toxin;
SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=VENOM GLAND;
Zhu S., Li W.;
                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=VENOM GLAND;
Li W., Zhu S.;
Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhu S., Li W.;
"the full-length cDNA encoding a from BmK.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=34649;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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Similarity 100.0%
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĀΑ;
Scorpion_toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9319
                                                                                             Scorpion_toxin.
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Pred. No. 26
); Mismatches
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Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                putative mammalian neurotoxin
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26;
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                                                                                                                                                                                                                                                                 g D.H., Ma
scorpion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                        databases
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                                                                                                                                                                                                                                                                 Mao X.;
on alpha-toxin
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RESULT Q9X00X DD Q0 DD Q0 DD Q0 DD Q0 DD Q0 OC Q

NCBI_TaxID=5811;

Eukaryota; Alveolata;

Apicomplexa;

Coccidia; Eimeriida;

Sarcocystidae

Gutell R., Aiello D.P.,

Chloroplast

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Kissinger J.C., Donald R.G., Moulton A.L., Gutell R., ALELLO, Kissinger J.C., Donald R.G., Moulton A.L., Gutell R., ALELLO, Kissinger J.C., Donald R.G., Moulton A.L., Gutell R., ALELLO, Complete Sequence annotation of the 35-kb glastid genome of Toxoplasma gondii.",

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; U87145, AAD41142.1;

InterPro; IPR000473; Ribosomal_L36.

Pfam; PF00444; Ribosomal_L36; 1.

Ribosomal protein; Chloroplast.

Ribosomal protein; Chloroplast.

SECOURAGE 37 AA; 4546 MW; EDD8C59BEEB5E6AD CRC64;

В γQ

34 EAFVKGK 40 ||||||| | 26 EAFVKGK 32

Q9XQQ5 Q9XQQ5; 01-NOV-1999 01-NOV-1999 01-JUN-2001

PRELIMINARY;

PRT;

37

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01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17, RIBOSOMAL PROTEIN L36.

Created)
Last sequence update)
Last annotation update)

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y Match . Local Similarity hes 7; Conserv

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DB 4; 5. 12;

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EMBL; Y17 NON_TER NON_TER SEQUENCE

34 AA;

4023 MW;

1F90377C28FA152D CRC64;

SEQUENCE FROM N.A.

MEDLINE=9929247; PubMed=10369878;

Gilley J. Fried M.;

"Extensive gene order differences within regions between the Fugu and human genomes: implications volution and the cloning of disease genes.";

Hum. Mol. Genet. 8:1313-1320(1999).

EMBL; Y17458; CAB44351.1; -.

NON_TER 34 34

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conserved synteny

RESULT
Q9NJC8
ID Q9
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Q9NJC8 Q9NJC8; 01-OCT-2000 01-OCT-2000

(TrEMBLrel.

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sequence

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PRELIMINARY;

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76 MKIRSSL 82

MKIRSSL

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Query Ma Best Loc Matches

Match

1 4.5%; Similarity 100.0% 7; Conservative

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Score 7; DB 8; Pred. No. 13; 0; Mismatches

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RESULT
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Best Local S
Matches 7
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Q9FCY3;
Q9FCY3;
Q1-MAR-2001 (TremBlrel. 16, Cr
Q1-MAR-2001 (TremBlrel. 17, Lr
Q1-JUN-2001 (TremBlrel. 17, Lr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9K6W1;
Q9K6W1;
01-OCT-2000
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SEQUENCE
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SIGNAL
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MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
SEQUENCE FROM N.A. Glerczynski R., Jagielski M.; Submitted (JUL-2000) to the E EMBL; AY004311; AAF97354.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000). EMBL; AP001519; BAB07332.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Pfam; PF02561; Flis; 1.
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                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horikoshi K.;
                                                                                                   NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 LTLMLYN 108
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Similarity 100.0%
7; Conservative
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PROTEIN (FRAGMENT).

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Last annotation update
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                   EMBL/GenBank/DDBJ
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NEUROTOXIN BMK11.
C08EA4859A30B7B6
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., Kuhara S
                                                                                                                                           Enterobacteriaceae;
                     databases
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RESULT
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CG9337 PROTEIN.
CG9337.
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01-MAY-2000
01-MAY-2000
01-MAY-2000
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MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayn Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Ga George R.A., Lewis S.E., Richards S., Ashburner M., Hend Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000758; Enterovir_OMP.
PRINTS; PR00316; ENTEROVIROMP.
PROSITE; PS00694; ENT_VIR_OMP_1; 1
NON_TER 1 1
NON_TER 1 141
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                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional prediction of the coding sequences of 33 new by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF118076; AAF22020.1; -. SEQUENCE 175 AA; 20393 MW; 7F1365992AD04B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       He F.
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                                                                                                                         SEQUENCE FROM N.A. STRAIN-BERKELEY;
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Mammalia; Eutheria;
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                                                                                                                                            EQUENCE FROM
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141 AA;
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15593 MW;
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Primates;
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O9FMX7

O9FMX7

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OPFMX7

O1-MAR-2001 (TrEMBLrel. 16, Created)

O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)

O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)

O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)

GENOMIC DNA, CHROMOSOME 5, P1 CLONE: HXD15.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                             "Structural analysis of a sequence features of the physically assigned pl cl DNA Res. 4:401-414(1997).
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S., Kaneko T.,
                                                                                             of Arabidopsis the regions of Pl clones.";
Isochorismatase
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STRAIN-DELTA H;
STRAIN-DELTA H;
MEDLINE=98037514; PubMed=9371463;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M.,
Smith D.R., Doucette-Stamm L.A., DeLoughery C., Gilbert
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Oli
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prab
Jiwani N., Caruso A., Bush D., Safer H.
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Q9CKL7;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
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O26109;
O1-JAN-1998 (TREMBLrel.
O1-JAN-1998 (TREMBLrel.
O1-JUN-2001 (TREMBLREL.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
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                                                                                                                                                                                                                                               NCBI_TaxID=145262;
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EMBL; AE006197; AAK03679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella multocida.
Bacteria; Proteobacteria;
Pasteurella.
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R., Gilbert K.,
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimhl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9CVR9 PRELIMINARY;
Q9CVR9;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Methar deltaH: functional analysis and com J. Bacteriol. 179:7135-7155(1997). EMBL; AE000795; AAB84510.1; -... InterPro; IPR003750; DUF171. pfam; PF02598; DUF171; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            InterPro; IPR001394; UCH-2.
Pfam; PF00443; UCH-2; 1.
PROSITE; PS00973; UCH_2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
EMBL; AK006800; BAB24746.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1700055M05RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                PROSITE; PS00973; UCH_2_2; 1. PROSITE; PS50235; UCH_2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1921520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1700055M05RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Functional annotation of a full-length mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 KEILIEP 155
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34 EAFVKGK 40
                                                                                       Similarity 7; Conserv
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ilarity 100.0%;
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                                                                                                                                                                                                                                          34632 MW;
                                                                                                                                                   4.5%;
                                                                                       Score 7; DB 1; Pred. No. 80; 0; Mismatches
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                                                                                                                                                                                                                                          343E53F1A9B5F482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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o. 80;
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5. 72;
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                                                                                                                                            Length 305;
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                                                                                          Indels
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20 STRAIN-NCTC 11168;

20 STRAIN-NCTC 11168;

21 STRAIN-NCTC 11168;

22 STRAIN-NCTC 11168;

23 Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

24 Parkhill J., Wren B.W., Mungall K., Feltwell T., Holroyd S.,

25 Basham D., Chillingworth T., Davles R.M., Feltwell T., Holroyd S.,

26 Basham D., Chillingworth T., Davles R.M., Feltwell T., Pann C.W.,

27 Augels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

28 Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,

29 Auhitehead S., Barrell B.G.;

20 Whitehead S., Barrell B.G.;

21 Treveals hypervariable sequences.";

22 Repal; Ali39074; CAB7236.1;

23 Repal; L.139074; CAB7236.1;

24 RinterPro; IPR001107; Band_7.

26 RinterPro; IPR001107; Band_7.

27 RinterPro; IPR001107; Band_7.

28 PRINTS; PR00679; PROHIBITIN.

29 SART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O94671 PRELIMINARY; PRT; 376 AA.
O94671;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE HOMOSERINE DEHYDROGENASE (EC 1.1.1.3) (HDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9PIM7:
01-OCT-2000 (TrEMBLrel. 15, Cre
01-OCT-2000 (TrEMBLrel. 15, Las
01-JUN-2001 (TrEMBLrel. 17, Las
PUTATIVE TRANSMEMBRANE PROTEIN.
                                                                                                                                             Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases -i- CATALYTIC ACTIVITY: L-HOMOSERINE + NAD(P)(+) = L-ASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPBC776.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PIM7
                                                                                                                                                                                                                                                                  STRAIN-972
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota;
Schizosaccharomycetales; Schi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome
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NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campylobacter jejuni.
Bacteria; Proteobacte
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                                                                                                                                                                                                    Wambutt R.;
                                                                                                                                                                                                                                   yne M., Rajandream M.A., Barrell B.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 NEPVELR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                        CATALYTIC ACTIVITY: L-HOMOSERINE + NAD(P)(+) = L-ASPARTATE BETI SEMIALDEHYDE + NAD(P)H.

SEMIALDEHYDE + NAD(P)H.

PATHWAY: THIRD STEP IN CONVERSION OF L-ASPARTATE TO HOMOSERINE. HOMOSERINE PARTICIPATES IN THE BIOSYNTHESIS OF THREONINE AND THE SISOLEUCINE AND IN THE BIOSYNTHESIS OF METHIONINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; epsilon subdivision; Campylobacter group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%; L
100.0%; Pr
0;
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Pred. No. 93;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomycetes;
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Barbert Table

발 타

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CC -1- SIMILARITY: TO OTHER SPECIES HOMOSERINE DEHYDROGENASE.

DR EMBL; AL035263; CAA22876.1; -
DR Interpro; IFR001342; Homoserine_dh.

DR Pfam; PF00742; Homoserine_dh.

DR PROSITE; PS01042; Homoserine_dh.;

DR PROSITE; PS01042; Homoserine_dh.;

EM Oxidoreductase; NADP; Threonine biosynthesis; Isoleucine biosynthesis;

KW Methionine biosynthesis.

PT NP_BIND

SQ SEQUENCE 376 AA; 40037 MW; 3A2BC3A2CBA9263C CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 96;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps. 0;

QY 45 EKEGKVV 51

Db 287 EKEGKVV 293

Search completed: January 31, 2002, 13:37:37

Job time: 162 sec
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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
  33109877777
                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
627.5
459.5
459.5
429.5
424.5
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seq length: 2000000000
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Match
 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_39:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-957-709-19
1998
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                             Length
 В
         DEP_MYCTU
DEP_ECOLI
DEP_STRMU
DEP_STRMU
HLJB_ARATH
HLJB_ARATH
YII3_YEAST
EPID_STAEP
SIS2_YEAST
EPID_STAEP
SIS2_YEAST
YKIB_YEAST
YKIB_YEAST
YKIB_YEAST
YKIB_YEAST
YKIB_YEAST
YKIB_YEAST
YKIB_YEAST
YEAST
CESM_HOMAN
Y730_METUMAN
Y730_METUMAN
Y730_METUMAN
Y730_METUMAN
Y730_METUMAN
Y730_METUMAN
HS60_CACET
CLPC_CYACA
EFGL_THEMA
HS60_SCHPO
NIFD_CLOPA
PRIA_BACSU
CLPB_HELPJU
MYS3_DICDI
CPSM_RANCA
Y373_HUMAN
ACKA_CLOTS
CH60_DROME
                                                                                                                                                                                                                                                                            DFP_BORBU
DFP_HAEIN
DFP_SYNY3
 PRE_BACSP
                                                                                                                                                                                                                                                                                                          DFP_METJA
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                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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RX Fraser C.M., Casjens S., Huang W.A., Sutton G.G., Clayton R.A.,

RA Fraser C.M., Casjens S., Huang M.A., Dodson R., Hickey E.K., Gwinn M.,

RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

RA Peterson J., Kerlavage A.R., Ouackenbush J., Salzberg S., Hanson M.,

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RA Peterson J., Kerlavage A.R., Ouackenbush J., Salzberg S., Hanson M.,

RA Peterson J., Watthey L., McDonald L., Artiach P., Bowman C.,

RA Van Vugt R., Watthey L., McDonald L., Artiach P., Bowman C.,

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RT Genomic Sequence of a Lyme disease spirochaete, Borrelia

RT Genomic Sequence of a Lyme disease spirochaete, Borrelia

RT Wature 390:580-586(1997)

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051752;
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15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed=7542800;

MEDLINE-95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFP_HAEIN STANDARD; PRT; 400 AA.
p44953;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA/PANTOPHENATE METABOLISM FLAVOPROTEIN HOMOLOG
DFP OR H10953.
                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
Bacteria; proteobacteria; gamma
Haemophilus.
NCBI_TaxID=727;
            EMBL; U32776; AAC22614.1; TIGR; HI0953; -.
                                                                                                                                                                                                             Science 269:496-512(1995).
-I- FUNCTION: FLAVOPROTEIN AFFECTING SYNTHESIS OF DNA AND PANTOTHENATE METABOLISM (BY SIMILARITY).
                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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MBL outstation -
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Best Local
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K.,

Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,

Yamada M., Yasuda M., Tabata S.;

Yamada M., Yasuda M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFP_SYNY3
P73881;
                          entities
or send a
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1097 (Rel. 40, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.
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137; Conserv
                                an
                          requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Pred. No. 1.9e
84; Mismatches
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P71661;
01-NOV-1997
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMO
DFP OR RV1391 OR MT1436 OR MTCY21B4.08.
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Pfam; PF02441; Flavoprotein; 1.
Flavoprotein; Complete proteome.
SEQUENCE 402 AA; 43419 MW; 7E3
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., E
Peterson J., DeBoy R., Dodson
                                                                                                                                        Sulston J.E., Taylor K., Whi "Deciphering the biology of complete genome sequence."; Nature 393:537-544(1998).
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Pred. No. 3
                                  Eisen
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  n J.A.,
Gwinn №
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        M.L.,
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        Carpenter
M.L., Haft
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O.,
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RESULT 6

DFP_ECOLI STANDARD; PRT; 406

AC P24285; P76718;

DT 01-MAR-1992 (Rel. 21, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence updat

DT 20-AUG-2001 (Rel. 40, Last annotation upd

DE DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN.

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EMBL; AE007015; AAK45701.1; -.
TIGR; MT1436; -.
TubercuList; Rv1391; -.
Tubercyro; IPR003382; Flavoprotein.
InterPro; IPR003382; Flavoprotein; 1.
Pfam; PF02441; Flavoprotein; 1.
Flavoprotein; Complete proteome.
SEQUENCE 418 AA; 43577 MW; 48BDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FLAVOPROTEIN AFFECTING SYNTHESIS OF DNA AND PANTOTHENATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., S
Delcher A., Utterback T., Weidman J., Khouri H., Gill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                               VTLI--RTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPR-----IEEGRAKVASIDEI-- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRIPKQVIVGVSGGIAA--YKACT-VVRQLTEASHRVRVIPTESALRFVGAATFEALSGE 61
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                                                                                                                                                                                                                                                                                                                             ARAKLRRKGCDLLVVNAVGEGRAFEVDSNDGWLLASDGTESALQHGSKTLMASRIVDAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVCTDVFADVPAVPHVHLG----QQADLVVVAPATADLLARAAAGRADDLLTATLLTA-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTLTAGHTAGLVDPAGVEVV--HVSSAQQLADAVSK--HAPTADVLVMAAAVADFRPAQV
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Query Match 21.2%;
Best Local Similarity 33.4%;
Matches 138; Conservative 7
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EMBL; AE000441; AAC76663.1; ALT_INIT.
EMBL; V01578; ; NOT_ANNOTATED_CDS.
ECOGene; EC10004; dfp.
InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Flavoprotein; Complete proteome.
SEQUENCE 406 AA; 43438 MW; CBD11B9347E8C6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-K12 / MG1655;
MEDLINE-93315143; PubMed-7686882;
MEDLINE-93315143; PubMedt G. III, Daniels D.L., Blattner F.R.;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84057777; PubMed=6139280;
Lundberg L.G., Thoresson H.O., Karlstroem O.H.,
"Nucleotide sequence of the structural gene for
Escherichia coli K-12.";
ESCHERICHI 867-971(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                  RKNLDLICANDVSQPTQGFNSDNNALHLFWQDGDKVLPLERKELLGQLLLDEI
                                                                                                                                                IK----SGRSITIELVPXNPKI---IDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIE-
                                                                                                                                                                                                                                                                                                                                                VDMAVAHFSPVNDLKHLNIMITAGPTREPLDPVRYISNHSSGKMGFAIAAAAARRGANVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGP------RIEEGRAKVASIDEIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EI----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHI 129
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                                                      RAKADLYVGNTL----EAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEI
                                                                                                             IKKQATQGDELTIKMV-KNPDIVAGVAALKDHRP--YVVGFAAETNN---VEEYARQKRI
                                                                                                                                                                                                                               LVSGPVSLPTPPFVK-RVDVMTALEMEAAVNASVQQQ--NIFIGCAAVADYRAATVAPEK
                                                                                                                                                                                                                                                                                         LIRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVAVLPAMNQQMYRAAATQHNLEVLASRGLLIWGPDSGSQACGDIGPGR-----MLDPLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLDPAAEAAMGHIELG----KWADLVILAPATADLIARVAAGMANDLVST-ICLATP-A 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 424.5; DB 1;
; Pred. No. 2.7e-19;
71; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF DNA AND PANTOTHENATE
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Best Local Similarity
Matches 55; Conserv
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HALJB OR AT1648610 OR T1N15.24.

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Streptophyta;
                                                 HL3B_ARATH STANDARD; PRT; 201 AA P94063; 091P62; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat HALOTOLERANCE PROTEIN HAL3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
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"Insertional mutagenessis and recovery of interrupted genes of Streptococcus mutans by using transposon Tn917: preliminary characterization of mutants displaying acid sensitivity and
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Q54433;
Q1-NOV-1997 (Rel.
                                                                                                                                                ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nutritional requirements.";
J. Bacteriol. 178:4166-4175(1996).
-!- FUNCTION: FLAVOPROTEIN AFFECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flavoprotein.
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                                                                                                                                                                                                                                        131 IMIAPAMHETMYRHPIVRENIERLKKLG 158
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                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                    76 I----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIP 130
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                                                                                                                                                                                                          KFFAPAMNTKMYENPITQSNITLLKKFG
                                                                                                                                                                                                                                                                                                                                                    KKIVXXXPGSIAALDVKACE---GLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITE
                                                                                                                                                                                                                                                                                                                                    KKILLAVSGSIAA--YKAADLSHQLTKLGYHVNVFMTNAAKQFIPPLTLQVLSKNPVYSN
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145
145 AA;
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35, Last sequence update)
35, Last annotation updat
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15819
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                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                           Score 199; DB 1; L
Pred. No. 5.1e-06;
Mismatches 57;
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                                                                 update)
      Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 145;
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RX MEDLING-2016719; Pubmed-11130712;

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Dubler E., Chan A., Chao Q., Chen H., Cheuk R.F., Crin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Hunter J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Liee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis

RT Tallainan",

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a
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Pfam; PF02441; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC020889; AAF79709.1; ALT_INIT Mendel; 12633; Arath;1833;12633.
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:816-820(2000).
-i- FUNCTION: INVOLVED IN PLANT GROWTH AND SALT AND OSMOTIC TOLERANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Espinosa-Ruiz A., Belles J.M., Serrano R., Cu
"Arabidopsis thaliana AtHAL3: a flavoprotein
osmotic tolerance and plant growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. COLUMBIA;
MEDLINE=20117504; PubMed=10652125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                          Flavoprotein; FMN.
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64 YTDEDEWSSWN-KIGDPVL----
                                          62
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TISSUE SPECIFICITY: EXPRESSED IN ROOTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAY CATALYZE THE ALPHA, BETA-DEHYDROGENATION OF A CELLULAR PARTNER (BY SIMILARITY). COPACTOR: FMN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKL088W.
                                                                                  TVTRK----PRILLAASGSVASIKFSNLCHCFSEWAEVKAVASKSSLNFVDKPSLPQNVTL
                                        -----YAWNLPTGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGID
                                                                                                                                                                                                                                                                                                                                                                                                                 U80192; AAB53106.1;
                                                                                                                                                                          l Similarity
46; Conserv
                                                                                                                                                                                                                                                                                                                                              IPR003382; Flavoprotein.
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                                                                                                                                                                                                                                                                                 201 AA;
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                 22415 MW;
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                                                                                                                                                                        Score 162; DB 1;
Pred. No. 0.0014;
3; Mismatches 5
                                                                                                                                                                                                                                                                                 7962655E408FA64C CRC64;
HIEL ---- RRWADVMIIAPLSANTLAKIAGGLC 110
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                                                                                                                                                                                                                Length 201;
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                                                                                                                                                                        Gaps
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DTPVTTVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGP

164

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RESULT
HL3A_ARATH
ID HL3A_ARATH
AC Q9SWE5;
20-AUG-200
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**WEDLINE=20444410; PubMed=10986463;

**X MEDLINE=20444410; PubMed=10986463;

**X A Albert A., Martinez Fipoll M., Espinosa-Ruiz A., Yenush L.,

**A Culianez-Macia F. A., Serrano R.;

**The X-ray structure of the FN.-binding protein AtHal3 provides the structural basis for the activity of a regulatory subunit involved in signal transduction.";

**Structural Dasis for the activity of a regulatory subunit involved in signal transduction.";

**Structural Dasis for the activity of a regulatory subunit involved in signal transduction.";

**Structural Dasis for the activity of a regulatory subunit involved in structure 8:961-969(2000).

**Corection: Involved In PLANT GROWTH AND SALT AND OSMOTIC TOLERANCE.**

**C HANG CATALYZE THE ALPHA, BETA-DEHYDROGENATION OF A PEPTIDYL CYSTEINE C. I. COPACTOR: FMN.

**C I. SUBUNIT: HOMOTRIMER.**

**C I. SUBUNIT: HOMOT
EMBL; AF166262; AAD51616.1; -.
EMBL; AB026641; BAB01331.1; -.
PDB; 1E20; 11-SEP-00.
InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Pfampprotein; FMN; 3D-structure.
SEQUENCE 209 AA; 23355 MW; 3AB1B
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HALOTOLERANCE PROTEIN HALJA.
HALJA OR ATGS1803 OR MEGIA 2.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety
TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20117504; PubMed-10652125;
Espinosa-Ruiz A., Belles J.M., Serrano R., Culianez-Macia F.A.;
"Arabidopsis thaliana AtHAL3: a flavoprotein related to salt and
osmotic tolerance and plant growth.";
Plant J. 20:529-539(1999).
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Res. 7:217-221(2000).
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                                 3AB1BB364F8E40DE CRC64;
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В δÃ В Qy

62

EFIDLQYSLKRNKIVLITSGGTTVPLENNTVRFIDNFSAGTRGASSAEQFLANGYSVIFL 121

VIKKLHKKTLEGKRVLVTAGATREYID--PIRFITNASSGKMGVALAEEADFRG-AVTLI 239

PHIPIMIAPAMHE--TMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIV--YR 182

PPLPVLNRPQIHTSVTEISHAIDRTIKEELFPVAYTTEEEQYFKTNPKPAYIDELIKDAK

183

Matches Query Match Best Local

l Similarity 77; Conser

7.5%; ilarity 23.2%; Conservative 5

; Score 150.5; DE; pred. No. 0.015; 50; Mismatches 1

120; DB 1;

Indels Length

85;

Gaps

14;

61

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YII3_YEAST
ID YII3_YEAST
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  р40506;
01-FEB-1995 (Rel. 31
01-FEB-1995 (Rel. 32
01-OCT-1996 (Rel. 3.
                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             STRAIN=S28BC / AB972;
Barrell B.G., Badcock K., Bankler A.T., Bowman S., Brown D., Barrell B.G., Badcock K., Bosell T., Dear S., Devlin K., Fraser Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.;
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID-4932;

[1]
Hypothetical protein.
SEQUENCE 365 AA; 41893 MW; D67655A7A3DDDDAB CRC64;
                               EMBL; Z46728; CAA86711.1; -. SGD; S0001345; YIL083C.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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les 52; Conserv
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31, Last sequence update)
34, Last annotation update)
KDA PROTEIN IN SDS3-THS1 INTERGENIC
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RESULT 11
EPID_STAEP
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AC P30197;
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Query Match
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Matches 51; Conserv
                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                  Goetz F., Entian K.-D.;
"Analysis of genes involved in the epidermin.";
                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
STRAIN=TU 3298 / DSM 3095;
MEDLINE=92355511; PubMed=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-TU 3298 / DSM 3095;
MEDLINE-92155237; PubMed=1740156,
Schnell N., Engelke G., Augustin
                                                              Oxidoreductase; Flavoprotein; FMN; Plasmid.
MUTAGEN 93 93 G->D: LOSS OF FMN I
SEQUENCE 181 AA; 20825 MW; 126830E0B987CE2C
                                                                                                InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
                                                                                                                                         EMBL;
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                                                                                                                             PIR; S23418; S23418
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NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
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15-JUL-1999
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                                                                                                                                           X62386; CAA44255.1;
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3 (Rel. 25, Last :
9 (Rel. 38, Last :
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                          PubMed=1644762;
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             7.5%;
30.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
Score 149.5; DB 1;
Pred. No. 0.0072;
1; Mismatches 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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                      DB 1;
                                                                            BINDING
                                                                CRC64;
                        Length 181;
 Indels
 19;
 Gaps
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RESULT 12
SIS2_CANTR
ID SIS2_C
AC Q12600
DT 01-NOV
DT 01-NOV
DT 02-AUG
DE SIS2 0
OS Candid
OC EUKARY
OC Saccha
OX NCBL_T
RN [1]
RP SEQUEN
RX MEDLIN
CC -!-SI
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                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X88900; CAA61362.1; -.
InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tropicalis with long acidic Yeast 12:1321-1329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez P.L., Ali R., Serrano R.; "CtCdc55p and CtHal3p: two putative regulatory proteins from Candida tropicalis with long acidic domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; 
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida tropicalis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIS2 PROTEIN (HALOTOLERANCE SIS2 OR HAL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q12600;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIS2_CANTR
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5482;
404
                                               142 YRHPIVREN---
                                                                                                 348
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                                                                                                                            82 HVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPIMIAPAMHETM 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAY STIMULATE EXPRESSION OF CERTAIN GENES THAT A PERIODICALLY EXPRESSED DURING LATE G1. ALSO MODULATES THE EXPRESSION OF THE ENAI ATPASE (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR OR CYTOPLASMIC (BY SIMILARITY SIMILARITY: TO YEAST SIS2/HAL3 AND TO YEAST YKLO88W. SOME, A.THALIANA HAL3A AND HAL3B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPATANTISKIACGIDDTPVTTVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLG
  YSSSTTKRQLRLIADDMPWIEVLKPLEKVF-GSYGDIGMGGMTDWNEIVNRIVMKL
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                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                  531 AA;
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246
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                 -RRWADILLVCPLTANTLAKISLGICDNLLTNVIRAWNSSYPILLAPAMDSHS
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                          484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ascomycota; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35, Created)
                                                                                                                                                                                                                                                                                                                                                          240
249
513
                                                                                                                                                                                                                        7.3%;
                                                                                                                                                                                                                                                                                                                                  58171 MW;
                                               IERLKKLGVEFIGPRIEEGRAKVASIDEIVYRVIKKL
                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                        Score 145.5; DB 1; Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (HIGHLY ACIDIC).
D5FF196B8B957B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          POLY-THR
                                                                                                                                                                                                                                                                                                                                                                                  POLY-THR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ere are no rest
as its content
                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
88W. SOME, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                   531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                                                                                                                                                                   15;
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                                               187
  458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
                                                                                                                                                                                                 Gaps
                                                                                                 403
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RESULT

13

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ID SIS2 YEARY
AC P36024
AC
                                                                                                                QΥ
                                                                   B
                                                                                                                                                                               Query Match 7.3%;
Best Local Similarity 29.2%;
Matches 40; Conservative
                                                                                                                                                                                                                                                      or send an emainer.

or send an emainer.

EMBL; U01878; AAA80000.1; -.

EMBL; U01878; AAA80000.1; -.

EMBL; Z28297; CAA82151.1; -.

PIR; S38149; S38149.

SGD; S0001780; SIS2.

InterPro; IPR003382; Flavoprotein.

Pfam; PF02441; Flavoprotein; 1. Nuclear protein.

Pfam; PF02441; Flavoprotein; 1. Nuclear protein.

ASP/GLU-RICH (HIGHLY ACIDIC).

ASP/GLU-RICH (HIGHLY ACIDIC).

A96 553

ASP/GLU-RICH (HIGHLY ACIDIC).

A97 57 MW; 19A9A475145DA7AB CRC64;
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P36024;
01-JUN-1994
01-JUN-1994
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-NOV-1994 (Rel. 29, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).
SIS2 OR HAL3 OR YKRO72C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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MEDLINE-96009574; PubMed=7565698;
Ferrando A., Kron S.J., Rios G., Fin
Fegulation of cation transport in S:
salt tolerance gene HALJ.";
MOL Cell Biol 15:5470-5481(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION AS INHIBITORY SUBUNIT OF PPZ1.

IDENTIFICATION AS INHIBITORY SUBUNIT OF PPZ1.

MEDILINE-98301578; pubMed-9636153;

de Nadal E., Colotet J., Posas F., Serrano R., Gomez N., Arino J.;

"The yeast halotolerance determinant Hallp is an inhibitory subunit of the prain Ser/The protein phosphatase.";

Proc. Natl. Acad. Sci. U.S.A. 95:7357-7362(1988).

1- FUNCTION: MAY STIMULATE EXPESSION OF CERTAIN GENES THAT ARE PERIODICALLY EXPRESSED DURING LATE G1. ALSO MODULATES THE EXPRESSION OF THE ENAI ATPASE. INTERACTS WITH THE C-TERMINAL DOMAIN OF THE SERINE-HIREDNINE PROTEIN PHOSPHATASE PPZ1 AND ACTS AS AN INHIBITORY SUBUNIT OF PPZ1.

1- SUBCELLULAR LOCATION: NUCLEAR OR CYTOPLASMIC.

1- SIMILARITY: TOC. TROPICALIS SISZ/HALJ AND TO YEAST YKL088W. SOME,

TO A. THALLIANA HALJA AND HALJB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-95220693; PubMed-7705654;

di Como C.J., Bose R., Arndt K.T.;

"Overexpression of SIS2, which contains an increases the expression of SWI4, CLN1 and genetics 139:95-107(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                           29;
                                                                                                                                                                                       Score 145; DI
Pred. No. 0.0:
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fink G.R., Serrano R.;
in Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 AA
                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                               Length 562;
                                                                                                                                                                                              Indels
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                                                                                                                                                                                              Gaps
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RESULT 15
CPSM_HUMAN S
ID CPSM_HUMAN S
AC p31327; O43774;
DT 01-JUL-1993 (Rel
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YKI8_YEAST
                                                                                                       γ
                                                                                                                                Вp
                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 47
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P36076;
01-JUN-1994 ()
01-JUN-1994 ()
20-AUG-2001 ()
HYPOTHETICAL ()
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 228088; CAA81926.1; -.
PIR; S37913; S37913.
SGD; S0001571; YKL088W.
InterPro; IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKLO88W.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Hypothetical,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 RAWNPSYPILLAPSMVSSTFNSMMTKKQLQTIKE---EMSWVTVFKPSEKVMDINGDIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASI------
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                                                                                                                                 467
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                                                                                                                                                                          QVLKPVEKVLICGD----IGMGGMREWTDIVEIVRRRINEIRKARDEETGDKEQEQEEQEG
                                                                                                                                                         RVIKKLHKKTLEGKRVLVTAGATREYIDPIRF-----ITNASSGKMGVALAEEADFRG
                                                                                                                                                                                           VTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIVY 181
                                                                                                          235
                                                                                                                                                                                                                                                                             ch 6.9%; l Similarity 26.0%; 47; Conservative 3
                                                                                     524
                                                                                                                                                                                                                                                                                                                                     al protein.
508 570 ASP/GLU-RICH (HIGHLY ACIDIC).
571 AA; 65238 MW; 9C674C2394EFCEAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
L 65.2 KDA PROTEIN IN MIF2-CYT2 INTERGENIC REGION
  (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                         STANDARD;
                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                             Score 138.5; DB 1;
Pred. No. 0.14;
2; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                          1500
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                                                                                                                                                                                                                                                                                Gaps
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S

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InterPro;
InterPro;
                           PRINTS; PRO0098; CPSASE.
PRINTS; PRO0099; CPSGATASE.
PROSITE; PS00866; CPSASE_1; 2.
PROSITE; PS00867; CPSASE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90282;
EMBL; Y15793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and sequence of a cDNA e synthetase I: molecular analysis Gene 107:335-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CARBAMOYL-PHOSPHATE SYNTHASE [AMMONIA], MITOCHONDRIAL PRECURSOR
(EC 6.3.4.16) (CARBAMOYL-PHOSPHATE SYNTHETASE I) (CPSASE I).
                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JQ1348; JQ1348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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Homo sapiens (Human)
Ligase; Repeat; Transit peptide; Mitochondrion; ATP-binding;
                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Prenatal diagnosis of carbamoyl phosphate synthetase identification of a missense mutation in CPS1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finckh U., Kohlschuetter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98375696; PubMed=9711878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., VARIANT CPS1 DEF. MET-544, AND VARIANT ALA-344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92084128; PubMed=1840546;
Haraguchi Y., Uchino T., Takiguch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuda I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: PRIMARILY IN THE LIVER AND SMALL INTESTINE.
DISEASE: DEFECTS IN CPS1 ARE THE CAUSE OF AN AUTOSOMAL RECESSIVE
METABOLIC DISORDER THAT, CAUSE A TYPE OF HYPERAMMONEMIA. CLINICAL
SYMPTOMS ARE VOMITING:IN'INFANCY, PROTEIN INTOLERANCE.
INTERMITTENT ATAXIA, SEIZURES, LETHARGY, AND MENTAL RETARDATION.
SIMILARITY: TO OTHER CARBANOYL-PHOSPHATE SYMPHETASES. ALSO
COMTAINS A GLUTAMNINE ANLODTRANSFERASE-LIKE DOMAIN BUT THE CYSTEINE
RESIDUE WHICH IS ESSENTIAL FOR AMIDO TRANSFERASE ACTIVITY, IS
MISSING IN THIS PROTEIN SO THIS DOMAIN IS NO LONGER ACTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: 2 ATP + NH(3) + CO(2) + H(2)O = ORTHOPHOSPHATE + CARBAMOYL PHOSPHATE.
ENZYME REGULATION: REQUIRES N-ACETYLGLUTAMATE AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            natal diagnosis or carrier in CPS1.";
Itlfication of a missense mutation in CPS1.";
Mutat. 12:206-211(1998).
FUNCTION: INVOLVED IN THE UREA CYCLE OF UREOTELIC ANIMALS WHERE
FUNCTION: DIAYS AN IMPORTANT ROLE IN REMOVING EXCESS AMMONIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                     PS; M38.971; -. 237300; -.
                                                                                                                                PF00988; CPSase_sm_chain;
PF00117; GATase; 1. •
PF02142; MGS; 1.
                                                                                                                                                                                    PF00289; CPSase_L_chain; 2. PF00988; CPSase_sm_chain; 1.
                                                                                                                                                                                                                                  IPRO01317; CPS_GATase.
IPRO00901; CPSase.
IPRO02474; CPSase_sm_chain.
IPRO0091; GATase_1.
IPR00091; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAA14328.1;
CAA75785.1;
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Primates;
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SIMATED
                                                VLVTA-----GATREYIDPIRFITNASSGKMGVALAEEADFRGAVTLIRTKGSVKAFR
                                                                                                                                                                                                                                                                                          ATKSRKLVGKKIVXXXPGSIAALDV----KACEGLIRHGAEVHAVMSEAATKIIHPYAWN
                  AFGSEENQVVLIGRDFTKELPKMKKRELAERI
                                    -TVYFLPITPQFVTEVIKAEQPDGLILGMGGQTALNCGVELFKRGVLKEYGVKVLGTSVE
                                                                                                IRKIKLKVETVEEML-----SAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKSGRS
                                                                                                                  TTITSVLPKPALVASRVEVSKVLIL---GSGGLSIGQAGEFDYSGS-
                                                                                                                                                         MHES---KPF----FAVQF-HPEVTPGPIDTEYLFDSFFSLIKK-----
                                                                                                                                                                           MHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIVYRVIKKLHKKTLEGKR 196
                                                                                                                                                                                                GAKTYKMSMANRGQNQPVLNITNKQAFITAQNHGYALDNTLPAGWKPLFVNVNDQTNEGI 364
                                                                                                                                                                                                                                       HDFTKMEYDGILIAGGPGNPALAE - - PLIQNVRKILESDRKEPLFGI - - STGNLITGLAA . 304
                                                                                                                                                                                                                                                                             STKDVKVYGK----GNPTKVVAVDCGIKNNVIRLLVKRGAEVHLV
                                                                             MKEENVKTVLMNPNIASVQTNEVGLKQAD
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                                                                                                                                                                                                                                                                                                                              6.7%;
20.6%;
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ROLFSDKLNEINEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disease mutation.
                                                                                                                                                                                                                                                                                                                                                              A -> T (IN REF. 1).
E -> G (IN REF. 1).
EH -> AT (IN REF. 1).
EH -> EN (IN REF. 1).
GD -> EN (IN REF. 1).
F -> S (IN REF. 1).
F -> S (IN REF. 1).
M -> L (IN REF. 1).
A -> V (IN REF. 1).
7 -> N (IN REF. 1).
19 MW; E53A22D7756396:
                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> S (IN REF. 1
R -> Q (IN REF. 1
G -> C (IN REF. 1
RLSRS -> KMSPN ()
                                                                                                                                                                                                                                                                                                                             Score 134;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (1)
ATP (2)
ATP (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_006834.
T -> M (IN CPS1 D
/FTId=VAR_006835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLUTAMINE AMIDOTRANSFERASE-LIKE CARBAMOYL-PHOSPHATE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITOCHONDRION (BY SIMILARITY). CARBAMOYL-PHOSPHATE SYNTHASE [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMOLOG
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                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                   -TAFPH-----IPIMIAP----
                                                                                                                                                                                                                                                                                                                                                                     E53A22D77563961D CRC64;
 56
                  394
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                                                                                                                                                                                                                                                                                                                    134;
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                                                                                                                  ----QAVKA--
                                                                                                                                                                                                                                                                                                                   162;
                                                                                                                                                                                                                                                                             ---- PWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [AMMONIA].
                                                                                                                                                         -GKA
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                                                                                                                                                         403
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protein search, using sw model protein

January 31, 2002, 13:07:53 Run on:

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US-08-957-709-19 1998

Title: Perfect score: Sequence:

MLHHVKLIYATKSRKLVGKK............KMKKRELAERIWDEIEKXLS 403

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

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summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

PIR_68:* •• Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

probable DNA/panto flavoprotein dfp {
DNA/pantothenate m
DNA/pantothenate m
pantothenate metab
pantothenate metab dna/pantothenate m pantothenate metab pantothenate metab pantothenate metab pantothenate metab pantothenate metab pantothenate metab DNA /pantothenate flavoprotein [impo pantothenate metab thymidylate syntha DNA/pantothenate m pantothenate metab pantothenate metab pantothenate metab hypothetical prote Description B70371 A72498 F83963 A82351 A72223 D69878 A81058 D81819 G64104 H75501 S75082 A64414 C84215 C70201 G71018 B82982 DB Query Match Length 1667.5 1649.5 735 731 627.5 626 543.5 535.5 494.5 494.5 494.5 473.5 473.5 473.5 473.5 439 424.5 424.5 424.5 404.5 351 350 301 224.5 223 176.5 Score No.

241 299 588

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hypothetical prote	lantibiotic epider	hypothetical prote	hal3 protein - yea	SIS2 protein - yea	hypothetical prote	carbamoy1-phosphat	hypothetical prote	translation initia	chromosome assembl	probable membrane	conserved hypothet	hypothetical prote	carbamoy1-phosphat	carbamoy1-phosphat	conserved hypothet
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365	181	270	531	562	571	1500	186	594	1156	674	880	237	1500	557	316
7.5	7.5	7.5	7.3	7.3	6.9	6.8	9.9	9.9	6.5	6.5	6.4	6.3	6.3	6.1	0.9
150.5	149.5	149.5	145.5	145	138.5	136	132	132	130.5	129	127	126	126	121.5	120.5
30	31	32	33	34	32	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

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A;Reference number: A69250; MUID:98049343
A;Accession: D69455
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Redidues: 1-404 <KLES
A;Cross-references: GB:AE000989; GB:AE000782; NID:92689312; PIDN:AAB89597.1; PID:9264
C;Superfamily: pantothenate metabolism flavoprotein dfp
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                                                                                                                        RESULT 2

dn 7514

c; Species: Pyrococcus abyss1

c; Species: Pyrococcus abyss1

c; Species: Pyrococcus abyss1

c; Species: Pyrococcus abyss1

c; Accession: E7514

R; anonymous, Genooscope

submitted to the EMBL Data Library, July 1999

A; Description: Pyrococcus abyss1 genome sequence: insights into archaeal chromosome struce number: A75001

A; Reference number: A75001

A; Residues: preliminary

A; Residues: 1-401 < KAW>
A; Residues: 1-401 < KAW>
A; Residues: 1-401 < KAW>
A; Experimental source: strain Orsay

C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: pantothenate metabolism flavoprotein dfp
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Patcher at metabolism flavoprotein dfp homolog AF1645 - Archaeoglobus fulgidus
Patcherate names: probable aspartate 1-decarboxylase activase
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus
C;Species: Archa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 401;
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pantothenate metabolism flavoprotein dfp homolog MTH1216 - Methanobacterium thermoaut Nalternate names: probable aspartate 1-decarboxylase activase Nathanobacterium thermoautotrophicum c)species: Methanobacterium thext_change 29-Sep-1999 (S)Semith, D. R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Glu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Glbson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C., Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7133-7155, 1997 (MID:98037514 (MID:98037514 (MID:98037514 (MID:98028)) (MID:98037514 (MID:98028) (MID:98037514 (MID:98028) (MID:98
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C;Genetics:
                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 RVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AWNLPTGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVV 122
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Query Match 36.8%; Score 735; DB 2; Length 404; Best Local Similarity 45.0%; Pred. No. 2e-37; Matches 182; Conservative 74; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 36.6%; Score 731; DB 2; Length 386; Best Local Similarity 44.0%; Pred. No. 3.28.37; Matches 176; Conservative 62; Mismatches 122; Indels 3
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C;Superfamily: pantothenate metabolism flavoprotein dfp
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Thu Jan 31 13:32:15 2002

Db 239 EVITAMGLEPPYYIKNHKVLTAKEMLNKAIELAKDFDIIISSAAISDFTVE-SFE 292 Qy 296 GKIKSGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKA 353 :	C;pace 102-reb-2001 #sequence_revision 02-reb-2001 #text_change_10-reb-2001 C;pace 102-reb-2001 #sequence_revision 02-reb-2001 #text_change_10-reb-2001 C;Accession: C84215 *	. Он Н	Qy 134 APAMHETMYRHDIVRENIERIKKLGVEFIGPRIEEGRAKVASIDEIVYRVIKKLHKKTLE 193 D 121 VPAMHEDMYDHPGVRDAIDRYSSWGVSVVDPRIEEGRAKLPRESTIVHETARAAGEQPLA 180 Qy 194 GKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIRTKGSVKAFR 249 I	Qy 362 EAFGSEENQVVLIGRDFTKELPKMKKRELAERI 394
79 FIEHVELAGEHENKADLILUCPATANTISKIACGIDDTPUTTVYTTAF-PHIPIMIAPAM	DD 234AETAEEMAERVRELVADHDVFLSAAVADERP-VYTERKISSSEERSVELKP 284 QY 311 XNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADLVVGNTLEAFGS 366	C; Species: Methanococcus jannaschii. C; Date: 13-Sep-1996 #text_change 21-Jul-2000 C; Species: Methanococcus jannaschii. C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C; Accession: A6444 R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Riut, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Seon, D.J.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A; Reference number: A64300; MUID:96337999 A; Accession: A6444 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-403 kBUL> A; Cross-references: GB:U67535; GB:L77117; NID:92826348; PIDN:AAB98918.1; PID:91591587; C; Genetics:	CyberPation: REV84592-844581 C; Superfamily: pantothenate metabolism flavoprotein dfp C; Reywords: flavoprotein Query Match Best Local Similarity 39.6%; Pred. No. 6.2e-31; Matches 163; Conservative 82; Mismatches 138; Indels 29; Gaps 16; Qy 1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAALDV-KACEGLIRHGAEVHAVNSEAATKII 59 :: : : : : : : :	120 TVVTTAFPHIPMAPAMHETMYRHPIVRENIEELK-KIGVEFIGPRIEEGRAKVASIDE 1 1 1 1 1 1 1 1 1

13;

Gaps

Indels

Length 388;

81

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W/459 probable DNA/pantothenate metabolism flavoprotein APE1959 - Aeropyrum pernix (strain probable DNA/pantothenate metabolism flavoprotein APE1959 - Aeropyrum pernix (Species: Aeropyrum pernix (Species: Aeropyrum pernix (Species: Aeropyrum pernix A7499 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C. Accession: A72499 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C. Accession: A72499 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 A7499 #sequence of an aerobic pyper-thermophilic Crenarchaeon, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999 #sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A7469 A74450; MUD:99310339 A74619 A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 -LKVETVEEMLSAIENELRSKKY-DVVIMAAAVSDFRPKIKAEGKIKSGRSITIELVPXN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYRHPIVRENIERLKKLGVEFIGPRI-----EEGRAKVASIDEIVYRVIKKLHKKTLEG 194
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                                                                                                                                                                           27 GSIAALDVKACE---GLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITEITGFIE--
                                                                                                                                                                                                                                       GGIAS--YKVCELVRELKRKGHSVKTILTPFAEKFMSPLTFQTLSGNKAYTDKDWEEEPL
                       26.8%; Score 535.5; DB 2; 37.2%; Pred. No. 2.2e-25; ive 74; Mismatches 137;
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                       Query Match 26.8%
Best Local Similarity 37.2%
Matches 142; Conservative
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C; Accession: C70201
Siraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Gatland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
Nature 390, 580-586, 1997
A.Authors: Smith, H.O.; Venter, J.C.
A.Accession: C70201
A.Reference number: A70100; MUID:98065943
A.Accession: C70201
A.Residuer: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-390 cKLE>
A.Residues: 1-390 cKLE>
A.Residues: 1-390 cKLE>
A.Cross-references: GB:AR001179; GB:AR000783; NID:92688738; PIDN:AAC67145.1; PID:9268873
C; Superimental source: strain B31
C; Superimental source: strain B31
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N.Alternate names: probable aspartate 1-decarboxylase activase
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 29-Sep-1999
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; OV
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70301; MUD:9819666
A;Reference number: A70301
A;Molecule type: DNA
A;Residues: 1-388 <AQF>
A;Cross-references: GB:AEO00708; NID:92983356; PIDN:AAC06944.1; PID:92983357; GB:AE00065
A;Experimental source: strain VF5
G;Genetics:
A;Gene dfp
C;Superfamily: pantothenate metabolism flavoprotein dfp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GF----IEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPIMI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KHILIGICGGIASYKSVYIVSSLVKLGYKVKVIMTQNATKFITPLTLETISKNKIITNLW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKIVXXXPGSIAAL-DVKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITEIT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : ::| |: |::|:|| | | ||||||: :| |:|||| ||:||
EFNQKDYLKNKKILITASRTEELIDPIRYFSNTSTGKMGFCLAQEAVKLGAQVTIITGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NENDPECVNIIKIKTAMEMYKEALKIY-----NKFEIIIGAAAVADFKPKHIFNSKIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEG-----RAKVASIDEIVYRVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 KLHKKT-LEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLI---R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GR--SITIELVPXNPKIIDRIKEIQ-PNVFLVGFKAETSKEKLIEEGKRQIERAKADLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 NKINRLYIKLV-KNPDIIQHIGHNKLKNQIVIGFCAENSK-NLIQKAKEKLKKKNLDFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.2%; Score 543.5; DB 2; Best Local Similarity 36.3%; Pred. No. 7.3e-26; Matches 144; Conservative 81; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 GNTLEAFGSEENQVVLIGRDFTKELPKMKKRELAERI 394
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                                                                                                                                                                                                                                                                 134 APAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIVYRVIKKLHK--KT 191
                                                                                    18 GKKIVXXXPGSIA---ALDVKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
Length 437;
                                             Indels
Ouery Match
26.8%; Score 535; DB 2; I
Best Local Similarity 36.8%; Pred No. 2.7e-25;
Matches 150; Conservative 66; Mismatches 152;
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                    A;Molecule type: DNA'
A;Residues: 1-399 <HBID
A;Cross-references: GB:AEO04111; GB:AE003852; NID:g9654614; PIDN:AAF93391.1; GSPDB:GN
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA/pantothenate metabolism flavoprotein PA5320 [imported] - Pseudomonas aeruginosa C;Speciaes: Pseudomonas aeruginosa C;Speciaes: Pseudomonas aeruginosa C;Speciaes: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B8938  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. addman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Nature 406, 959-964, 2000
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A:Accession: B82982
                                                                                                                                           A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833
18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDSLLDPAAEASMGHIELA----KWADLVLLAPATADLIARWAAGMGNDLLTTLILATSA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 FPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEE-----GRAKVASIDEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 VYRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKKSRDNDTLTIEMV-KNPDIVASVAALTENRPFTVGFAAETQDVETYARSK--LVRKNL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ITEI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVV--TTA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 IRTKGSVK-AFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKSGR---SITIELVPXNPKIIDRIKEIQPN-VFLVGFKAETSKEKLIEEGKRQIERAKA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 RKLVGKKIVXXXPGSIAALD-VKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:: | : | | : | : | : | | : | DMICANDVSIAGQFENSNDNALTLFWKEGQHSLPLTSKDALASAVMHLIHEQM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLVVGNTL - - - EAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXL
                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1
C;Superfamily: pantothenate metabolism flavoprotein dfp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%; Score 490.5; DB 2; 35.1%; Pred. No. 1.2e-22; iive 69; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 35.1%
Matches 145; Conservative
                                                                                                                                                                                                                   A;Status: preliminary
                        C; Accession: A82351
                                                                                                                                                                                          A; Accession: A82351
                                                                                                                                                                                                                                                                                                                                                            A; Gene: VC0215
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                                                                                                                                                                                                                                                                                                                                                                                              flavoprotein dfp [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C;Accession: F83363
FTakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20263314
A;Accession: F83963
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-404 <STO>
A;Cross-references: GB;AP001515; GB;BA000004; NID:g10174886; PIDN:BAB06229.1; GSPDB;GNOCA; A;Cross-references: Strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                      LEGIRALVTLGSTREWIDRVRFISNPSSGVMGLEAALELYARGAEVDVVAGYTSVEIPHL 280
                                                                                                                                           311 XNPKIIDRIKEIQPNVFLVGFKAE--TSKEKLIEEGKRQIERAKADLVVGNTLEAFG--- 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EI----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVTTAFPHI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEE-----GRAKVASIDEIVYRV 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LVGKKIVXXXPGSIAALDVKA-CEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | |::|| ::|::|
DIFSEPDPSEIAHIQLA----DWADVIIIAPATANLIGKLANGVADDMLSTMLLAT--KA
                                                                          RKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKSGRSITIELVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOGKRVVLGVSGGIAAFKSAAFASKLVQAGAEVKVVMTEGAKKFVTPLTFQALTRHPVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 IKKLH----KKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEA-DFRGAVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 404;
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                                                                                                                                                                                                                                                                     397 ASPLLDVLMLDVSGEAVLKG-SFHKEI-----VAAVIADEIAKLLS 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: pantothenate metabolism flavoprotein dfp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%; Score 494.5; DB 2;
33.5%; Pred. No. 7e-23;
Live 84; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.55
Matches 138; Conservative
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A;Gene: dfp
C;Superfamil)
  221
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15;

Gaps

39;

Indels

Length 399;

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <STO>
A;Cross-references: GB:AE004944; GB:AE004091; NID:g9951628; PIDN:AAG08705.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                            A;Gene: dfp; PA5320
                                                                                                                                                                                C; Genetics
                                                                                                                                                                          DNA/pantothenate metabolism flavoprotein VC0215 [imported] – Vibrio cholerae (strain N16
                                                                                                                                                                                                            C; Species: Vibrio cholerae
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M.J.; K.; L

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RESULT 14

Datothenate metabolism flavoprotein dfp homolog yloI - Bacillus subtilis

NiAlternate names: probable aspartate 1-decarboxylase activase

C;Spaces: Bacillus subtilis

C;Space: 05-Dec.1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Space: 05-Dec.1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Space: 05-Dec.1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Date: 05-Dec.1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Bron, S;Brouillet, S;Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.;

A.; Brnich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

Natures: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y; Funa, S; Galizzi, A; Gal

Ecch, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Rabret, C.; Ferrari,

Natures: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y; Funa, S; Galizzi, A; Gal

Ecch, J; Harwood, C.R.; Hanaut, A.; Hilbert, H.; Holsappel, S.; Hana,

Natures: Lauber, J; Lazarevic, V.; Lee, S.H.; Levine, A.; Liu, H.; Masuda, S.; Mau

N; M; Ogdwaa, R.; Oglwara, A.; Ogdwaa, R.; Serocha, B.; Rose, M.; Sarro, V.; Pohl, T.M.; Parkoth, N.; Rivolta, C.; Rocha, E.; Roche, E.; Rose, M.; Sakiquchi, J; Sekowska, A.; Sekowska, A.; Terpstra, P.; Tosato, V.; V; Chanare, R.; Schikawa, H.; Danchin, A.; Tanaka, A.; Tanaka, T.; Terpstra, P.; Tosato, V.; V; V; Molecule Genome sequence of the Gram-positive bacterium Bacillus subtill A; Accession: D69878

A; Restaus: preliminary; nucleic acid sequence not shown; translation not shown

A; Roseidues: 1-406 <a href="mailto:refarences: GB:Z99112">refarences: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13443.1; PID:g26339

A; Geneticar, Vol.
                                                                                                                                                                                                                        H----KKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIRTK 242
   ILVPTMNYRMYSNKLFQENLEKLKNNGWFVVEP--EEGHLACGEVGKGRYPENEKIVEAV 171
                                                                                                                                                                                                                                                                                           SITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADLVVGN-TL 361
                                                                                                                                                                                                                                                                                                                                            NDLVLHLERTKDILKELGQRKSNQILVGFAAEV--ENFEENAVKKLREKNLDLLVLNDAR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEE------GRAKVASIDEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYRVIKKLHKKT----LEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ITEI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LVGKKIVXXXPGSIAALDVKAC---EGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPV 72
                                                                                                          GSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 406;
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C,Superfamily: pantothenate metabolism flavoproteln dfp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.7%; Score 473.5; DB 2; ilarity 34.1%; Pred. No. 1.3e-21; Conservative 73; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                               362 EAFGSEENQVVLIGRD-FTKELPKMKKRELAERIWDEI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                    348
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A72223
pantochenate metabolism flavoprotein dfp homolog TM1687 - Thermotoga maritima (strain M5
N;Alternate names: probable aspartate 1-decarboxylase activase
C;Specias: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72223
R;Melson, K.E.; Clayton, R.A.; Gotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Tttle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316
A;Accession: A7223
A;Accession: A7223
A;Residues: 1-394 cARN>
A;Residues: 1-394 cARN>
A;Residues: 1-394 cARN>
A;Residues: 1-394 cARN>
A;Residues: 1-344 cARN>
A;Coperimental source: strain MSB8
A;Gene: TM1687
C;Superfamily: pantothenate metabolism flavoprotein dfp
                                                                                                                                17;
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                                                                                                                                                                                                                                                                                                                                                                                                AFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRI-----EEGRAKVASIDE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                              115 T--DAQIALAPAMNQAMWRDTATQANAELLRQRGFHLFGPAAGSQACGDVGLGRMLEAEE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 IVYRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 LIRTKGSV---KAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGKIK----SGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIER 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 AHKLKKDPTSGEGLLLQLV-RNPDILATLAQREDRPFSVGFAAET--ENLLDYAARKLKD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPVITEI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIVY----RVIKKL 187
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                 RKLVGKKIVXXXPGSIAALDVKACEGLIR----HGAEVHAVMSEAATKIIHPYAWNLPTG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 AKADLVVGNTLE----AFGSEENQVVLIGRD-----FTKELPKMKKRELAERIWDEIEK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 KIVXXXPGSIA---ALDVKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITE-
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24.1%; Score 482.5; DB 2; Length 394;
Best Local Similarity 36.2%; Pred. No. 3.6-2;
Matches 144; Conservative 67; Mamatches 154; Indels 33;
                                                                               Length 402;
                                                                         Query Match
24.2%; Score 483.5; DB 2; Length And Thoral Similarity 33.4%; Pred. No. 32e-23.
Matches 140; Conservative 81; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: TM1687
Superfamily: pantothenate metabolism flavoprotein dfp
C; Superfamily: pantothenate metabolism flavoprotein dfp
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848058
DNA/pantothenate metabolism flavoprotein NWB1658 [imported] - Neisseria meningitidis (st C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C; Accession: A81058
R; Tettellin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
If, H.; Qin, H; Vamathevan, J.; Gill, J.; Scarlato, V; Masignani, V; Pizza, M.
A; Hilogolist, Son, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID: 20175755

A; Accession: A81058
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 < TET>
A; Cross-references: GB: AE002516;

A,Cross-references: GB:AE002516; GB:AE002098; NID:g7226905; PIDN:AAF42007.1; PID:g722691 A,Experimental source: serogroup B, strain MC58

A;Gene: NMB1658 C;Superfamily: pantothenate metabolism flavoprotein dfp

38; Length 394; Query Match 23.7%; Score 473; DB 2; Length 39 Best Local Similarity 35.0%; Pred. No. 1.4e-21; Matches 143; Conservative 69; Mismatches 159; Indels

15;

Gaps

17 VGKKIVXXXPGSIAALDVKACEGLIR----HGAEVHAVMSEAATKIIHPYAWNLPTGNPV 72 셤 à

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128 HIPIMIAPAMHETMYRHPIVRENIERLKKIGVEFIGPRI-----EEGRAKVASIDEIVY 181

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182 RVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIR 240

241 TKGSVKAFRIRKIKLKVETV - - EEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKI 298 --GQLQTALPFGISDTVQAVSAENMHRAVHRLI--DKQDAFISVAAVSDYRVKNRSTQKF 287

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---KSGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADL 355 299

356 VVGNTLE-AFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXLS 403

Search completed: January 31, 2002, 13:08:39

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:39:13; Search time 46.78 Seconds (without alignments) 122.268 Million cell updates/sec Run on:

156 1 MLPDWKIRKEILIEPFSEE......PYRGNYOGSTRLAFSKRKKL 156 US-08-957-709-71 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	pyrococ	Q9uxs8 pyrococcus		P39739 bacillus su	P16454 yersinia en	Q56957 yersinia ps	sulfolobu	Q58927 methanococc								P47386 mycoplasma				endle	P49224 anabaena va		•	P34328 caenorhabdi	P03900 xenopus lae	Q9ux95 sulfolobus	P31478 manduca sex	_	P36546 escherichia	-	P54439 bacillus su		Q9hkkO thermoplasm
SUMMARIES	ID		DCD_PYRAB	ODO2_BUCAI	FLIS_BACSU	AIL_YEREN	AIL_YERPS	TDXH_SULSO	HIS4_METJA		CYSM_AQUAE	QUIX_ACICA	ALN_YEAST	NTP2_FOWPV	NTP2_MCV1	UBPK_HUMAN	Y140_MYCGE	DPOL_ADEG1	SYV_FUGRU	CENF_HUMAN	RK36_EUGGR	RS21_ANAVA	HKL8_MAIZE	EM2_WHEAT	YKZ1_CAEEL	NU3M_XENLA	RL24_SULSO	VATF_MANSE	VG46_BPMD2	OMPX_ECOLI	OMPX_ENTCL	YRKL_BACSU	RP18_RAT	DCD_THEAC
	DB		Н	-	Н	-	-	٦	-	Н	Н	Н	-	Н	-	-	-	-		П	Н	,-	٦	П	П	-		7	П	Н	-	-	-	Н
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	Score		22	æ	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	9	9	Q	9	9	9	Q	9	9	9	9	9	9	Q
	Result No.	-	7	m	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

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Gaps ; ;

Query Match
23.7%; Score 37; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.9e-31;
Matches 37; Conservative 0; Mismatches 0; Indels

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RESULT

P57209 buchnera ap Q92hd8 buchnera ap P2848 escherichia P57891 pasteurella P4784 haemophilus Q02196 saccharomyc O59366 pyrococcus P53363 borrelia bu O7477 schizosacch Q12657 penicillium P20571 haloarcula Q57596 methanococc	S AA.	te) Jate) INASE (EC 3.5.4.13) (DCTP	DEPARIAMS). DEPARIAMS PYTOCOCCUS horikoshii. Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus. NCBI_TaxID=53953;	n H., Haikawa Y., Hino Y., Kosugi H., Hosoyama A., Nagai Y., awa H., Takamiya M., Ohfuku Y., amazaki J., Kushida N., Oguchi A.,	nizuya H., Kikuchi H.; uence and gene organization of the genome of a hyper- archaebacterium, Pyrococcus horikoshii OT3."; -76(1998). ACTIVITY: DCTP + H(2)O = DUTP + NH(3). Y: BELONGS TO THE DCTP DEAMINASE FAMILY.	produced through a collabities and the EMBL outstere are no restrictions as its content is in usage by and for com: . Usage by and for com: thttp://www.isb-sib.ch/an	393A985 CRC64;
DCD_BUCAL DCD_BUCAP DCD_ECCLI DCD_PASMU DCD_HAEIN MCAPS_TEAST KTHY_PYRHO GIDB_BORBU RLI3_SCHPO KAPS_PENCH TLI3_SCHPO KAPS_PENCH	ALIGNMENTS FRT; 156	057706; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE	occales;	STRAIN-OT3: MEDLINE-9873; MEDLINE-9874137; PubMed-9679194; MEXARADAGAS Y., Sawada M., Horikawa H., Hai Yamamoto S., Sekine M., Baba SI., Kosugi H Sakai M., Ogura K., Otsuka R., Nakazawa H., Funahashi T., Tanaka T., Kudoh Y., Yamazaki Aoki KI., Yoshizawa T., Nakamura Y., Robb	Kikuchi H.; gene organization erium, Pyrococcus DCTP + H(2)O = Di	This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institution. There a mose by non-profit institutions as long as a mosified and this statement is not removed. Us entities requires a license agreement (See http or send an email to license@isb-sib.ch).	nse. ; 1. 96B2C2C50393A985
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193 193 194 195 205 208 208 211 214 220	STANDARD;	40, C. 40, L. 40, L. IDINE	shii. aeota;	PubMee Sawada ne M., ., Otsi aka T.	zuya H., nce and chaebact 6(1998). CTIVITY: BELONGS	ntry is cop s Institute nformatics it institu statement a license to license	BAA31124.1; 5323; dCTP_deamins 41428; dUTPase. 1UTPase. 1. 5; dCTP_deaminse; lete proteome. 94; 17871 MW; 96
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୰ ୰୰୰୰୰୰୰୰୰୰	YRHO	057706; 20-AUG-2001 20-AUG-2001 20-AUG-2001 PROBABLE DEO:	DEAMINASE). DCD OR PH1997. Pyrococcus horikoshii Archaea; Euryarchaeot NCBI_TaxID=53953;	SEQUENCE FROM N.A. STRAIN-OT3; MEDLINE-98344137; Kawarabayasi Y., & Yamamoto S., Sekii Sakai M., Oguran M., Oguran K. Funahashi T., Yoran K. Ti., Yoshii K. Ti., Yoshii K. Ti., Yoshii K.	Masucni Y., Shizuya H., "Complete sequence and (thermophilic archaebact. DNA Res. 5:55-76(1998)!- CATALYTIC ACTIVITY: -!- SIMILARITY: BELONGS	This SWISS-PROT ent between the Swiss the European Bioinf use by non-profit modified and this s entities requires a or send an email to	AF Propropropropropropropropropropropropropr
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DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARITY).

-! CATALYTIC ACTIVITY: SUCCINYL-COA + DIHYDROLIPOAMIDE - COA + S-SUCCINYLDIHYDROLIPOAMIDE.

-! COPACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL COPACTOR (BY SIMILARITY).

-! SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL SYMMETRY (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.

-! SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
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InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR001009; Biotin_lipoyl.
Pfam; PF00198; 2-0xoacid_dh; 1.
Pfam; PF001364; biotin_lipoyl.
ProDom; PD001115; 20xoacid_dh; 1.
PROSTTE; PS00189; LIPOYL; FALSE NEG
Glycolysis; Transferase; Acyltransferase; Lipoyl; Complete proteome.
ACT_STE 391 391 POTENTIAL.
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STRAIN=168 / HB2058;
STRAIN=168 / HB2058;
Chen L. Helmann J.D.;
The Bacillus subtilis sigma D-dependent operon encoding the flagellar proteins FilD, FilS, and Filt";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 420;
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NOT KNOWN.
-!- SIMILARITY: BELONGS TO THE FLIS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E0028D647A5CE34C CRC64;
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o. 1.4;
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01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FLAGELLAR PROTEIN FLIS.
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100.0%; Pred. No. 1.4
tive 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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Bacillus subtilis.
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62 EKEGKVVI 69
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ID FLIS_BACSU
AC P39739;
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DE57389.
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDROLIPOMAIDE SUCCINVLIENSFERSE COMPONENT OF 2-OXOGLUTARATE
BUCHOR BUJGJ,
BUGGIL CALL (Subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
Bucterial; Proteobacterial; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi.
Archaea; Buryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
MCB1_TaxID-29292.
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STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu sequence of the endocellular bacterial symbiont of aphids
"Genome sequence of the endocellular Sandrain Symbione of aphids
                                                                                         20-A0G-2001 (Rel. 40, Created)
20-A0G-2001 (Rel. 40, Last sequence update)
20-A0G-2001 (Rel. 40, Last annotation update)
PROBABLE DEOXXCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DCD OR PABLIE.
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14.1%; Score 22; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 22; Conservative 0; Mismatches 0; Indels
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ProDom: PD004900; dCTP_deaminse; 1?
Hydrolase; Complete proteome: SEQUENCE 154 AA; 17758 MW; C031BEE419094DDB CRC64;
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InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
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                                      STANDARD;
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                                  DCD_PYRAB
Q9UXS8;
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"Nucleotide sequence of the Yersinia enterocolitica ail gene and
characterization of the Ail protein product.";
J. Bacteriol. 172:1062-1069(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 E0E80476A96F14D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
ATTACHMENT INVASION LOCUS PROTEIN PRECURSOR.
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100.0%; Pred. No. ...
0; Mismatches
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Pred. No. 5.7;
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MEDLINE-90130261; Pubmed=1688838;
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                                                                                                                                                          or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                  EMBL; 231376; CAA83249.1; -.
EMBL; U56901; AAC44954.1; -.
EMBL; 299122; CAB15550.1; -.
SubtiList; BG10922; fils..
InterPro; IPR003713; Flis..
Pfagella; Complete proteome.
SEQUENCE 133 AA; 15131 MW;
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Matches 7; Conservative
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23 LTLMLYN 29
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P16454;
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4.5%; Score 7; DB 1; Length 178;

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or send an email to license@isb-sib.ch).
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"The pasa locus is responsible for thermoinducible binding of Yersinia pseudotuberculosis to cultured cells.";
Infect. Immun. 64:2483-2489(1996).
-: FUNCTION: THIS MEMBRANE ASSOCIATED PROTEIN PROMOTES INVASION OF PATHOGENIC BACTERIA INTO EUKARYOTIC CELLS BY AN UNKNOWN MECHANISM (BY SIMILARITY).
                            Gaps
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EE7A4A20E4D8975C CRC64;
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE AIL/OMPX/PAGC/LOM FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ATTACHMENT INVASION LOCUS PROTEIN PRECURSOR.
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20-ANG-2001 (Rel. 40, Last annotation update)
PROBABLE PEROXINEDOXIN.
S020121 OR C02015 OR C02_016.
Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%; Score 7; DB 1;
100.0%; Pred. No. 7.5;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                       182 AA.
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                               Mismatches
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PRINTS; PR00316; ENTEROVIROMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00694; ENT_VIR_OMP_1; 1. PROSITE; PS00695; ENT_VIR_OMP_2; 1.
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MEDLINE=96294755; PubMed=8698470;
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15-JUL-1999 (Rel. 38, Last sequ
15-JUL-1999 (Rel. 38, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wersinia pseudotuberculosis.
                            7; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
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65 GVIGSFA 71
                                                                                     86 GVIGSFA 92
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ID AIL_YERPS
AC Q56957;
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                               Matches
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131 KEGKVVI 137
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P44652;
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REQUIRED CONTROL OF STRAIN-ATCG 35092 / DSM 1617 / P2;

REDINE-21313296; PubMed-11427726;

RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Awayez M.J., Chan-Weiher C.C.**., Cardon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Coost J.;

RI The complete genome of the crenarchaeon Sulfolobus Solfataricus P2.";

RT. For. Matl. Acad. Sci. U.S.A 98:7835-7840(201).

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                                                       SEQUENCE FROM N.A.
SERAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-ATCC 35092 / DSM 1617 / P2;
MEDLINE-9055432; PubMed-8899719;
Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
Doollittle W.F., Ragan M.A., Charlebols R.L.;
"Organizational characteristics and information content of an archaeal genome: 156 kb of sequence from Sulfolobus solfataricus
Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
NCBL_TaxID=2287;
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HISA_METJA STANDARD; PRT; 237 AA.
AC 658274
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1097 (Rel. 40, Last annotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DT 20-AUG-SYLPORMININO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOMERASE (EC 5.3.1.16).
ISA OR MJ1532.
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcaeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 215;
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5210477EF4C9607B CRC64;
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Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                     Microbiol. 22:175-191(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, Y08256; CAA69447.1; --
EMBL, AL512975; CAC23765.1; --
EMBL, AE006819; AA442300.1; --
HSSP, P30041; LPRX,
InterPro; IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA; I.
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24 RIKLPDD 30
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SEQUENCE
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Bulf C.J. White O. Olsen G.J. Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayfon R.A., Gocayne J.D., Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Naysen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klomk H.-P., Fraser C.M., Snith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                       Jannaschii.
Science 273:1058-1073(1996).
-!-CATALYTIC ACTIVITY: N-(5'-PHOSPHO-D-RIBOSYLFORMIMINO)-5-AMINO-1-
-!-CATALYTIC ACTIVITY: N-(5'-PHOSPHO-D-1'-
(5'-PHOSPHORIBOSYL)-4--
RIBULOSYLFORMIMINO)-5-AMINO-1-(5''-PHOSPHORIBOSYL)-4-
IMDAZOLECARBOXAMIDE.
-!-PATHWAY: FOURTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
-!-SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
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MEDIATE=P$550630; PubMed=7542800;
Pleischmann R.D., Addams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D., Widman J.F., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., "Whole-genome random sequencing and assembly of Haemophilus
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Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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InterPro: IPR00570; His_biosynth.
Pfam. PF00977; His_biosynth; 1.
Isomerase: Histidine biosynth; 1.
Isomerase: Alstidine biosynth; 26132 MW; DIIE3AD24C01AC2A CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 340, Last annotation update)
FERREDOXIN-TYPE PROTEIN NAPG HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5%; Score 7; DB 1;
100.0%; Pred. No. 9.4;
ative 0; Mismatches
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TIGR; MJ1532; -.
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NCBI_TaxID=471;
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 ACETATE
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QUIX_ACICA
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               Science 269:496-512(1995).
-!- FUNCATION: INVOLVED IN ELECTRON TRANSFER.
-!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
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-i- CATALYTIC ACTIVITY: O-ACETYL-L-SERINE + H(2)S = L-CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
CYSTEINE SYNTHASE (EC 4.2.99,8) (0-ACETYLSERINE SULFHYDRYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 279;
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CON-SULFUR 4 (4FE-4S) (BY
F77B6801E220955A CRC64;
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Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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PROSITE: PS00198; 4FE4S_FERREDOXIN; 1.
Electron transport; Iron-sulfur; 4Fe-4S; Comparate 72 72 IRON-SULFUR 1 METAL 75 180N-SULFUR 1 METAL 78 78 IRON-SULFUR 1 METAL 78 78 IRON-SULFUR 1
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30227 MW;
                                                                                                                                                                                                                                                        EMBL; U32719; AAC22006.1; -. HSSP; P00198; 1FCA.
TIGR; HI0345; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
Les 7; Conservative
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 influenzae Rd.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYSM OR AQ_1556
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067507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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CYSM_AQUAE
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                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro, 1.10, 2.10, 2.10, 1.

Prosite; PS00901; CYS_SYNTHASE; 1.

Lyase; Cysteine blosynthesis; Pyridoxal phosphate; Complete proteome.

Lyase; Cysteine blosynthesis; Pyridoxal phosphate; Camplete proteome.

BINDING 65 65 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elsemore D.A., Ornston L.N., "Unusual ancestry of dehydratases associated with quinate catabolism
                               PATHWAY: CYSTEINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in Acinetobacter calcoacéticus.";
J. Bacteriol. 177:5971-5978(1995).
-!- FUNCTION: COULD POTENTIALLY BE INVOLVED IN THE TRANSPORT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE PORIN QUIX.
B332A322F3130F79 CRC64;
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100.0%; Pred. No. 12;
ative 0; Mismatches
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
10-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001216; Cys_synthase.
InterPro; IPR001926; PALP.
COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BD413 / ADP1;
MEDLINE-96011389; PubMed-7592351;
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Matches 7; Conservative
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                                                                                                 SYNTHASE FAMILY.
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439 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 KEGKVVI 52
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RESULT 13
NTP2_FOWPV
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                                     ö
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S286G / AB372;
STRAIN-S286G / AB372;
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentches C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsenl T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
--- FUNCTION: UTLIZATION OF PURINES AS SECONDARY NITROGEN SOURCES, WHEN PRIMARS SOURCES ARE LIMITING.
--- CATALYTIC ACTIVITY: ALLANTOIN + H(2)0 - ALLANTOATE.
--- COFACTOR: ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                    01-CT-1993 (Rel. 27, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
DALION YINROZIO.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyceiles, Saccharomycotina; Saccharomyceteles; Saccharomyceteles; Saccharomyceteles; Saccharomyceteles;
                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-92206070; PubMed=1803816;
Buckholz R.G., Cooper T.G.;
"The allantoinase (DML1) gene of Saccharomyces cerevisiae.";
  Length 439;
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATABOLISM).
Score 7; DB 1;
Pred. No. 16;
0; Mismatches
                                                                                                                                                                                                       460 AA
                                                                                                                                                                                                   PRT;
Query Match 4.5%; Soc
Best Local Similarity 100.0%; P:
Matches 7; Conservative 0;
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Yeast 8:239-239(1992).
                                                                                                                                                                                                       STANDARD;
                                                                                                110 LTLERIK 116
                                                                      61 LTLERIK 67
                                                                                                                                                                                                     ALN_YEAST
P32375:
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MEDLINE=20193820; PubMed=10729156;
MEDLINE=20193820; PubMed=10729156;
MEDLINE=20193820; PubMed=10729156;
MEDLINE=20193820; PubMed=10729156;
"The genome of fow]pox virus:";
1 virol: 74:3815-3811(2000).
1 virol: 74:3811(2000).
1 virol:
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Binns M.M., Bourson M.B.G., Skinner M.A.;
Gene translocations in poxviruses: the fowlpox virus thymidine kinase
gene is flanked by 15 bp direct repeats and occupies the locus which
in vaccinia virus is occupied by the ribonucleotide reductase large
subunit gene. "I.
Virus Res. 24:161-172(1992).
                                                                                          Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Avipoxvirus.
NCBI_TaxID-10261;
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                                                                                     0; Indels
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NUCLEOSIDE TRIPHOSPHATASE II (EC 3.6.1.15) (NUCLEOSIDE
TRIPHOSPHATE PHOSPHOHYDROLASE II) (NPH II).
4.5%; Score 7; DB 1;
100.0%; Pred. No. 17;
ive 0; Mismatches
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                                          Similarity 100. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                          REGVIGS 90
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     Query Match
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Matches 7
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TISSUE-Brain;
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  RESULT 15
UBPK_HUMAN
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1-FUNCTION: ESSENTIAL FOR VIRAL REPLICATION. PLAYS AN IMPORTANT ROLE DURING TRANSCRIPTION OF EARLY MRNAS, PRESUMABLY BY PREVENTING R-LOOP FORMATION BEININD THE ELONGATING RNA POLYMERASE. ACTS AS NTP-DEPENDENT HELICASE THAT CALSES UNIDIRECTIONAL UNWINDING OF 3'TAILED DUPLEX RNAS. MIGHT ALSO PLAY A ROLE IN THE EXDORT OF NEWLY SYNTHESIZED MRNA CHAINS OUT OF THE CORE INVO THE CYTOPLASM. REQUIRED FOR PROPAGATION OF VIRAL PRATICLES (BY SIMILARITY).
-1-CATALYTIC ACTUVITY: NTP + H(2)O = NDP + ORTHOPHOSPHATE.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molluscum contagiosum virus subtype 1 (MCVI).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Molluscipoxvirus.
                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-NUG-2001 (Rel. 40, Last annotation update)
NUCLEOSIDE TRIPHOSPHATASE II (EC 3.6.1.15) (NTPASE II) (NUCLEOSIDE TRIPHOSPHOYDROLASE II) (NPASE II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-96325459; PubMed-8670425;
Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of a human tumorigenic poxvirus: prediction of specific host response-evasion genes."; Science 273:813-816(1996).
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100.0%; Pred. No. 24;
.ive 0; Mismatches 0; Indels
                       Length 682;
                                                                 0; Indels
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SMART; SM00490; HELICC; 1.
PROSITE; PS00690; DEAL_ATP_HELICASE; 1.
ATP-binding; Helicase; Hydrolase; Transcription.
305 520 HELICASE.
    4.5%; bcc.
100.0%; Pred. No. ...
0; Mismatches
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INTERPO: IPR001410; DEAD.
INTERPO: IPR001464; DEAH_ATP_helcse.
InterPro; IPR001650; Helicase_C.
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Ouery Match
Best Local Similarity 100.،
المالية 7; Conservative
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Matches 7; Conservative
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263 PVELRYG 269
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INTP2_MCV1
INTP2_MCM01
INTP2_MCV1
INTP2_MCM01
INTP2_M
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MEDLINE=99246063; PubMed=10231032;
Nagase T., Ishikawa K.I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
**Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 580-802 AND 838-913 FROM N.A.
MEDLINE-99299247; PubMed=10369878;
Gilley J., Fried M.;
Gilley J., Fried M.;
Extensive gene order differences within regions of conserved synteny between the Fugu and human genomes: implications for chromosomal evolution and the cloning of disease genes.";
Hum. Mol. Genet. 8:1313-1320(1999).
-!- CATALYTIC ACTIVITY: UBLQUITIN C-TERMINAL THIOLESTER + H(2)0 = UBLQUITIN + A THIOL.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19; ALSO KNOWN AS FAMILY 2 OF UBLQUITIN CARBOXXL-TERMINAL HYDROLASES.
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UBPR_HUMAN STANDARD; PRT; 913 AA.

UBPR_HUMAN STANDARD; PRT; 913 AA.

O972K6; 0900N8; 0900P0;

20-AUG-2001 (Rel. 40, Lrst sequence update)

20-AUG-2001 (Rel. 40, Last sequence update)

UBIQUITIN CARBOXYL TERMINAL HYDROLASE 20 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 20) (UBIQUITIN SPECIFIC PROCESSING PROFEASE 20)

(DEUBIQUITINATING ENZYME 20).
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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H -> Q (IN REF. 2).
R -> M (IN REF. 2).
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Pfam; PF00443; UCH-2; 1.
Pfam; PF00248; zf-UBP; 1.
PROSTIE; PS00972; UCH_2_1; 1.
PROSTIE; PS00973; UCH_2_2; 1.
PROSTIE; PS00973; UCH_2_2; 1.
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InterPro; IPR001394; UCH-2.
InterPro; IPR001607; zf-UBP.
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EMBL; Y17459; CAB44352.1; -
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	DDEL TWINNBY.		(TrEMBLrel,	(TrEMBLrel.	401AA LONG HYPOTHETICAL		Pyrococcus horikoshii.	Archaea; Euryarchaeola; NCBI TaxID=53953;		N.A.	STRAIN=OT3; MEDLINE=98344137; PubMed=9679194;	., Sar	ekine	а. К.,	Tanaka	shizav	izuya	"Complete sequence and gene organization of the genome of a hyper-	thermophilic archaebac	BAA	InterPro; IPR003382; Flavoprotein.	Pfam; PF02441; Flavoprotein; 1	ome.	401 AA;		al Similarity 100 72; Conservative	TGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFP	TGNPVTTFTTGFTEHVELAGEHENKADLTLVCPATANTISKTACGTDDTPVTTAVTTAPP	
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RESULT	U39114 TD 050114	059	01-	01-	401	PHI	Pyr	NCB	[1]	SEO	MED	Kaw	Yam	Sak	Fun	Aok	Mas	ပ္	the	EMB	Int	Pfa	Com	SEO	Query Match	Best Loc Matches	9	Ċ	•
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STATISHMESS / SEROGROUP B;
A BISTON N.C., Gauton M.D., Heidelberg J., Jeffries A.C., Nelson K.E.,
A BISTON W.C., Gauton M.L., DeBoy R., Peden J.F., Dodson R.J.,
A Melson W.C., Gauton M.L., DeBoy R., Peterson J.D., Hickey E.K.,
A Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Oln H., Vamathevan J.,
A Sanilato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58 ...
RCMB1, ABOS1819-1815(2000).
REMEL, ABOS2516; AAR42007.1; -
REMEL, REMEL, ABOS2516; AAR42007.1; -
REMEL, REMEL, REMELSER, REMELS
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STRACHS_224J / SEROGROUP A / SEROTYPE 4A;
STRACHS_224J / SEROGROUP A / SEROTYPE 4A;
MEDIINE—20222556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Peltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OT-2001 (TrEMBLrel. 17, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN.
NMB1658.
NABSEATA meningitidis (serogroup B).
Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.
                           Gaps
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN NMA1916.
Pred. No. 0.0029;
; Mismatches 0;
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   100.08;
   Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                              200 RFITNASSGKMG 211
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208 SSGKMGVALA 217
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STRAILWASSB (J. DSM 3109;
MEDLINE-99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Fyidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Mature 399:323-329(1999).
Mature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                             Pyrococus abyssi.
Archaea: Euryarchaeota: Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID-29292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.9%; Score 60; DB 1; Length 401 Best Local Similarity 100.0%; Pred. No. 3.1e-51; Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ484285; CAB49630.1;
InterPro; IPR003382; Flavoprotein.
Pfam; PF0241; Flavoprotein: 1.
Complete proteome.
SEQUENCE 401 AA; 44290 MW; 96cCD5A190C1FA5D CRC64;
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                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2001 (TrEMBLrel. 17, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN (DFP)
PAB1897
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DNA/FANTOTHENATE METABOLISM FLAVOPROTEIN.
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                                                                                                                                      PRT;
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   129 HIPIMIAPAMHE 140
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MEDLINE=98049343; PubMed=9389475; Klerk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klerk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Klerk H.-P., Cayton R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Verterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weildman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Wenter J.C.,
Luo Y., Pfister P., Leisinger T., Wasserfallen A.;
"The genome of archaeal prophage psiM100 encodes the lytic enzyme responsible for autolysis of Methanothermobacter wolfeii.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF301375; AAG39941.1; -.
InterPro: IPR003812; Flavoprotein.
Pfam: PF02441; Flavoprotein; 1.
SEQUENCE 382 AA, 41207 MW; 8E792042DFDFA3AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphatereducing archaeon Archaeoglobus fulgidus.";
Mature 390:364-370(1997).
EMBL; AE000989; AABB95597.1; --
TIGR; AF1645; --
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Archaeoglobus.
                                                                                                                                                                                           Length 382;
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Pfan; PF02441; Flavoprotein. 1.
Hypothetical protein; Complete proteome.
SEQUENCE 404 AA; 44885 WW. E5A2B899C3E6A66F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. 2.9;
ative 0; Mismatches
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257 AAAVSDFRP 265
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Matches 9; Conserv
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanobacterium wolfei.
Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
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 Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491."; Mature 404.502-506(2000).
EMBL; ALI62757.
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                                                                                                                                                                                                                                               2.5%; Score 10; DB 2; Length 394 100.0%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                Interpro: IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Hypothetical protein; Complete proteome
SEQUENCE 394 AA, 42238 MW; E19917C24E62B087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02441; Flavoprotein; 1.
SEQUENCE 399 AA; 43395 MW; 566E98FF6F07F7EB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.
DPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 AA
                                                                                                                                                                                                                                                                                          Mismatches
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100.0%; Pre
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                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                208 SSGKMGVALA 217
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MEDIATRE-96174815; PubMed=8599938;
MEDIATRE-96174815; PubMed=8599938;
KRIGHTRE-96174815; PubMed=8599938;
KRIGHTRE-96174815; PubMed=8599938;
REMIGHT OF STATE AS A STATE AS A RESPECTION OF THE ASSP. 10.51934;
MESSP. 10.21933; AACS9859.1;
INTERPRO: IPRO00135; Highmoblty_12.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Saxifragales; Hamamelidaceae; Hamamelis.
NCBI_TaxID=4397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Membibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-FRUCTOFURANOSIDASE (EC 3.2.1.26) (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HIGH MOBILITY GROUP PROTEIN-1.
      0;
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ilarity 100.0%; Pred. No. 13;
Conservative 0; Mismatches (
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      Mismatches
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      8; Conservative.
                                                                                                                                                                                                                                          PRELIMINARY;
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les 8; Conserv
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                                                    152 ERLKKLGV 159
                                                                                      66 LPTGNPVI 73
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Q91596;
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Q91596
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                                 Caenorhabditis elegans.
Bukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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SEQUENCE FROM N.A.
STRAIN-1925/SVJ;
Weinman E.J., Steplock D.A., Zhang X., Akhter S., Shenolikar S.;
Weinman E.J., Steplock D.A., Zhang X., Akhter S., Shenolikar S.;
"Molecular cioning of the cDNA and promoter sequences for the mouse sodium-hydrogen exchanger regulatory factor.";
Biochim. Biophys. Acta 0:0-0(1999).
EMBL, ARISH4912; AAA49224.1;
InterPro: IPRO01478; PDZ.
InterPro: IPRO01478; PDZ.
Pfam: PFC00595; PDZ: 1.
SWART: SM00228; PDZ: 1.
SWART: SM00228; PDZ: 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID-10090;
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                                                                                                                                                                                                                                       Lennard N.; submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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09R1A1, 01-MAY-2000 (TEMBLEE] 13, Created)
01-MAY-2000 (TEMBLEE] 13, Last sequence update)
01-JUN-2001 (TEMBLEE] 17, Last annotation update)
SODIW-YPDROGEN EXCHANGER REGULATORY FACTOR (FRAGMENT):
SLC9A3R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
EMBL; 281567; CAB04589.1; -.
SEQUENCE 127 AA; 14638 MW; B169A1E75006C2CE CRC64;
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SEQUENCE 142 AA; 15376 MW; A8994D6A865B283A CRC64;
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
80699-6 PROTEIN.
80869-6
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100.0%; Pred. No. 10;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Best Lągal Similarity
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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85 FRIRKIKL 92
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AC 09R1A1
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Gaps

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us-08-957-709-19.rspt

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HSSP, Q12923; 3PDZ.
MGD; MGI:13494842; S1C993rl.
InterPro; IPR001478; PDZ.
Pfam; PF00595; PDZ; 2.
SMART; SM0228; PDZ; 2.
SMART; SM0228; PDZ; 2.
SROUTE: PS50106; PDZ; 2.
SEQUENCE 355 AA; 38600 MW; 331F6BEE31DA0A11 CRC64;
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Q9X8S5;
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Q9X8S5
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"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
InterPro: IPR001345; PG_mutase.
Pfam; PF0001345; PG_mutase.
Complete proteome.
SEQUENCE 227 AA; 25954 MW; B0928CC777B5C6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                Query Match 2.0%; Score 8; DB 13; Length 210; Best Local Similarity 100.0%; Pred. No. 16; Matches 8; Conservative 0; Mismatches 0; Indels
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Weinman E.J., Steplock D.A., Shenolikar S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U74079; AAB17569.1; -.
          ALICETEL, TELLO,                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last sequence update)
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MEDLINE-21145866; PubMed-11248100;
  InterPro; IPR000910; HMG_12_box.
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01-FEB-1997 (TIEMBLEEL 0
01-JUN-2001 (TIEMBLEEL 1
PROTEIN CO-FACTOR.
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P70441;
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P70441
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049754; CAB42045.1;
HSSP; Q56232; 1BKG.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
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Murphy L., Harris D.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Wb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                               Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iransferase, Aminotransferase.
SEQUENCE 396 AA; 42785 MW; 727DBF14C347EBDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                             Score 8; DB 11;
Pred. No. 27;
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100.0%; Pred. No. 30;
ative 0; Mismatches
2.0%; Scor.
v 100.0%; Pred. No. ...
o; Mismatches
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MEDLINE=97000351; PubMed=8843436;
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Matches 8; Conservative
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Job time: 158 sec

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Thu Jan 31 13:32:30 2002

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:20:06; Search time 78.64 Seconds (without alignments) 151.109 Million cell updates/sec

156 1 MLLPDWKIRKEILIEPFSEE......PYRGNYQGSTRLAFSKRKKL 156 US-08-957-709-71 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched: Total number of hits satisfying chosen parameters:

0

Word size :

219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries PIR_68:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	37	23.7	156	7	E71216	dCTP deaminase (EC
7	22	14.1	154	7	G75030	deaminase
m	æ	5.1	420	7	D84965	dihydrolipoamide S
4	7	4.5	133	-	140398	flagellar protein
S	7	4.5	133	~	E84101	flagellar protein
9	7	4.5	178	7	A35123	ail protein precur
7	7	4.5	215	7	S74033	alkyl hydroperoxid
æ	7	4.5	237	7	C64491	phosphoribosylform
σ	7	4.5	268	Н	A69000	conserved hypothet
10	7	4.5	279	7	A64149	hypothetical prote
11	7	4.5	327	~	A70435	cysteine synthase
12	7	4.5	362	7	C81445	
13	7	4.5	376	7	T40673	homoserine dehydro
14	7	4.5	439	7	I39524	probable porin - A
15	7	4.5	460	-	S48489	allantoinase (EC 3
16	7	4.5	587	7	H83748	two-component sens
17	7	4.5	661	7	A69252	3-hydroxyacyl-CoA
18	7	4.5	999	7	D82386	methyl-accepting c
19	7	4.5	682	Н	G48563	I8 protein - fowlp
20	7	4.5	684	~	T30652	probable RNA helic
21	7	4.5	782	~	D81281	probable nucleotid
22	7	4.5	874	7	н86167	hypothetical prote
23	7	4.5	1017	7	PC4035	ģ
24	7	4.5	1113	~	E64215	hypothetical prote
25	7	٠	1921	7	T13827	
56	9	3.8	34	~	S77646	hypothetical prote
27	9		35	~	C70256	cal
28	9	3.8	37	П	R5EG36	U
29	9	3.8	55	N	H70228	hypothetical prote

ribosomal protein		hypothetical prote	embryonic abundant	conserved hypothet	hypothetical prote	L71-2 protein - fr	hypothetical prote	hypothetical prote	MADS-box protein (C14B9.1 protein -	NADH dehydrogenase	protein secretion	hypothetical prote	H+-transporting AT
I39622	T29319	G82600	VUWTEM	B82436	G83729	S62334	T21642	T24886	A84659	S44755	QXXL3M	H72655	T27846	A53055
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30	3 2	33	34	35	36	37	38	39	40	41	42	43	44	45

dCTP deaminase (EC 3.5.4.13) PH1997 [similarity] - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

Cyaccession: E71216
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137
A;Ression: E71216
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-156 <KAM>
A;Residues: 1-156 <KAM>
A;Cross-references: GB;AP000007; NID:93236134; PIDN:BAA31124.1; PID:93258441
A;Cross-references: GB;AP000007; NID:93236134; PIDN:BAA31124.1; PID:93258441
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa

A,Gene: PH1997 C,Superfamily: dCTP deaminase C,Keywords: hydrolase

Gaps ó Length 156; Indels DB 2; Le 8.5e-31; 0; Mismatches 23.7%; Score 37; 100.0%; Pred. No. Conservative Query Match Best Local Similarity Matches 37; Conserva Matches

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1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVGREAFV 37 ŏ

1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVGREAFV 37 Db

RESULT

dCTP deaminase (EC 3.5.4.13) PAB1164 [similarity] - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C:Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C;Accession: G75030

R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A;Reference number: A75001 A;Accession: G75030

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-154 < KAM>
A; Residues: 1-154 < KAM>
A; Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50685.1; PID:g545
A; Experimental source: strain Orsay
C; Genetics:
C; Genetics:
C; Superfamily: dCTP deaminase

Thu Jan 31 13:32:30 2002

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Ouery Match 4.5%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches
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Matches 7; Conservative
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23 LTLMLYN 29
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C;Datecles: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: 140398; E69625
R;Chen, L.; Helmann, J.D.
J. Bacteriol. 16, 3093-3101, 1994
A;Title: The Bacillus subtilis sigma D-dependent operon encoding the flagellar proteins.
A;Reference number: 140396; MUID:94252974
A;Accession: 140398
A;Status: pre-fulminary; translated from GB/EMBL/DDBJ
A;Residues: 1-133 <RES>
A;Cross references: EMBL:231376; NID:9499379; PIDN:CAA83249.1; PID:9499382
A;Cross references: EMBL:231376; NID:9499379; PIDN:CAA83249.1; PID:94999382
A;Cross references: EMBL:231376; NID:9499379; PIDN:CAA83249.1; PID:94999982
A;Croulger, D.; Fritz, C.; Fulita, M.; Fulita, Y.; Funma, S.; Galizzi, E.
A; Ehrlich, S.D.; Emmerson, P.T.; Entington, J.; Fabret, S.; Hosono, S.; Hullo, M.; Kottler, D.; Kritz, C.; Fulita, M.; Fulita, Y.; Puma, S.; Hosono, S.; Hullo, M.; Kottler, P.; Roulger, M.; Bark, A.; Bark, M.; Sadole, Y.; Sato, Y.; Sato, A.; Bark, C.; Rocha, E.; Rocha, E.; Rache, B.; Rack, M.; Sadole, Y.; Sato, M.; Sato, M.; Sato, M.; Sato, M.; Sato, M.; Sato, M.; Seror, A; Authors: Schleich, S.; Schroeter, R.; Yamanoto, H.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
B04465
d149drolipoamide S-succinyltransferase (EC 2.3.1.61) [imported] - Buchnera sp. (strain 12.5 pecies: Buchnera sp. (c. Species: B04965 and B04966 and B0496 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Gene: sucB; BU303
C.Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C.Keywords: acyltransferase; coenzyme A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó;
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0
                                                                                                                                             Length 154;
                                                                                                                                             / Match 14.1%; Score 22; DB 2; Length 154 Local Similarity 100.0%; Pred. No. 3.4e-15; hes 22; Conservative 0; Mismatches 0; Indels
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Cispecies: Bacillus halodurans (strain C-125)
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A; Reference number: A69580; MUID: 98044033
A; Accession: E59625
A; Status: nucleic acid sequence not shown; translation not shown
A; Status: nucleic acid sequence not shown; translation not shown
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: L133 < KMN>
A; Residues: L133 < KMN>
A; Cross-references: GB: Z99122; GB: AL009126; NID: 92636029; PIDN: CAB15550.1; PID: 926360
A; Experimental source: strain 168
A; C; Superimental source: strain 168
C; Superimental source: strain 168
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tive 0; Mismatches
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Matches 7; Conservative
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conserved hypothetical protein MTH1 - Methanobacterium thermoautotrophicum.(strain Delta C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A69000
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B;Experimental source: strain P2.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase C22 prot
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phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase - Methanococcus
c;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Caccession: G64491
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.M.; Shithe: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
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C;Superfamily: N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidaz
                                                                                                                                                      alkyl hydroperoxide reductase homolog - Sulfolobus solfataricus
N;Alternate names: protein c0215
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: S74033
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: A;Reference number: S73076; MUID:97055432
A;Reference number: S74033
A;Status: nucleic acid sequence not shown; translation not shown
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A;Accession: C64491
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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| 131 KEGKVVI 137
86 GVIGSFA 92
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24 RIKLPDD 30
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-268 <MTH>
A; Cross-references: GB-AE000795; GB:AE000666; NID:g2621036; PIDN:AAB84510.1; PID:g262
A; Experimental source: strain Delta H
C; Genetics:
A; Gene: MTH1
C; Superfamily: conserved hypothetical protein MTH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gorayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.E.;
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                                                                                                                                          A; Reference number: A69000; MUID: 98037514
A; Accession: A69000
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Aquifex aeolicus
C;Abecies: Aquifex aeolicus
C;Accession: A70435
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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States and the control of the EMBL Saccharomyces cerevisiae)

N.Alternate names: protein XIR027c
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
R.Rowcesion: S48489; S28649
R.Rowley, K.
A.Reference number: S48478
A.Accession: S48489
A.Accession: S48489
A.Accession: S48489
A.Accession: S48489
A.Accession: S4849
A.Accession: S4849
A.Accession: S4849
A.Accession: S4849
A.Accession: S4849
A.Accession: S4849
A.Accession: S28649; MUD:92206070
A.Title: The allantolnase (DALI) gene of Saccharomyces cerevisiae.
A.Title: The allantolnase (DALI) gene of Saccharomyces cerevisiae.
A.Title: The allantolnase (DALI) gene of Saccharomyces cerevisiae.
A.Accession: S28649
A.Molecule type: DNA
A.Residuces: LAN
A.Residuces: LAN
A.Residuces: LAN
A.Residuces: S4849; MUD:92206070
A.Accession: S28649
A.Molecule type: DNA
A.Residuces: BABL:MG9294; NID:9171365; PIDN:AAA34553.1; PID:9171366
A.Cross-references: SGD:S0001466; MIPS:YIR027c
A.Cross-references: SGD:S0001466; MIPS:YIR027c
A.Cross-references: Bacillus dihydroorotase homology
C.Superfamily: allantoinase; Bacillus dihydroorotase homology
C.Keywords: hydrolase
F.56-447/Domain: Bacillus dihydroorotase homology
                                                                                                                                                                                                                                                                                                                                  probable porin - Acinetobacter calcoaceticus
probable porin - Acinetobacter calcoaceticus
C;Species: Acinetobacter calcoaceticus
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 18-Sep-1998
C;Accession: 139524
J. Bacteriol. 177, 5971-5978, 1995
A;Title: Unusual ancestry of dehydratases associated with quinate catabolism in Acine
A;Reference number: 139522, MUID:96011389
A;Accession: 139524
A;Accession: 139524
A;Accession: 139524
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-439 - REES-
A;Cross_references: EMBL:U20284; NID:9644872; PID:9644875
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Superfamily: Pseudomonas porin oprB
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ilarity 100.0%; Pred. No. 35;
Conservative 0; Mismatches
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Matches 7; Conserv
                                                                                                    287 EKEGKVV 293
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                                             45 EKEGKVV
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GRA445

probable transmembrane protein Cj0268c [imported] - Campylobacter jejuni (strain NCTC 11)

C. Species: Campylobacter jejuni
C. Species: Campylobacter jejuni
C. Species: Sandylobacter jejuni
C. Species: Sandylobacter jejuni
C. Mar. 2000 #text_change 31-Mar-2000
C. Accession: C81445

N. Farkhili, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C. W.; Quail, W.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A. Accession: C8144
A. Accession: C8144
A. Accession: C8144
A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A. And A.
A;Cross-references: EMBL:AL035263; PIDN:CAA22876.1; GSPDB:GN00067; SPDB:SPBC776.03
A;Experimental source: strain 972h-; cosmid c776
C;Genetics:
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T40673
T40673
C; Dacard dehydrogenase - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C; Accession: T40673
R; Lyne, M; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Kutzner, M.; Wambutt, Submitted to the EMBL Data Library, January 1999
A; Accession: T40673
A; Accession:
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100.0%; Pred. No. 26;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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A;Map position: 2
A;Introns: 14/1
C;Superfamily: homoseri
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217 NEPVELR 223
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Search completed: January 31, 2002, 13:20:08 Job time: 109 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:06:08; Search time 33.61 Seconds (without alignments) 888.174 Million cell updates/sec Run on:

Title: Perfect score:

US-08-957-709-19 1998 1 MLHHVKLIYATKSRKLVGKK:......KMKKRELAERIWDEIEKXLS 403

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

/SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT:>/SIDS2/gcgdata/geneseq/geneseqp/AA1990.DAT:> /SIDS2/gcgdata/geneseq/geneseqp/AA1994_DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA1995_DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA1996_DAT: /gcgdata/geneseq/geneseqp/AA1997.DAT: /SIDS2/gcgdata/geneseg/genesegp/AA1998.DAT: /SIDS2/gcgdata/geneseg/genesegp/AA1999.DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA1992.DAT: | SIDS2/gcgdata/geneseq/geneseqp/AA1980.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1981.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1981.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1983.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1984.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1986.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1986.DA1 | SIDS2/gcgdata/geneseq/geneseqp/AA1988.DA1 /SIDS2/gcgdata/geneseq/geneseqp/AA1991 A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegp/AA2001.DAT:

SUMMARIES

					SUMMARIES	
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Result		Query				
NO.	Score	Match	Match Length DB ID	DB	ID	Description
-	1985			19	AAW72844	Polymerase enhanci
7	461.5			22	AAG82741	S. epidermidis ope
٣	444			22	AAB79946	Corynebacterium ol
4	439			22	AAG91520	C qlutamicum prote
5	197			19	AAW98418	H. pylori GHPO 319
9	166.5			22	AAB94179	Human protein sequ
7	165.5			22	AAM39470	Human polypeptide
8	165.5			22	AAM41256	Human polypeptide
6	165.5			21	AAY32199	Human receptor mol
10	162	8.1	217	21	AAY96816	A. thaliana Vb89 (
11	160			22	AAB93850	Human protein segu



	bidopsis t	s re	pro	hCPSI. Homo sapie	Polymerase enhanci	LO.	Human T1405 carbam	Human carbamyl pho	ಹ	enh		Plasmodium falcipa		Polymerase enhanci	Amino acid sequenc	micu	Candida glabrata H	ø	Histidine tagged C				Merosin major subu			laminin	Novel bone marrow		ORF85	thali	sis th		Human partial merc	
AAG11382	\mathbf{m}	AAY43439	AAR39345	963	AAW72841	AAB49222	AAB49223	AAB49224	AAB49225	AAW72860	AAY23924	AAB18324	AAW72863	AAW72843	AAY23920	AAG90216	AAB01278	AAB01277	AAB01279	AAW13491	AAB19794	AAB19792	AAR71730	AAY15460	AAB19791	AAB19793	AAU14603	AAU14697	AAB41087	AAG04547	AAG43327	AAR63681	AAW39206	
21	21	20	14	14	19	22	22	22	22	19	20	21	19	13	20	22	21	21	21	18	21	21	16	20	21	21	22	22	21	21	21	12	18	
199	209	181	181	1500	31	1500	1500	1500	1500	35	268	1558	24	24	582	463	548	268	268	751	3088	3089	3110	3110	3110	3110	5373	5447	2541	331	331	337	337	
•	•			•	•	•	•	•	6.7	•			٠				•		•		•	•	•	•	٠	•	•	٠	٠	•	•	•		
158	158	151.5	4	136	135	134	134	134	134	129	119.5	119	116	116	111.5	109.5	107	107	107	106	105	105	105	105	105	105	. 105		103.5	103		102.5	0	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication. Polymerase enhancing factor P50 component. /note= "encoded by NNN" Pyrococcus furiosus strain DSM 3638 Location/Qualifiers Ä. AAW72844 standard; Protein; 403 (first entry) Key Misc-difference 23 Misc-difference 24 01-MAR-1999 AAW72844;

/note= "N-terminal peptide used to generate primers" /note= "encoded by NNN" /note= "encoded by NNN" /note= "encoded by CCN" 311 /note= "encoded by NNN" 275..291 Misc-difference 310 Misc-difference Misc-difference Peptide Peptide

/note= "internal peptide used to generate /note= "internal peptide used to generate primers Peptide

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This is the amino acid sequence of the P50 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. The sequence is predicted from a DNA sequence (see AAW73847) are the from genomic DNA by PCR. P50 and P45 (see AAW72847) are the predominant components of PEF, which acts to enhance the activity of P furiosus DNA polymerase, thereby providing replication products of greater length and purity. P50 is similar in structure to a bacterial flavoprotein. The invention provides movel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies raised against P45 or P50. Also included are methods for identifying compositions with Polymerase enhancing activity, for proteins and complexes that function to enhance polymerases to proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase reactions can be enhanced (claimed) by composition having polymerase enhacing activity. Kits are provided for replicating nucleic acid sequencing or amplification composition having nucleic acid sequencing or amplification site-directed mutagenesis, nucleic acid sequencing or amplification or amplification or amplification or amplification or amplification or amplification or amplification.
                                                                                                                                                                                                                                                                                                                                                                     Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases,
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 46; Page 36; 161pp; English.
                                                                                                                        98WO-US05497
                                                                                                                                                             97US-0957709
97US-0822774
                                                                                                                                                                                                                                                                    Hansen CJ, Hogrefe H;
                                                                                                                                                                                                                                                                                                         WPI; 1998-542284/46.
N-PSDB; AAV63859.
                                                                                                                                                                                                                           (STRA-) STRATAGENE.
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                                         WO9842860-A1
                                                                                                                        20-MAR-1998;
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                                                                               01-OCT-1998.
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for

PYAWNLPTGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTT 120 1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAALDVKACEGLIRHGAEVHAVMSEAATKIIH 60 99.3%; Score 1985; DB 19; Length 403; 99.8%; Pred. No. 1.1e-184; tve 1; Mismatches 0; Indels 0; Best Local Similarity 99.8 Matches 402; Conservative Query Match q ò

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VVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIV 180 YRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGAVTLIR 240 TKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKS 300 121 181 121 181 241 oy Oy oy Oy Q

GRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADLVVGNT 360

301

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81150, from Staphylococcus epidermidis.

(II), given in AAG81154 to AAG83120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH5509 represent specifically claimed S. epidermidis genomic DNA antibious contained sequences from the present invention. AAH55091 to AAH5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N. B. The present invention specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing of the present specification, though sequences are given in the sequence listing of the present specification, though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no even the present for SEQ ID NO:4465 to 4472, Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis S. epidermidis open reading frame protein sequence SEQ ID NO:2576. Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis. 361 LEAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXLS 403 Claim 18; Page 675; 2188pp; English. AAG82741 standard; Protein; 399 AA 09-NOV-2000; 2000WO-US30782. 03-SEP-2001 (first entry) Staphylococcus epidermidis (GLAX) GLAXO GROUP LTD. WPI; 2001-316495/33. N-PSDB; AAH53591. WO200134809-A2. 09-NOV-1999; Kimmerly WJ; 17-MAY-2001. AAG82741; RESULT g QQ δ

16; Gaps 19 KKIVXXXPGSIAALD-VKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT--- 74 Ouery Match 23.1%; Score 461.5; DB 22; Length 399; Best Local Similarity 34.3%; Pred. No. 2.4e-36; Matches 141; Conservative 75; Mismatches 148; Indels 47; Query Match οy

Sequence 399 AA;

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                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
               174 kfftqqknvvkssfsgkralvtagptvevidpvryvsnrssgkmgyaiaealrdkgaivt 233
                                                                                                              LIRTKGSVKAFRIRKIK-LKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEG 296
                                                                                                                                            KIK---SGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKA 353
                                                                                                                                                     2 khillavtggiaaykaidltskligsgydvrvmlsdhaqefvtplafgaisrnpvytntf
                                               MIAPAMHETMYRHPIVRENIERLKKLGVEFIGP------RIEEGRAKVASIDE
                                                                                                                            li--sgpthlslpeginvvkvesaddmfqavte--rfakgdivikaaavsdytpmdileh
                                                                              IVYRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VT
                                                                                                                                                                                                                                                                                                                                   carbohydrate; aromatic compound; cofactor; polyketide; enzyme
                                                                                                                                                                           DLV----VGNTLEAFGSEENQVVLIGRDFTK-ELPKMKKRELAERIWDEIE 399
                                                                                                                                                                                     |:: ||:| | |::|:: | 345 dvissnovgdtsigfssddneltmhfknnekvnikkqkksalahqiieile 395
                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum MP protein sequence SEQ ID NO:626
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                                                                                                                                                                                                                                  AAB79946 standard; Protein; 422
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99DE-1031424.
99DE-1031428.
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99DE-1031634
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08-JUL-1999;
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleocides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases –
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids from Corynebacterium glutamicum encoding metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.2%; Score 444; DB 22; Length 422; 31.7%; Pred. No. 1.3e-34; ive 85; Mismatches 146; Indels 5.
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99DE-1033005.
99DE-1040764.
99DE-1040765.
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Matches 132; Conservative
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N-PSDB; AAF72065.
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27-AUG-1
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                     LIRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGK 297
                                                                                                                                                                                              298 IKSGRS-----ITIELVPXNPKII-DRIK-----EIQPNVFLVGFKAETSKE--KLIEE 343
                                                                                                                                                                                                                        PIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGP---RI----EEGRAKVASIDEIVYRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                 344 GKRQIERAKADLVVGNTL---EAFGSEENQ-VVLIGRDFTKELPKMKKRELAERIWD 396
                                                                                                                                                                                                                                                                                      :::::: ||::| : ||:|| 358 arkklqkkgcdllmcnevgmgkvfgqkhnegwildahggvvdvehgsklevaaqiwd 414
                                                                                   IKKLH-----KKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C glutamicum protein fragment SEQ ID NO: 5274.
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                                                                                                                                                                                                                                                                                                                                                                                AAG91520 standard; Protein; 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum.
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N-PSDB; AAH66739.
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Tateishi N,
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specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                 Gaps
                                                                                                                                                                  75 EI---TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDD--TPVTTVVTTAFPHI 129
                                                                                                                                                                                                                PIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGP---RI---EEGRAKVASIDEIVYRV 183
                                                                                                                                                                                                                                                              184 IKKLH-----KKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VT 237
                                                                                                                                                                                                                                                                                                            238 LIRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGK 297
                                                                                                                                                                                                                                                                                                                          298 IKSGRS-----ITIELVPXNPKII-DRIK-----EIQPNVFLVGFKAETSKE--KLIEE 343
                                                                                                                                                                                                                                                                                                                                                                        19 KKIVXXXPGSIAALDVKACEGLIR----HGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Helicobacter polynucleotides - used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                     :::::: ||::|::||::|| 356 arkklqkkgcdllmcnevgmgkvfgqkhnegwildahggvvdvehgskievaaq1wd 412
                                                                                                                                                                                                                                                                                                                                                                                                       344 GKRQIERAKADLVVGNTL---EAFGSEENQ-VVLIGRDFTKELPKMKKRELAERIWD 396
                                                                                             54;
                                                                     Length 420;
                                                                   Score 439; DB 22; Length 42C
Pred. No. 4e-34;
; Mismatches 147; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                 22.0%; Sco
31.7%; Pre
tive 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW98418 standard; Protein; 228
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97US-0833457.
97US-0881227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori GHPO 319 protein
                                                                              Best Local Similarity 31.78
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                  420 AA;
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N-PSDB; AAX14137
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01-APR-1997;
24-JUN-1997;
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                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW98418;
                                                                       Query Match
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full-length cDNAs

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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of gattic and duodenal ulcers. They can also be detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                       73 ITEITGFIEHVELAGEHEN-------KADLILVCPATANTISKIACGIDDTPVT-T 120
                                                                                                                                                                                                                                                                                                                                                                                             121 VVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPR-----IEEGRAKVA 174
                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                               14 RKLVGKKIVXXXPGSIAAL-DVKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto
                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                        Length 228;
 the diagnosis, prevention and treatment of Helicobacter
                                                                                                                                                                                                                                                     88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K, Y
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 SIDEIVYRVIKKLHKKT-LEGKRVLVTAGATREYIDPIRFITN 216
                                                                                                                                                                                                                      Query Match
9.9%; Score 197; DB 19;
Best Local Similarity 28.3%; Pred. No. 5.6e-11;
Matches 63; Conservative 44; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sogai T, Nishikawa T, Hayashi K,
Sugiyama T, Wakamatsu A, Nagai F
                infections and gastrointestinal diseases
                                        Claim 8; Page 700-701; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein sequence SEQ ID NO:14492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB94179 standard; Protein; 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                                                                                                                                                228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999;
11-JAN-2000;
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                                                                                                                                                                                  Seguence
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5.-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5.-end sequence and an oligonucleotide comprises a 3-end sequence. The complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13613 to AAH13632 to Febreacht human amino acid sequences; and AAH13632 to AAH13632 to Febreacht human amino acid sequences; and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 VITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hantington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 MIAPAMHETMYRHPIVRENIERLKKLG---VEFIGPRI---EEGRAKVASIDEIVYRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |||: |: || : :::|| | : : : :|| :| :| 134 lfcpamntamwehpitaqqvdqlkafgyveipcvakklvcgdeglgamaevgtivdkv 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.3%; Score 166.5; DB 22; Best Local Similarity 28.1%; Pred. No. 4.4e-08; Matches 50; Conservative 30; Mismatches 65;
                                              8; SEQ ID 14492; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention.
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chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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AAY32199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system diseases, such as lateriar solerosis, and Shy-Drager Sydrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activit/inhibin activity, chemotectic/chemokinetic activity, democratic/chemokinetic activity, dand thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 VITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPI 131
                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GSIAALDVKACEGLIRH--GAEVHAVMSEAATKIIHPY------AWNL--PTGNP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 MIAPAMHETMYRHPIVRENIERLKKLG---VEFIGPRI---EEGRAKVASIDEIVYRV 183
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Zhang J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.3%; Score 165.5; DB 22; Length; Best Local Similarity 28.1%; Pred. No. 5.5e-08; Matches 50; Conservative 30; Mismatches 65; Indels
                                                                                                                                                                                                                                  Qian XB,
Yang Y,
                                                                                                                                                                                                                                Chen R, Ma Y, (Xu C, Xue AJ, R, Drmanac RT;
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                                                                                                                                                                                                                             Liu C, Asundi V, Che
Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
25-APR-2000, 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-062312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0653191.

19-CCT-2000; 2000US-069391.

29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                    WPI; 2001-442253/47.
N-PSDB; AAI58626.
                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA;
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                                                                                                                                                                                                                             Tang YT,
Wang J, W
Zhao QA,
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system diseases, such as Albeimer's, Parkinson's disease, Huntingfon's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotexic/chemokinetic activity, demonstric/chemokinetic activity, and thrombolytic activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 165.5; DB 22; Length 309;
ilarity 28.1%; Pred. No. 1e-07;
Conservative 30; Mismatches 65; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F, W.
Zhang J;
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                              21-JAN-2000, 2000US-0488725.
25-APR-2000, 2000US-0552117.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-065312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-OCT-2000; 2000US-0653191.
29-NOV-2000; 2000US-0633036.
                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US34263
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N-PSDB; AAI60412.
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AA;
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C.N.S disorders.
                                                                                                          WO200153312-A1.
                                                        Homo sapiens.
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                                                                                                                                                                   26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
Wang J, W
Zhao QA,
Leukaemia.
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including but not limited to, production disorders, and compositions of the observed and reduction disorders, infertility including tubal disease, ovulatory defects, endometriosis, disruptions of the oestrous and menstrual cycles, polycystic ovary sydrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic pregnancy, teratogenesis, breast cancer, fibrocystic breast disease, galactorrhoea, disruptions of spermatogenesis, abnormal sperm physiology, testis cancer, prostate cancer, benign prostatic hyperplasia, prostatitis, Peyonie's disease, male breast carcinoma and gynecomastia; gastrointestinal disorders including, but are not limited to, dysphagia, peptic oesophagitis, oesophageal spasm and stricture, oesophageal carcinoma, dyspepsia, indigestion, gastritis, gastric carcinoma, anorexia, nausea, emesis, gastroparesis, intestinal stricture, oesophageal carcinoma, dyspepsia, indigessio, discrease, mallory-Weiss syndrome, irritable bowel syndrome, short bowel syndrome, diarrhoea, constipation, cirrhosis, jaundice, and hepatic vein thombosis; nervous cancer and constipation, diarrhoea, constipation, cirrhosis, jaundice, and hepatic vein thombosis; nervous cancer and constipation, diarrhoea, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human receptor molecules used in the diagnosis, treatment and prevention of neoplastic, immunological, reproductive gastrointestinal, nervous, smooth muscle and musculoskeletal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               including muscular dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, inclusion body myositis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amnesia, bipolar disorder, catatonia, cerebral neoplasms, Down's syndrome, and dystonias; smooth muscle cell disorders including, but not limited to, angina, anaphylactic shock, arrhymia, cardiovascular shock, migraine, and pheochromocytoma; musculoskeletal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thyrotoxic myoapathy, and ethanol myopathy; immunological disorders including AIDS, Addison's disease, adult respiratory distress syndrome, allergy, ankylosing spondylitis, amyloidosis, anamemia, asthma, atherosclerosis, autoimmune hemolytic anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human receptor molecule (REC) encoded by Incyte cDNA clone 202379. The invention provides human RECs and polynucleotides which identify and encode REC, as well as vectors, host cells, antibodies, agonists and antagonists. Human vectors, host colls, antibodies, agonists and antagonists. Human reproductive gastrointestinal, nervous, smooth muscle and agonists, and compositions can be used to treat: a reproductive disorder,
                                                                                                                                                                                                                              Receptor; REC; human; diagnosis; therapy; neoplastic disorder; immunological disorder; reproductive disorder; nervous disorder; gastrointestinal disorder; smooth muscle disorder;
                                                                                                                                                                           Human receptor molecule (REC) encoded by Incyte clone 2022379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corley NC;
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AAY32199 standard; Protein; 326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 71-72; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US09191.
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                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                     musculoskeletal disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-052971/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9957270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1999;
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cc emphysema, episodic lymphopenia with lymphocytocoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, costeoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, costeoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogram's systemic syndrome, rheumatoid arthritis, scleroderma, Sjogram's Reiter's syndrome, complications ulcerative colitis, uveitis, werner syndrome, complications of cancer, haemadialysis, and infections; trauma; and neoplastic disorders including adenocarcinoma, infections; trauma; and neoplastic disorders including adenocarcinoma, cleukemia, melanoma, malenoma, and various cancers. The REC polynucleotide is a source of probes and primers which bind may be used to detect REC in a sample from a patient (claimed). They may also be a dministered as part of a gene therapy regime.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin-dependent protein kinase; CDK; CDC2a; CDC2b; Vb89; HAL3; cell cycle; interacting protein; environmental stress; growth regulator; herbicide; nematode resistance; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 VITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GSIAALDVKACEGLIRH--GAEVHAVMSEAATKIIHPY------AWNL--PTGNP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 gsvaalklpllvsklldipglevavvtterakhfyspqdipvtlysdadewemwksrsdp 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding plant cell cycle interacting proteins, useful for regulating plant growth and in recombinant DNA protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 MIAPAMHETMYRHPIVRENIERLKKLG---VEFIGPRI---EEGRAKVASIDEIVYRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%; Score 165.5; DB 21; Length 326; 88.1%; Pred. No. 1.1e-07;
atopic dermatitis, dermatomyositis, diabetes mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. thaliana Vb89 (HAL3) CDC2b interacting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.3%; Score 165.5; I
Best Local Similarity 28.1%; Pred. No. 1.1e-
Matches 50; Conservative' 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Veylder L, Boudolf VKCK,
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N-PSDB; AAA51412.
                                                                                                                                                                                                                                                                                                                                                              326 AA;
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Yamamoto

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The Vb89 clone encodes the Arabidopsis thaliana HAL3 homologue, a halotolerant gene isolated in Saccharomyces cerevisiae. The Vb89 clone interacts with A. thaliana CDC2D (a cyclin-dependent protein kinase (CDC2) and CDC2D are the only CDK genes to have been characterized in decail in Arabidopsis thaliana. They were used as bait in a two-hybrid strening assay with a cDNA library of a plant cell suspension as previous plant a coll cycle interacting proteins identified were designated correcting assay with a cDNA library of a plant cell suspension as previous the protein substant cell suspension as previous vectors comprising them, the proteins they express, antibodies that blind to them and or inhibitors of their protein expression and/or activity may be used for modulating the cell cycle in an animal or plant, plant cell division and/or growth, for influencing the activity of cell cycle proteins in a plant or animal cell, as positive or negative regulators of cell proliferation, for influencing the growth inhibition caused by environmental stress conditions (e.g. to improve growth of plants in normal or suboptimal nutrient conditions, especially phosphorus), for use in a screening method for inhibitors or activators of cell cycle protein, as growth regulators, herbicides and/or for inducting nematode resistance in plants. The DNA sequences and their regulatory sequences may also be used as markers in plant or animal cell and regulatory sequences may also be used for the expression of heterologous DNA sequences during a stage of the cell cycle.
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8.1%; Score 162; DB 21; Length 217; 27.1%; Pred. No. 1.3e-07; Live 33; Mismatches 59; Indels 32 Query Match
Best Local Similarity 27.1
Matches 46; Conservative

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Gaps

32;

-----YAWNLPTGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGID 114 61 11 TKSRKLVGKKIVXXXPGSIAALDVKACEGLIRHGAEVHAVMSEAATKIIHP------DTPVTTVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGP 164 115 62 ò g õ

Human; primer; detection; diagnosis; antisense therapy; gene therapy. Human protein sequence SEQ ID NO:13699. AAB93850 standard; Protein; 284 (first entry) 26-JUN-2001 AAB93850;

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99JP-0300253. 2000JP-0118776. 2000JP-0183767. 2000JP-0241899. 28-JUL-2000; 2000EP-0116126. 99JP-0248036 27-AUG-1999; 11-JAN-2000; 02-MAY-2000; 09-JUN-2000; Homo sapiens EP1074617-A2 29-JUL-1999; 07-FEB-2001

(HELI-) HELIX RES INST

The present invention describes primer sets for synthesising 5602

(ull-length CDNsA defined in the Specification. Where a primer set

(ull-length CDNSA defined in the Specification. Where a primer set

to the complementary strand of a polynucleotide which comprises one of

the \$602 nucleotide sequences defined in the specification, where the

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 3'-end sequence complementary to a

journaleotide which comprises a 3'-end sequence where the

oligonucleotide comprises a 1-end sequence which comprises of

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers and also of the full-length

AB493831 represent human amino acid sequences; AA892446 to

AA8938931 represent human amino acid sequences; and AAH3632

of the present invention. ner sets for synthesizing polynucleotides, particularly the 5602 -length cDNAs defined in the specification, and for the detection or diagnosis of the abnormality of the proteins encoded by the Saito K, Otsuki Claim 8; SEQ ID 13699; 2537pp + CD ROM; English. Isogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K, WPI; 2001-318749/34. full-length cDNAs Ota T, I Ishii S, and/or

284 AA; Sequence

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15;
                                                             160 EFIGPRIEEGRAKVASIDEIVYRVIKKLHKKTLEGKR-VLVTAGATREYID--PIRFITN 216
                                                                                                                                            217 ASSGKMGVALAEE--ADFRGAVTLIRTKGS-----VKAFR----IRKIKLKVE 258
                              78; Gaps
                                                                               ----YDVVIMAA
                                                                                                                                                                                                                  120 aeenalpgfaealrsyqeaaaagtflavefttladylhllqaaaqalnplgpsamfylaa
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26.8%; Pred. No. 3.1e-07;
.ive 43; Mismatches 92; Indels 78
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 Query Match
Best Local Similarity
Matches 78; Conserv
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Arabidopsis thaliana protein fragment SEQ ID NO: 10077

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24 - 70N - 1999;
28 - 70N - 1999;
30 - 70N - 1999;
01 - 70L - 1999;
02 - 70L - 1999;
06 - 70L - 1999;
08 - 70L - 1999;
09 - 70L - 1999;
                                                                                                                                                                                                                                                                                                          04-AUG-1999;
05-AUG-1999;
 rrotein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
                                                                                990S-0121825.
990S-0123180.
99US-0123548.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0127462.
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99US-0129845.
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99US-0132484.
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99US-0137724.
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990S-0135124
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                                Arabidopsis thaliana
                                                                     25-FEB-2000;
                                                                                 25 - FEB - 1999;
05 - MAR - 1999;
23 - MAR - 1999;
25 - MAR - 1999;
01 - APR - 1999;
06 - APR - 1999;
06 - APR - 1999;
16 - APR - 1999;
12 - APR - 1999;
21 - APR - 1999;
21 - APR - 1999;
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28-APR-1999;
30-APR-1999;
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04-MAY-1999;
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07-MAY-1999;
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18-JUN-1999;
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10-JUN-1999;
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21-JUN-1999;
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99US-0149722. 99US-0149723. 99US-0149929. 99US-0149902. 99US-0149930.

3-AUG-1999

990S-0151065. 990S-0151066. 990S-0151080. 990S-0151303.

27-AUG-1999 30-AUG-1999

99US-0148684. 99US-0149368. 99US-0149175. 99US-0149426.

L7-AUG-1999; L8-AUG-1999;

12-AUG-1999; 13-AUG-1999;

.3-AUG-1999

AUG-1999

.0-AUG-1999

AUG-1999

06-AUG-1999

-AUG-1

us-08-957-709-19_1.rag

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                Arabidopsis thaliana protein fragment SEQ ID NO: 10076.
                                                                                                                                             25-FEB-2000; 2000EP-0301439
                17-OCT-2000 (first entry)
                                                                               Arabidopsis thaliana.
                                                                                               EP1033405-A2.
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
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990S - 0152363
990S - 0153163
990S - 0154039
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99US-0153758.
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23-AUG-1999;
25-AUG-1999;
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17-AUG-1999
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Gaps

Indels 44; Length 209;

us-08-957-709-19_1.rag

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The present invention describes the oxidative decarboxylation of a terminus the amino acid sequence (1) with EpiD; X1-X2-X3-X4-X5-X6-C (1) where X1, X2, X3 and X4 = any one of the 20 common amino acids; X5 = verwinus the amino acid sequence (1) with EpiD; X1-X2-X3-X4-X5-X6-C (1) where X1, X2, X3 and X4 = any one of the 20 common amino acids; X5 = ryr, Val, Met, Phe, IIe, Leu or Trp; and X6 = Cys, Ala, Ser, Val or Thr C (2) responding that the carboxy terminus of the peptide is not sequence compounds to the preparation of derivatives of known peptides and hormones with a cystelne residue in the unmodified peptide replaced or supplied experimental purposes or for the formation of novel compounds for experimental purposes or for the formation of known compounds for experimental purposes or for the formation of known compounds for experimental purposes or for the formation of known compounds for experimental purposes or for the formation of known compounds for experimental purposes or for the formation of known compounds for experimental purposes or for the formation of known compounds for experimental purposes or for the formation of known compounds for experimental minion and acid residues and/or and also be analyor and also be analyor and also be achieved using this method retain the biological activity of the parent compound but we have increased stability and improved half-lives. Ant/43418 to AA443475, of the present invention.
                                                                                                                                                                             Staphylococcus epidermis; epidermin; epiA; epiB; epiD; epiP; epiQ; epiY'; epiY''; oxidative carboxylation; flavoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidative decarboxylation of peptides by the flavoprotein EpiD
                                                                                                                                       S. epidermis reading frame epiD protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                         (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
               AAY43439
ID AAY43439 standard; Protein; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 9; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                             96US-0645193.
                                                                                                                                                                                                                                                                                                                                                                            96US-0645193.
                                                                                                                                                                                                                                  Staphylococcus epidermis.
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                                                                    AAY43439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
  14
RESULT
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6
                                                                   16 LVGKKIVXXXPGSIAALDVK-ACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
7.6%: Score 151.5; DB 20; Length 181;
29.5%: Pred. No. 1.1e-06;
Live 37; Mismatches 76; Indels 21;
      Local Similarity 29.5
Query Match
        Best Loca
Matches
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7;
               ---RIEEGRAK----VASIDEIVYRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of EpiD which is involved with EpiB and EpiC in the four enzymatic modification reactions involved in the product of epidermin, (1) water elimination by a serincy/threonine dehydratase, (2) sulphur addition by a lanthionine synchase, (3) C-terminal decarboxylation by a cysteine decarboxylase and (4) double bond formation.
                                                                                                                                                                                                                                                                                                                                                                                  K, Gotz F, Jung G, Kaletta C;
Rosenstein R, Schnell N, Wieland B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 CPATANTISKIACGIDDTPVTTVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 LIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITEITG-FIEHVELAGEHENKADLILV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 lkqhfdevnilfspssknfintdvlklfcdn-lydelkdpllnhinivenhe----yilv. 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%: Score 149.5; DB 14; Length 181; 30.9%; Pred. No. 1.7e-06; .ive 31; Mismatches 64; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D, P or Q epidermin.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA molecule - encoding Epi B, C, involved in biosynthesis of lantibiotic
134 APAMHETMYRHPIVRENIERLKKLGVEFIGP-
                                                                                                   RESULT 15
AAR39345
ID AAR39345 standard; Protein; 181 AA.
                                                                                                                                                                                                                  Epidermin; derivatives; lantibiotic.
                                                                                                                                                                                                                                                                                                                                                                              Augustin J, Engelke G, Entian
Klein C, Kellner R, Kupke T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Fig 9; 52pp; English.
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                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                       (THOM ) THOMAE GMBH KARL.
                                                                                                                                                                                                                                         Staphylococcus epidermis.
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                                            184 IKKLHKKTLE 193
                                                                 173 inn-ekrpid 181
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N-PSDB; AAQ42541.
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                                                                                                                                                                      15-SEP-1993
                                                                                                                                                                                            EpiD protein
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Search completed: January 31, 2002, 13:07:05

159 VEFIGP-----RIEEGRAK----VASIDEIVYRVIKKLHKKTLE 193

δy

Job time: 57 sec

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January 31, 2002, 13:07:08; Search time 19.24 Seconds (without alignments) 471.353 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-08-957-709-19 1998 1 MLHHVKLIYATKSRKLVGKK......KMKKRELAERIWDEIEKXLS 403 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

212252 seqs, 22503292 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 19, Appl	51,	52,	24,	22,	22,	46,	6, 2	48,	4, 7	4	'n	'n	m	ω,	'n	Sequence 11, Appl	11,	o,	Sequence 11, Appl	8	4	7	o,	35,	35,	
SUMMARIES	ID	US-08-822-774-19	US-08-822-774-51	US-08-822-774-52	US-08-645-193B-24	-08-392-625-2	US-08-466-961A-22	US-08-822-774-46	US-08-822-774-6	US-08-822-774-48	US-08-460-309-4	US-08-125-077-4	US-08-822-774-3	US-08-317-223-3	US-09-059-849A-3	US-09-213-632-3	PCT-US95-12675-3	US-07-814-964-11	US-08-258-442-11	US-08-328-809-6	PCT-US92-11107-11	US-08-973-462-8	US-08-445-135-4	US-09-091-117-2	US-08-973-462-9	US-08-467-822-35	US-08-432-697-35	US-08-466-248-35
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	US/08822774 Holly Holly Extracts, PEF Protein Complexes, Ise and Methods for Purifying and Ident, 61 S. Kulik, Evenson, McKeown, Edwards, P.L.L.C. eet, N.W. Suite 700 eet, N.W. Suite 700 Release #1.0, Version #1.25 ATS ATS ATS ATS ATION: 3 86,576 MBER: 1486/43163 ATION: 3 36,576 MBER: 1486/43163 ATION: 1 36,576 ATION: 1 36,576 ATION: 1 36,576 ATION: 1 19: 1 19: 1 10: 1	••
ω .	g Fact if ying McKeow	DB 4; 3.5e-181 les 0;
ALIGNMENTS	US/08822774 Holly Polymerase Enhancing Factc Extracts, PEF Protein Compand Methods for Purifying S: Kulik, Evenson, McKeowr P.L.C.C. eet, N.W. Suite 700 M: Y disk Ompatible PC-DoS/MS-DOS Release #1.0, Version #1. ATATA: US/08/822,774 R-1997 ATION: J. 36,576 MBER: 1486/43163 ORMATION: J. 36,576 MBER: 1486/43163 ORMATION: LES: ACION: J. 105: ACION: LES: ACION: ACION	ore 1988; red. No. 3. Mismatches
ALIC	122-774-19 nce 19, Application US/08822774 t No. 6183927 t No. 618392 TLE OF INVENTION: Extracts, PEF Pro TLE OF INVENTION: Extracts, PEF Pro TLE OF INVENTION: Extracts, PEF Pro TLE OF INVENTION: Extracts, PLC. C. TLE OF INVENTION: Extracts, PLC. C. STRESPONDENCE ADDRESS: 61 RRESPONDENCE PORM: MEDURE READABLE FORM: RRESPERICATION DATA: APPLICATION DATA: APPLICATION NAMER: US/08/822,774 REGISTRATION NUMBER: 1486/43163 RECORNEY/AGENT INFORMATION: TELEPHONE: (202) 628-8800 TELEFRAX: (202) 628-8800	SG .
	1 1 22-774-19 nce 19, Application US/08822774 RAL INFORMATION: PLICANT: HOGREE, Holly TLE OF INVENTION: Extracts, PEF TLE OF INVENTION P. L. L. C. STREET: 1200 G Street, N.W. Sui TLE PROMPTER: IBM PC compatible OPPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAPLICATION NUMBER: US/08/822,7 TELEFAX: (202) 628-8840 TREISTRATION NUMBER: 136,576 TELEFAX: (202) 628-8840 TREISTRATION NUMBER: 36,576	99.5%; 100.0%; ive 0
	lication US/088 97 OGREFE, Holly NTION: Dolymer NTION: Extract Lenahan, P.L.L. 00 G Street, N. ington Ingt	vat
	122-774-19 nnce 19, Application US/06 RAL INFORMATION: FLICANT: HOGREFE, HOlly TLE OF INVENTION: Extract MADRESSEE: Lenahan, P.L. STRAFF: 1200 G Street, P.L. STRAFF: 1200 G Street, P.L. STRATE: D.C. STRAFF: D.C. STRAFF: D.C. STRAFF: D.C. COMPUTER: ENDANCE: PC-DOS SOFTWARE: Floppy dis) COMPUTER: ISPM C COMPATA: MEDIUM TYPE: Floppy dis) COMPUTER: ISPM C COMPATA: MEDIUM TYPE: Floppy dis) COMPUTER: ISPM C COMPATA: MEDIUM TYPE: PLOPPY dis) CLENGTICATION NUMBER: US/C SOFTWARE: ATTORN NUMBER: US/C CLASSIFCATION: 436 CLASSIFCATION NUMBER: US/C CANDATION NUMBER: US/C COMPUTED NUMBER: US/C	99. larity 100 Conservative
	122-774-19 nnce 19 Applit No. 6183997 TELE OF INVENT TLE OF INVENT TLE OF INVENT TLE OF INVENT THE O	Simi 3;
	SULT 1 -08-822-774-19 Sequence 19, Application US/08822774 Sequence 19, Application US/08822774 Sequence 19, Application US/08822774 BAPLICANT: HOGREFE, Holly TITLE OF INVENTION: BALTACKS, PE TITLE OF INVENTION: and Methods NUMBER OF SEQUENCES: 61 CORRESPONDENCE ADDRESS: ADDRESSE: Lenahan, P.L.L.C. STREET: 1200 G Street, N.W. Su CITY: Washington STATE: D.C. ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: PATCHIN DATA: APPLICATION NUMBER: US/08/822, FILING DATE: 21 MAR-1997 CLASSIFICATION: 436 ATTORNEY/AGENT INFORMATION: NAME: KULLK, DAVId J. REGISTRATION NUMBER: 36,576	
	RESULT 1 US-08-822-774-19 Sequence 19, A Sequence 19, A Fatent No. 618 APPLICANT: TITLE OF IN TITLE TITLE OF IN TITLE TITLE OF IN TITLE OF IN TITLE TITLE OF IN TITLE T	Query Ma Best Loca Matches

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APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005
                                                                                                                                                                                  DTPVTTVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLK-KLGVEFIGPRIEE---- 168
                                                                                                                                                                                                        -GRAKVASIDEIVYRVIKKL-HKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVAL 226
                                                                                                                                                                                                                                                                        363 KELINRAKERLNKYNLNMIIANDLSKXXHYFGDDYIEVYIITKYEVEKISGSKKXEISER 422
                                                                                                                  60 HPYAWNLPTGNPVITEITGF-----IEHVELAGEHENKADLILVCPATANTISKIACGID 114
                                                                                                                                       65 GKEALKFGCGNEVYEEITGXXXXXDIEHILLYXXXXNECDCLLIYPATANIISKINLGIA 124
                                                                                                                                                                                                                                                                                                                    AEEADFRG-AVTLIRTKGSVKAFRIRKIKLKVETVEEMLS-AIENELRSKKYDVVIMAAA 284
                                                                                                                                                                                                                                                                                                                                                                                    VSDFRPKIKAEGKIKS----GRSITIELVPXNPKIIDRIKEIQPNV-FLVGFKAE--TSK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKLIEEGKRQIERAKADLVVGNTLEA----FGSEENQVVLIGRDFTKELPKMKKRELAER 393
                 29; Gaps
                                                1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAALDV-KACEGLIRHGAEVHAVMSEAATKII 59
                                                                     Pred. No. 2.3e-52;
; Mismatches 153; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATA
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 21-MR*1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David 36,576
RESTERENCE/DOCKET UNMER: 1486/43163
TELEFANION NUMBER: 36,576
TELEFANION NUMBER: 36,576
TELEFANION NUMBER: 36,576
TELEFANION FOR $20 ID NO: 52:
SEQUENCE CLARACTERISTICS:
LENGTH: 444 ARACTERISTICS:
LENGTH: 444 ARACTERISTICS:
LENGTH: 444 ARACTERISTICS:
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llarity 37.9%; Pri
Conservative 83;
 Best Local Similarity
Matches 162; Conserv
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423 IVEKVKK 429
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Patent No. 6183997

GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Extracts, PEFF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: ADDRESSE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005
                                                                                                                                             VVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIV 180
                                                                                                                                                                                                                 TKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 635.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRELATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLEASIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULLEY, David J.
REGISTRATION NUMBER: 1486/43163
TELEFORMUNICATION INFORMATION:
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acids
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococcus Jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM:
US-08-822-774-51
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US-08-822-774-51

    Query Match

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STREET: 1100 New CITY: Washington
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173 LNN-EKRPLD 181
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: U.S.A.
                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 56; Conserv
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                                                                                                                                                                                                              US-08-645-193B-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                               239 IRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 VSGPVSLPTPPFVK-RVDVMTALEMEAAVNXXASVQQQNIFIGCAAVADYRAATVAPEKI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K----SGRSITIELVPXNPKI---IDRIKEIQPNVFLVGFKAETSK-EKLIEEGKRQIE- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :||::||||| : :|::|| :|| || || 324 KKQATQGDELTIKMVKXNPDIVAGVAALKDHRP--YVVGFAAFTNNXXXXVEFYARQKRI 381
                                                                                                                                                                                                                                                                                                                              75 EI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHI 129
                                                                                                                                                                                                                                                                                                                                                                                                         130 PIMIAPAMHETMYRHPIVRENIERL-KKLGVEFIGPRIEEGRAKVASI-----DEIVYR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 VIKKLH---KKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 DMAVAHFSPVNDLKHLNIMITAGPTREPLDPVRYISNHSSGKMGFAIAAAAARRGANVTL 264
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                           16 LVGKKIVXXXPGSIAALDVKACEGLIR-HGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 RAKADLVVGNTL----EAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kupke, Thomas
APPLICANT: Gotz, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: TBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,193B
FILING DATE: 13-MAY-1996
                                                                                                                                                                      21.9%; Score 438.5; DB 4; 32.9%; Pred. No. 1.3e-33; tive 70; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08645193B Patent No. 5962253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W.
                                                                                                                                                                                                              Conservative
            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, K
unknown
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 136; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
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                                                                        ORIGINAL SOURCE:
                                                      ANTI-SENSE: NO
                              HYPOTHETICAL:
                                                                                           ; ORGANISM:
US-08-822-774-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-645-193B-24
TOPOLOGY:
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75 EITG-FIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPIMI 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       16 LVGKKIVXXXPGSIAALDVK-ACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
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                                                                                                                                                                                                                                                                                                       Length 181;
                                                                                                                                                                                                                                                                                                         7.6%; Score 151.5; DB 2; 29.5%; Pred. No. 7.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue
REFERENCE/DOCKET NUMBER: 0652.1540000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                    37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kellner, Roland
TITLE OF INVENTION: Blosynthetic Process F
TITLE OF INVENTION: Of Chemical Compounds
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entian, Karl-Dieter
G tz, Friedrich
Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/392,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Kaletta, Cortina
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Kupke, Thomas
                                                                                                                                                                      TOPOLOGY: single TOPOLOGY: not relevant MOLECULE TYPE: protein 1-645-193p-3
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, K
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WBER: US 07/876,791
30-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 CPATANTISKIACGIDDTPVTTVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLG 158
                                                                                                                                                                                                                                                                                                                                                                                                 40 LIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITEITG-FIEHVELAGEHENKADLILV 98
                                                                                                                                                                                                                                                                                                                                                                                                                              25 LKQHFDEVNILFSPSSKNFINTDVLKLFCDN-LYDEIKDPLLNHINIVENHE----YILV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wieland, Bernd
APPLICANT: Wieland, Bernd
APPLICANT: Wieland, Chinas
APPLICANT: Jung, G nther
APPLICANT: Jung, G nther
TITLE OF INVENTION: Blosynthetic Process for the Preparation of
TITLE OF INVENTION: Chamical Compounds
NUMBER OF SEQUENCES: 48
ADDRESSE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, NW
STATE: Reabilington
                                                                                                                                                                                                                                                                                                                                                            64; Indels 19;
                                                                                                                                                                                                                                                                                                                    Ouery Match 7.5%; Score 149.5; DB 2; Length 181; Best Local Similarity 30.9%; Pred: No. 1.1e-06; Matches 51; Conservative 31; Mismatches 64; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 VEFIGP-----RIEEGRAK----VASIDEIVYRVIKKLHKKTLE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,625
FILING DATE: 22-FEB 1995
PRIOR APPLICATION DATA:
                                                                                   0652.0980002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Entian, Karl-Dieter
G tz, Friedrich
Schnell, No. 5843709bert
Augustin, Johannes
Engelke, Germar
Rosenstein, Ralf
Kaletta, Cortina
Klein, Cora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08466961A Patent No. 5843709 GENERAL INFORMATION:
FILING DATE: 30-APR-1992

HATCAREY FAGENY INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.
FELECOMMUNICATION INFORMATION:
FELEPAX: (202) 371-260
FELEFAX: (202) 371-250
FELEFAX: ENGRATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERSTICS:
LENGTH: 181 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: 1050-22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-466-961A-22
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Sequence 46, Application US/08822774
Patent No. 61839397
TERENT INCORMATION:
APPLICANT: HGGREFE, Holly
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
STATE: D.C.
STATE: D.C.
STREET: 1200 G Street, N.W. Suite 700
STATE: D.C.
STATE: D.C.
STREET: P.C.
STREET: STATE: D.C.
STREET: STATE: STATE: STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 LIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITEITG-FIEHVELAGEHENKADLILV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 LKQHFDEVNILFSPSSKNFINTDVLKLFCDN-LYDEIKDPLLNHINIVENHE----YILV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.5%; Score 149.5; DB 2; Length 181; Best Local Similarity 30.9%; Pred. No. 1.1e-06; Matches 51; Conservative 31; Mismatches 64; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 VEFIGP-----RIEEGRAK----VASIDEIVYRVIKKLHKKTLE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: US/08/822,774
FILING DATE: US/08/822,774
ATONNEY/AGENT INFORMATION:
NAME: KULKK, DAVIG J.
RECISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163.
TELECOMMUNICATION:
FILING DATE: 30-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUBBER: US 07/784,234
FILING DATE: 31-OCT-1991
ATTOKNEY/ABCHT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 0652.0980004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 46:
SEGUINCE CHARACTERISTICS:
LENGTH: 31 amino acids
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amino acid
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APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
CORRESPONDENCE ADDRESS:
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APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C. STREET: 1200 G Street, N.W. Suite 700 CITY: Washington STATE: D.C. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.8%; Score 116; DB 4; Length 24; Best Local Similarity 100.0%; Pred. No. 8.6e-05; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHAX: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                         ; Sequence 48, Application US/08822774
; Patent No. 6183997
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 ADLVVGNTLEAFGSEENQVVLIGR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-460-309-4; Sequence 4, Application US/08460309; Patent No. 5837496
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                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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STRANDEDNESS: unl
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US-08-822-774-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PBF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same
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                                                                                                                                                                                                                Score 135; DB 4; Length 31;
Pred. No. 2e-06;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards
ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYZEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 8.6e-05; tive 0; Mismatches 0;
                                                                                                                                                                                                  6.8%; Scort
100.0%; Pred. No. 2c.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KOLIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8844
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAA 31
                                                                                                                                                                                                                                                                                                                              1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAA 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08822774
Patent No. 6183997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ADLVVGNTLEAFGSEENQVVLIGR 24
                                                                                                    ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-08-822-774-46
                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 31; Conservative
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Best Local Similarity 100.
Matches 24; Conservative
                      unknown
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                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
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TOPOLOGY: unknown
TYPE: amino acid
                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 120
CITY: Washi
STATE: D.C.
ZIP: 20005
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US-08-822-774-6
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1656 TK------VTADGEQTGQDAERTNTRAKSLGEFIKELARDAEAVNEKAIKLNE 1702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 KAEGKIKS---GRSITIELVPXNPKI------IDRIKEIQPNVFLVGFKAETSKEK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 PAMHETMYRHPIVRENI-ERLKKLGVEFIGP-----RIEEGRAK--VASIDEIVYRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKY------DVVIMAAAVSDFRPKI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.3%; Score 105; DB 2; Length 3111; Best Local Similarity '23.3%; Pred. No. 1.4; No. 1.4; Conservative 48; Mismatches 109; Indels 86; Gaps Matches 14; Conservative 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 ---LIEEGKRQIERAKADLVVGNTL----EAFGSEENQVVLIGRDFTKELPKM-----
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Filer, compatible COMPUTER: IBM PC Compatible OPERATUR SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: 05/08/125,077 FILING DATE: 22-SEP-1993
CLASSIFICATION NUMBER: US PCT/US 94/10730 FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US 94/10730 FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319 FILING DATE: 31-SEP-1994
PRIOR APPLICATION NUMBER: US 07/919,951 FILING DATE: 27-JUL-1992
PRIOR APPLICATION NUMBER: US 07/919,951 FILING DATE: 27-JUL-1992
PRIOR APPLICATION NUMBER: US 07/919,951 FILING DATE: 27-JUL-1992
ATTORNEY/GENT INCORMATION: NUMBER: Campbell, Cathryn A. REFERENCE/DOCKET NUMBER: P-LA 9721
TELEPHONE: (619) 535-9001
TYPE: amino acids

       NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1 0
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US-08-822-774-3
; Sequence 3, Application US/08822774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1703 TLGT----RDEAFERNLEGLQKEIDQMIKELRRKNLETQKEIAEDELVAAEALLKKVKKL 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 IKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASS-GKMGVALAEEADF--RGAVTLIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 KAEGKIKS---GRSITIELVPXNPKI-----IDRIKEIQPNVFLVGFKAETSKEK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 PAMHETMYRHPIVRENI-ERLKKLGVEFIGP-----RIEEGRAK--VASIDEIVYRV 183
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TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 3111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
5.3%; Score 105; DB 2; Length 311
Best Local Similarity 23.3%; Pred. No. 1.4; 109; Indels
Matches 74; Conservative 48; Mismatches 109; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
                                                                                                                                                                                                       FILING DATE:

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/125,077

FILING DATE: 22-5EP-1993

APPLICATION NUMBER: US PCT/US 94/10730

FILING DATE: 21-5EP-1994

APPLICATION NUMBER: US 07/472,319

FILING DATE: 30-7AN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/919,951

FILING DATE: 27-UL-1992

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,815

REGISTRATION NUMBER: 31,815

REGISTRATION NUMBER: 31,815

RECISTRATION NUMBER: 31,815

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

SEQUENCE CHARATICES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1875 IDDLSQEIKDRKLAEKV 1891
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08-125-077-4
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222 MGVALAEEADF--RGAVTLIRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKY--- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 FIKELARDAEAVNEKAIKLNETLGT----RDEAFERNLEGLQKEIDQMIKELRRKNLETQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 RIEEGRAK--VASIDEIVYRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASS-GK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 IKEIQPNVFLVGFKAETSKEK---LIEEGKRQIERAKADLVVGNTL----EAFGSEENQV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DVVIMAAAVSDFRPKIKAEGKIKS---GRSITIELVPXNPKI------IDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CELLULAR ATTACHMENT TO LAMININ 5-COATED TITLE OF INVENTION: TRANS-EPITHELIAL APPLIANCES NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 VLIGRDFTKELPKM------KKRELAERI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | :|||:
236 IDYVEDIQTKLPPMSEELNDKIDDLSQEIKDRKLAEKV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%; Score 102.5; DB 23.4%; Pred. No. 0.085;
                                                                                                   PULGATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/042,727
FILING DATE: 05-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/151,134
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,460
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: DESMOS.002CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ 1D NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09059849A
Patent No. 6034068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craig Halberstadt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE: CLONF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 337 amino aci
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                         CLASSIFICATION: 435
                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 65; Conserv
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APPLICANT: Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
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                                                           Polymerase Enhancing Factor (PEF)
Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CELLULAR ATTACHMENT TO TRANS-EPITHELIAL TITLE OF INVENTION: APPLIANCES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104; DB 4; Length 35; Pred. No. 0.0021;
                                                                                                                                                                              Evenson, McKeown, Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-WAR-1997
CLASSIFICATION: 436
ATTORNEY FAGENT INFORMATION:
NAME: KULIK, DAVIG J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKER NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ DI NO: 3:
SEQUENCE CHARCTERISTICS:
                                                                                                                          NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, MADRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.2%; Score 104; 70.0%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LLHHVKLIYATKXRXLVGKXIVLAIPGXXA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5885267
GENERAL INFORMATION:
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
APPLICANT: Tammura, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 70.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                     APPLICANT: HOGREFE, E
TITLE OF INVENTION: F
TITLE OF INVENTION: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-317-223-3
                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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us-08-957-709-19_1.rai

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222 MGVALABERADF---RGAVTLIRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKY--- 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 -----DVVIMAAAVSDFRPKIKAEGKIKS---GRSITIELVPXNPKI------IDR 318
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5.1%; Score 102.5; DB 3; Length 3
Best Local Similarity 23.4%; Pred. No. 0.085;
Matches 65; Conservative 42; Mismatches 102; Indels
                                                                                                                                                                                                               ZIP: 92660
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IND PC COMPATIBLE
OPERATING SYSTEM: PC DOGNAG-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,632
CLASSIFICATION DATA:
FLING DATE: 12-NOV-1993
FILING DATE: 13-NOV-1993
FILING DATE: 12-NOV-1993
FILING DATE: 13-NOV-1993
FILING DATE: 13-NOV-199
                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
CONTRY: USA
COUNTRY: USA
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :|| | : || |: INDLSQEIKDRKLAEKV 273
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FRAGMENT TYPE: int
IMMEDIATE SOURCE:
CLONE: merosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 FIKELARDAEAVNEKAIKLNETLGT----RDEAFERNLEGLQKEIDQMIKELRRKNLETQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 -----DVVIMAAAVSDFRPKIKAEGKIKS---GRSITIELVPXNPKI------IDR 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 IKEIQPNVFLVGFKABTSKEK---LIEBGKRQIERAKADLVVGNTL----EAFGSEENQV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.1%; Score 102.5; DB 3; Length 337; Best Local Similarity 23.4%; Pred. No. 0.085; Matches 65; Conservative 42; Mismatches 102; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
3C-09-213-33-3
$ Sequence 3, Application US/09213632
$ Sequence 8. Application US/09213632
$ Patent No. 6110711
$ FAPPLICANT: Jones, Jonathan C.R. APPLICANT: Jonashar Vito
$ APPLICANT: Tamura, Richard
$ APPLICANT: Tamura, Richard
$ TITLE OF INVENTION: CELLULAR ATTACHMENT TO TRANS-EPITHELIAL
$ TITLE OF INVENTION: APPLIANCES
                                                                  ZOUNTIL 0.SA
ZIP: 92660
ZIP: 92660
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/059,849A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 VLIGRDFTKELPKM--------KKRELAERI 394
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                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NOMBER:
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Istaelsen, Ned A.
REGISTRATION NUMBER: 29, 655
FELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 3:
FELECOMMUNICATION NO: 323-0176
INFORMATION FOR SEQ ID NO: 3:
LENGTH: 337 amino acids
STRANDEDNESS: single
MODECULE TYPE: peptide
ANTI-SENSE: NO
FRAGMENT TYPE: internal
MODECULE TYPE: peptide
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: mercain
US-09-059-849A-3
Newport Beach
                                                    USA
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Search completed: January 31, 2002, 13:07:51 Job time: 43 sec

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H. pylori ORP 05ae H. pylori ORP 05ae Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

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Polymerase enhanci Polymerase enhanci Signal transductio Pyruvate dehydogen S. pneumoniae prot

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Peptide #1311 enco
Peptide #1314 enco
Peptide #134 enco
Peptide #138 enco
Peptide #1286 enco
Peptide #1286 enco
Arabidopsis thalia
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Arabidopsis thalia
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DNA replication an Chlamydia pneumoni

Human polypeptide Human polypeptide

Cell cycle regulat Arabidopsis thalia

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/note= "N-terminal peptide used to generate
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/note= "internal peptide used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase enhancing factor; PEF; DNA polymerase; PCR;
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    primers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by NNN"
Misc-difference 25
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AAW72862
AAB92176
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AAG36085
AAG36084
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AAM14877
AAM27306
AAM27309
AAM27309
AAM02602
AAM02604
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AAG46240
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AAM42119
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AAY35142
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AAY11301
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AAE04541
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23
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1 MLHHVKLIYATKSRKLVGKK......KMKKRELAERIWDEIEKXLS 403
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                       January 31, 2002, 13:18:02
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AAW72863
AAW72843
AAW72842
AAW72860
AAW72866
AAW72865
AAW72865
                                                                                                  protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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and is derived by
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Pred. No.

Score

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361 LEAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXLS
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AAW72841
ID AAW7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the P50 component of the polymerase enhaning factor (PEF) of Pyrococcus furiosus DSM 3638.

The sequence is predicted from a DNA sequence (see AAV63859) obtained from genomic DNA by PCR. P50 and P45 (see AAW72847) are the predominant components of PEF, which acts to enhance the activity of predominant components of PEF, which acts to enhance the activity of P. furiosus DNA polymerase, thereby providing replication products of greater length and purity. P50 is similar in structure to a parterial flavoprotein. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies raised against P45 or P50. Also included are methods for identifying compositions with polymerase enhancing activity, for proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase reactions can be enhanced (claimed) by composition having polymerase enhancing activity. Kits are provided for replicating nucleic acid template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replication nucleic acid sequencing or amplification sylendiance. Site-directed mutagenesis, nucleic acid sequencing or amplification controlled acid sequencing or amplification controlled.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAALDVKACEGLIRHGAEVHAVMSEAATKIIH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 46; Page 36; 161pp; English.
                                                                                                                                                                           98WO-US05497.
                                                                                                                                                                                                                               97US-0957709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.8 Matches 402; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-542284/46.
N-PSDB; AAV63859.
                                                                                                                                                                                                                                                                                                                                                                                            Hansen CJ, Hogrefe
                                                                                                                                                                                                                                                                                                                                 (STRA-) STRATAGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 AA;
                                                    WO9842860-A1
                                                                                                                                                                                                                                   24-OCT-1997;
21-MAR-1997;
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YRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGAVTLIR 240

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q ò Q 301 GRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADLVVGNT 360

241 TKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKS 300

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This peptide comprises the N-terminal portion of the P50 component of the polymerase enhancing factor (PEF) of procedus furiosus furiosus of isolated P50 bNA (ase AAV0589) and corresponds to a chemically determined N-terminal peptide (see AAW07800). PEF, the predominant components of which are P50 and P45 (see AAW07807) proteins, enhances the activity of P furiosus DNA polymerase, thereby providing replication products of greater length and purity. The invention replication products of greater length and purity. The invention provides novel extracts, proteins and complexes that improve the provides novel extracts, proteins and complexes that improve the provides novel extracts, proteins and complexes that improve the provides any included are methods for identifying compositions of peptide. Also included are methods for identifying compositions and specific extracts, proteins and complexes that function to enhance polymerase activity. Nowlels acid of polymerase compositions, and specific extracts, proteins and complexes that function to enhanced (claimed) by mixing a nucleic acid compact cape activity. Kits are provided for replicating nucleic acid acids. The Kits can be used in site-directed mutagenesis, nucleic acid acids. The Kits can be used in site-directed mutagenesis, nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase enhancing factor proteins, extracts and complexes - improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication
                                                                                                                                                                                                                       Polymerase enhancing factor P50 component N-terminal peptide.
                                                                                                                                                                                                                                                        Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication.
/note= "unidentified amino acid"
Misc-difference 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                         /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                    Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 91; 161pp; English.
                                                                                                         AAW72841 standard; Peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US05497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0957709.
97US-0822774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRA-) STRATAGENE.
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 23
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21-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is a tryptic peptide of the P50 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. It was obtained by tryptic digestion of P50 protein isolated from a PEF complex. PEF, the predominant components of which are P50 (see AAW72844) and P45 (see AAW72847), enhances the activity of P. furiosus DNA polymerase. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These can be used to improve nucleic acid polymerases. These can be used to improve nucleic acid polymerases.
                                                                                                        Gaps
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improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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by any amino acid but is tentatively
assigned as indicated"
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                                                           Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                       Polymerase enhancing factor P50 component tryptic peptide.
                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhancing factor; PEF; DNA polymerase; PCR;
                                                           28; DB 19; I
No. 5.4e-21;
                                              6.9%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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amplification; sequencing; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus furiosus strain DSM 3638.
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                                                                                                                                                                                                                                                                                             AAW72863 standard; Peptide; 24 AA
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                                                                                                   31; Conservative
                                                                                 Similarity
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31
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21-MAR-1997;
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Sequence
                                                                                                                                                                                                                                                                                                                                     AAW72863;
                                                           Query Match
Best Local
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                                                                                                     Matches
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This peptide comprises an internal peptide of the P50 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. It is obtained from the translated sequence (see AAM7284) of isolated P50 DNA (see AAM72859) and corresponds to a chemically determined N-terminal peptide (see AAM72862). PEF, the predominant components of which are P50 and P45 (see AAM72847) proteins, enhances the activity of P. furiosus DNA polymerase, thereby providing replication products of greater length and purity. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These complexes may include proteins including the P50 internal peptide. Also included are methods for identifying compositions with polymerase enhancing activity, for purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase reactions can be enhanced (claimed) by maxing a nucleic acid cenhancing activity. Kits are provided for replication nucleic ending activity. Kits are provided for replicating nucleic acid cenhancing activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 Polymerase enhancing factor P50 component internal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus furiosus strain DSM 3638.
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1 adlvvgntleafgseenqvvligr
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                                                                                                                                                                                       AAW72843 standard; Peptide;
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Matches 24; Conserv
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Best Local Similarity 100. Matches 24; Conservative

Query Match

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Gaps

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0; Indels

Score 24; DB 19; Length 24; Pred. No. 5.1e-17;

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/note= "this residue may be deleted or substituted
by any amino acid but is tentatively
assigned as indicated"

Location/Qualifiers

(first entry)

"this residue may be deleted or substituted by any amino acid but is tentatively assigned as indicated"

"this residue may be deleted or substituted by any amino acid but is tentatively assigned as indicated"

"this residue may be deleted or substituted by any amino acid but is tentatively assigned as indicated"

"any amino acid"

/note=

"these residues may each be deleted or substituted by any amino acid but are tentatively assigned as indicated"

97US-0957709. 97US-0822774. 98WO-US05497.

Hogrefe H;

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Misc-difference 14
/note= "this residue may be deleted or substituted
by any amino acid but is tentatively
assigned as indicated"
                                                                Polymerase enhancing factor P50 component N•terminal peptide.
                                                                                                Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication.
                                                                                                                                               Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
Misc-difference 30
                                                                                                                                                                                                                                                                                                                             Misc-difference 16 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 29
                                                                                                                                                                               Key
Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1998;
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21-MAR-1997;
                                 01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hansen CJ,
 AAW72860
   of the polymerase enhancing factor (PEF) of pyrooccus furiosus of the polymerase enhancing factor (PEF) of pyrooccus furiosus of the polymerase enhancing factor (PEF) of pyrooccus furiosus of isolated P50 DNA (see AAV63859) and corresponds to a chemically deternihed betained from the translated sequence (see AAW73844) cof isolated P50 DNA (see AAW63859) and corresponds to a chemically deternihed Neternihal peptide (see AAW73847) proteins, enhances to exploration products of greater length and purity. The invention provides novel extracts, proteins and complexes that improve the provides novel extracts, proteins and complexes that improve the provides novel extracts, proteins and complexes that improve the provides are methods for identifying compositions with polymerase enhancing activity. For purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase crivity. Nucleic acid polymerase crivity. Rucleic acid polymerase crivity. Any expectation and complexes that function to enhanced (claimed) by mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acid acids. The kits can be used in site-directed mutagenesis, nucleic acid acids activity. The service of acids of acids or acids o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                              Polymerase enhancing factor P50 component internal peptide.
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                                                                                                                                                              Polymerase enhancing factor; PEF; DNA polymerase; PCR; smplification; sequencing; replication.
                                                                                                                                                                                                               Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 91; 161pp; English.
                              AAW72842 standard; Peptide; 17 AA.
                                                                                                                                                                                                                                                                                                            98WO-US05497.
                                                                                                                                                                                                                                                                                                                                          97US-0957709
97US-0822774
                                                                                                (first entry)
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Hansen CJ, Hogrefe H;
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                                                                                                                                                                                                                                                                                                                                                                                         (STRA-) STRATAGENE.
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21-MAR-1997;
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                                                            AAW72842;
RESULT
AAW72842
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This is an N-terminal peptide of the P50 component of the polymerase enhancing factor (PBF) of Pyrococcus furiosus DSM 3638. It was obtained by N-terminal sequencing of P50 isolated from a PEF complex. PEF, the predominant components of which are P50 (see AAW72844) and P45 (see AAW72847), enhances the activity of P. furiosus DNA polymerase. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These can be used to improve nucleic acid replication, polymerisation and amplification (especially in PCR or RT-PCR).
Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                   Example 5; Page 32; 161pp; English.
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Gaps ; 0

AAW72860 standard; Peptide; 35 AA.

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RESULT 6 AAW72860 ID AAW72

275 KYDVVIMAAAVSDFRPK 291

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us-08-957-709-19.rag

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Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is an N-terminal peptide of a 150 kDa component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. PEF, the predominant components of which are P50 (see AAW72844) and P45 (see AAW72847), enhances the activity of P. furiosus DNA polymerase. The invention provides novel extracts, proteins and complexes that improve the polymerastion activity of nucleic acid polymerases. These can be used to improve nucleic acid replication, polymerases.
                                                                                                                                                                                                                                        /note= "this residue may be deleted or substituted
by any amino acid but is tentatively
assigned as indicated"
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                                                             Polymerase enhancing factor 150 kDa protein N-terminal peptide.
                                                                                             Polymerase enhancing factor; PEF; DNA polymerase; PCR;
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Pred. No.
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                                                                                                              amplification; sequencing; replication
                                                                                                                                                                                                          'label= Gly, Ala, Met
                                                                                                                                          Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                            Location/Qualifiers
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100.0%; Pre
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                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hogrefe
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                         Misc-difference 11
                                                                                                                                                                                         Misc-difference l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
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                               01-MAR-1999
                                                                                                                                                                                                                                                                                                         WO9842860-A1
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 AAW72864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is an N-terminal peptide of the P50 component of the polymerase enhancing factor (PBF) of Pyrococcus furiosus DSM 3638. It was obtained by N-terminal sequencing of P50 isolated from a PEF complex. PEF, the predominant components of which are P50 (see AAW72844) and P45 (see AAW72847), enhances the activity of P. furiosus DNA polymerase. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These can be used to improve nucleic acid conjugation, polymerisation and amplification (especially in PCR or
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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0
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                Length 35;
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             ore 13; DB 19; Length 35
red. No. 1.2e-05;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                        Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication.
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               Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 33; 161pp; English
                                                                                                                                                                                         AAW72866 standard; Peptide; 13 AA.
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3.2%; Scu-
100.0%; Pre
0; '
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                                                                                                                                                                                                                                                         (first entry)
           Query Match 3.2
Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
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                                                                                             3 lhhvkliyatksr 15
                                                                           2 LHHVKLIYATKSR 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-542284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRA-) STRATAGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1997;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       W09842860-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1998;
                                                                                                                                                                                                                                                         01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1998
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                                                                                                                                                                                                                         AAW72866;
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Gaps

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RESULT 8
AAW72864 TID AAW72

à a

Length 15; Indels

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This is an N-terminal peptide of the P50 component of the polymerase enhancing factor (PEE) of pyrococcus furiosus DSM 3638. It was obtained by N-terminal sequencing of P50 isolated from a PEE complex. PEE, the predominant components of which are P50 (see AAW72844) and P45 (see AAW72847), enhances the activity of P. furiosus and complexes that improve the polymerastics proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These can be used to improve nucleic acid. The instanton and amplification (especially in PCR or
                                                                                                                                                                                                                                                                                                                                                                                      Polymerase enhancing factor proteins, extracts and complexes - improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication
                      "this residue may be deleted or substituted
by any amino acid but is tentatively
assigned as indicated"
                                                                                                                              Anote- "this residue may be deleted or substituted by any amino acid but is tentatively assigned as indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymerase enhancing factor P50 component N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10; DB 19; Length 15;
Pred. No. 0.006;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication.
                                                                           "any amino acid"
                                                                                                        "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 32; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW72871 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 2.5%; Sco
Best Local Similarity 100.0%; Pr
Matches 10; Conservative 0;
                                                                                                                                                                                                                                        98WO-US05497.
                                                                                                                                                                                                                                                                    97US-0957709.
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                                                                         Misc-difference 14
                                                                                                    /note=
Misc-difference 15
                       /note=
                                                                                                                                                                                                                                                                                                                                      Hogrefe H;
                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-542284/46.
                                                          Misc-difference 13
                                                                                                                                                                                                                                                                                                         (STRA-) STRATAGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LHHVKLIYAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 lhhvkliyat 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA;
                                                                                                                                                                                   W09842860-A1.
                                                                                                                                                                                                                                      20-MAR-1998;
                                                                                                                                                                                                                                                                24-OCT-1997;
21-MAR-1997;
                                                                                                                                                                                                               01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                     Hansen CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9842860-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                  δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XX
XX
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XX
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                                                                                                                                                                                                                                                                                                                                                                   Polymerase enhancing factor proteins, extracts and complexes - improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is an N-terminal peptide of a 100 kDa component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. PEF, the predominant components of which are P50 (see AAW72844) and polymerase. The invention provides novel extracts, proteins and complexes that improve the polymeration activity of p. furiosus DNA complexes that improve the polymeration activity of nucleic and polymerases. These can be used to improve nucleic acid replication polymerisation and amplification (especially in PCR or RT-PCR).
                                                                                            /Jabel= Lys, Leu
/note= "these residues may each be deleted or
substituted by any amino acid but are
assigned as indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase enhancing factor P50 component N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.7%; Score 11; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymerase enhancing factor; PEF; DNA polymerase; PCR; amplification; sequencing; replication
                                                                      /label= Gly, Ala, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "any amino acid"
Misc;difference 2
               Pyrococcus furiosus strain DSM 3638
                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 33; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus furiosus strain DSM 3638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW72858 standard; Peptide; 15 AA.
                                                                                                                                                                                                                     98WO-US05497.
                                                                                                                                                                                                                                                 97US-0957709
97US-0822774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                  Hansen CJ, Hogrefe H;
                                                                                                                                                                                                                                                                                                                                          WPI; 1998-542284/46.
                                                                                Misc-difference 13
                                                                                                                                                                                                                                                                                      (STRA-) STRATAGENE.
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2 lhhvkliyatk 12
                                                   Misc-difference 1
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                                                                                                                                                               WO9842860-A1
                                                                                                                                                                                                                    20-MAR-1998;
                                                                                                                                                                                                                                             24-OCT-1997;
21-MAR-1997;
                                                                                                                                                                                            01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Gaps

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(STRA-) STRATAGENE.

PAR A PAR A

24-OCT-1997; 21-MAR-1997;

20-MAR-1998;

01-OCT-1998

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The present invention relates to Aspergillus fumigatus N-myristoyl transferase (NMT) gene and its use in identifying anti-fungal agents. NMT is responsible for cotranslational modification of a variety of fungal proteins. NMT catalyses the attachment f a 14-carbon saturated fatty acid to the N-terminal glycine residue of cellular proteins. This modification is thought to be irreversible and essential for the full biological activity of myristoylated proteins. The present sequence is Aspergillus fumigatus N-myristoyl transferase (NMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is a H. pylori secreted protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and
N-myristoyl transferase, useful for identifying anti-fungal agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
                                                                                                                                                                                                                                                                                                                  Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori ORF 05ae30220_24882812_c3_103 secreted protein.
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                core 8; DB 22;
Pred. No. 16;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claims 14,94; Page 671-672; 1145pp; English.
                                                                                                                                                                                                                                                                                                                  2.0%; Score 8;
                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW55465 standard; Protein; 481 AA.
                                                                                                                                                                                                                                                                                                                                                       .,
                                       Claim 1; Fig 1; 23pp; English
                                                                                                                                                                                                                                                                                                                                       100.0%;
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96US-0625811.
96US-0758731.
96US-0736905.
96US-0738859.
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                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                        463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -OCT-1996
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW55465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alm RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW55465
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                                                                                                                                                                                                                                                                                                                                                                                                  δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid molecules, which encode Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                        This peptide is derived from an N-terminal peptide (see AAW72858) of the P50 component of the polymerase enhancing factor (PEF) of Pyrooccus furiosus DSM 3638. A degenerate primer (see AAW63871) based on the peptide has been used to amplify DNA (see AAW63871) coding for P50 protein (see AAW72844) from P. furiosus genomic DNA. PEF enhances the activity of P. furiosus DNA polymerase. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These can be used to improve nucleic acid replication, polymerisation and amplification (especially in PCR or RT-PCR).
                                                                                                                                                                                                                                                    Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transferase; NMT; identification; anti-fungal agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus fumigatus N-myristoyl transferase (NMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 19; I
Pred. No. 4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04541 standard; Protein; 463 AA.
                                                                                                                                                                                                                                                                                                                                       Example 6; Page 34; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cotranslational modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                     98WO-US05497
                                                                          97US-0957709
97US-0822774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0163444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                          Hansen CJ, Hogrefe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus fumigatus
                                                                                                                                                                                                                 WPI; 1998-542284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-431958/46.
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8 AA;

Sequence

3 HHVKLIYA 10

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12

AAE04541 RESULT

Bulawa CE;

Cook WJ,

30-SEP-1998;

26-JUN-2001

JS6251596-B1

12-SEP-2001

AAE04541;

N-myristoyl

30-SEP-1998;

N-PSDB; AAD09840

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The DNA and probes derived from it may be used for the diagnosis of diagnosis of H. Pylori infection. Wucleic acid sequences complementary to the DNA act as antisense sequences, and can be used to prevent the translation of H. Pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. Pylori mRNA. Antibodies against the protein can confirm the protein can mechanically shearing the bacterial DNA. The sequences were necessary shearing the bacterial DNA. The sequences were coding regions defined by computer evaluation. To identify likely sequences predicted from various ORF were analysed for significant compost to other known or exported membrane proteins. Having regions can be isolated from H. Pylori by PCR analysed for significant dentified and determined the sequences of interest, particular regions can be isolated from H. Pylori by PCR analification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
2.0%; Score 8; DB 18; Length 486;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 1075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG04881 standard; Protein; 490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              990S-0121825
990S-0123180
990S-0125788
990S-0126786
990S-0126785
990S-0127462
990S-012744
990S-013077
990S-013077
990S-013077
990S-013077
990S-013077
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990S-0132485.
99US-0132486.
99US-0132486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                     486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 SKEKLIEE 343
|||||||||||
286 skekliee 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2.
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05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
29-MAR-1999,
01-APR-1999,
08-APR-1999,
16-APR-1999,
16-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
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                                    $$$$$$$$$$$$$$$$$$$$$$$$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
can be used to prevent the translation of H. pylori mRNA. Antibodies addinstribution of H. pylori-specific antigens. The gronnic sequence of by modistribution of H. pylori-specific antigens. The gronnic sequence of by mechanically shearing the bacteral and Na. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions vaccine development. When the amino acid sequences predicted from various of membrane proteins. Having identified and determined the sequences of membrane proteins. Having identified and determined the sequences of amplification for significant homology to other known or exported interest, particular regions can be isolated from y sequences of amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; vaccine; prevention; treatment; infection; envelope; inflentification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a Helicobacter pylori protein of unspecified
                                                                                                                                                                                                                                                                                                                                     2.0%; Score 8; DB 18; Length 481;
100.0%; Pred. No. 17;
7ative 0; Mismatches 0; Indels
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9905-0145145. 9905-0145218. 9905-0145218. 9905-0145218. 9905-0145918. 9905-0145919. 9905-0145919. 9905-0145919. 9905-0145919. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0149930. 9905-0149930. 9905-0149930. 9905-0149930. 9905-0149930. 9905-0149930. 9905-0151303. 9905-0151303. 9905-0151303. 9905-0151303. 9905-0151303. 9905-0151303. 9905-0151303. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333. 9905-0151333.
23 - JUL 1999; 23 - JUL 1999; 23 - JUL 1999; 24 - JUL 1999; 27 - JUL 1999; 27 - JUL 1999; 27 - JUL 1999; 27 - JUL 1999; 28 - JUL 1999; 28 - JUL 1999; 29 - JUL 1999; 20 - AUG 1999; 31 - AUG 1999; 32 - AUG 1999; 33 - AUG 1999; 34 - AUG 1999; 35 - AUG 1999; 36 - AUG 1999; 37 - AUG 1999; 38 - AUG 1999; 38 - AUG 1999; 39 - AUG 1999; 31 - AUG 1999; 31 - AUG 1999; 32 - AUG 1999; 33 - AUG 1999; 34 - AUG 1999; 35 - AUG 1999; 36 - AUG 1999; 37 - AUG 1999; 38 - AUG 1999; 39 - AUG 1999; 31 - AUG 1999; 31 - AUG 1999; 32 - AUG 1999; 33 - AUG 1999; 34 - AUG 1999; 35 - AUG 1999; 36 - AUG 1999; 37 - AUG 1999; 38 - AUG 1999; 39 - AUG 1999; 31 - AUG 1999; 31 - AUG 1999; 31 - AUG 1999; 31 - AUG 1999; 32 - AUG 1999; 33 - AUG 1999; 34 - AUG 1999; 35 - AUG 1999; 36 - AUG 1999; 37 - AUG 1999; 38 - AUG 1999; 39 - AUG 1999; 31 - AUG 1999; 32 - AUG 1999; 33 - AUG 1999; 34 - AUG 1999; 35 - AUG 1999; 36 - A
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999US - 0134286 999US - 0134286 999US - 0134218 999US - 0134219 999US - 0134219 999US - 0134219 999US - 0134219 999US - 0134219 999US - 0135353 999US - 0135353 999US - 0135353 999US - 013536782 999US - 013536782 999US - 01359454 999US - 0139455 999US - 0140682 999US - 0140682 999US - 0144086 999US - 0144086
11 - MAY - 1999; 11 - MAY - 1999; 12 - MAY - 1999; 13 - MAY - 1999; 14 - MAY - 1999; 15 - MAY - 1999; 16 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - MAY - 1999; 20 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 23 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 23 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - MAY - 1999; 29 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 23 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 23 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - M
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161350.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-016193.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 90US-0161992.
PR 28-O
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Search completed: January 31, 2002, 13:18:03 Job time: 164 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

 protein search, using sw model OM protein Run on:

January 31, 2002, 13:20:02; Search time 78.64 Seconds (without alignments) 390.366 Million cell updates/sec

US-08-957-709-19

403 1 MLHHVKLIYATKSRKLVGKK.......KMKKRELAERIWDEIEKXLS 403 Perfect score: Sequence: Title:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

0

Word size :

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s Post-processing: Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	pantothenate metab	dna/pantothenate m	pantothenate metab	pantothenate metab	hypothetical prote	DNA/pantothenate m	pantothenate metab	hypothetical prote	lity	aroma	probable transamin	phosphoglycerate k	cag pathogenicity	cag island protein	probable membrane	sensory transducti	gene e19 protein -			hypothetical prote	methioninetRNA l	hypothetical prote	hypothetical prote	hypothetical prote	probable translati	probable translati	hypothetical prote	ribosomal protein	protein tyrosine p
	QI	G71018	E75114	A72223	A64414	D81819	A81058	D69455	T23443	S62355	E71125	T36548	TVWTGC	B64585	D71927	T36972	S75130	T03348	G69115	F69252	B85774	F70338	C70537	F75075	C64382	E75056	D71104	A96580	E71723	T10278
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	Length	401	401	394	403	394	394	404	127	210	391	396	480	481	481	794	1261	36	9	91	101	111	124	130	138	140	140	144	145	160
оÞР	Query	17.9	14.9	3.0	2.7	2.5	2.5	2.2	2.0	2.0	2.0	5.0	2.0	2.0		2.0	5.0		1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
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	ribosomal protein	disulfide bond for	nonhistone chromos	CLP proteinase (im	endopeptidase Clp	endopeptidase Clp	hypothetical prote	conserved hypothet	luxG protein - Vib	phosphoribosylform	5'-methylthioadeno	probable enoyl-(ac	hypothetical prote	probable hemein up	hypothetical prote	conserved hypothet	
	r43779	382818	B61611	086555	372067	B81672	T38480	A69864	A37830	D72304 .	D64307	I36778	r50916	381257	r48229	083425	
	2	~	~	7	~	7	7	7	7	7	7	2	7	7	2	7	
	170	173	186	191	191	196	203	209	236	241	252	255	255	268	270	274	
	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	
	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
`	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

pantothenate metabolism flavoprotein dfp homolog PH1444 - Pyrococcus horikoshii N;Alternate names: probable aspartate 1-decarboxylase activase C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 C;Accession: G71018

Rikawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Obluku, Y.; Funhiashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Refcerace number: A71000; MUID:98344137
A;Accession: G71008
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA A;Residues: 1-401 <KAM>
A;Residues: 1-401 <KAM>
A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30551.1; PID:g3257868

A; Experimental source: strain OT3 A; Note: this accession replaces an interim accession for a sequence replaced by GenBa

A;Gene: PH1444 C;Superfamily: pantothenate metabolism flavoprotein dfp

ö Gaps ; 0 DB 2; Lens.
3. 1e-62;
0; Indels Length 401; Mismatches Score 72; Pred. No. 17.9%; Sccilarity 100.0%; Pr Conservative 0; Similarity Query Match Best Local Simi Matches 72;

TGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFP 127 89 à

qq

HIPIMIAPAMHE 139 128 δλ

129 8

RESULT

dna/pantothenate metabolism flavoprotein (dfp) PAB1897 - Pyrococcus abyssi (strain Or

C;Spēcies: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C; Accession: E75114

A; Accession: E75114

Rjanonymous, Genoscope submitted to the EMBL Data Library, July 1999 A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A; Reference number: A75001

A; Status: preliminary

2

A.Experimental source: strain Orsay C.Genetics: A.Gene: PAB1897 C.Superfamily: pantothenate metabolism flavoprotein dfp

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A, Molecule type: DNA
A, Residues: 1-394 <TET>
A; Coss.references: GB: AE002516; GB: AE002098; NID: 97226905; PIDN: AAF42007.1; PID: 9722
A; Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA/pantothenate metabolism flavoprotein NMB1658 [imported] - Neisseria meningitidis Cispecies: Neisseria Mar-2000 #text_change 19-Jan-2001 Cispeciesion: A81058 M.J.; Harten, D.J.; Heidelberg, J.J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.J.; Fleischmann, R.D.; Dougherty, B. Science 287, 1809-1815, 2000.
Science 287, 1809-1815, 2000.
Altible: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
Altible: A81000; MUID:20175755
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                  Length 403;
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C;Superfamily: pantothenate metabolism flavoprotein dfp
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C;Superfamily: pantothenate metabolism flavoprotein dfp
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Pred. No. 0.13;
0; Mismatches
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                           2.7%; Score 11; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
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ilarity 100.0%;
Conservative 0
                           Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                             218 SSGKMGVALAE 228
                                                                                                                                                                                                                          219 SSGKMGVALAE 229
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
A7223
pantothenate metabolism flavoprotein dfp homolog TM1687 - Thermotoga maritima (strain M9 martothenate names: probable aspartate 1-decarboxylase activase
C; Specias: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C; Accession: A7223
R; Nalson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
C, M.
C, M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A; Accession: A72223
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-394 cARNA
A; Cross-references: GB:AE001809; GB:AE000512; NID:g4982257; PIDN:AAD36754.1; PID:g498226
C; Genetics:
C; Genetics: TM1687
C; Superfamily: pantothenate metabolism flavoprotein dfp
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A64414
pantochenate metabolism flavoprotein MJ0913 - Methanococcus jannaschii
N:Alternate names: probable aspartate 1-decarboxylase activase
C;Specias: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jui-2000
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jui-2000
C;Accession: A64414
R;Bult. C.J.; White, O; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Rsch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Stanc, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Sclance 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Tile: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Accession: A64414
A;Scatus: preliniary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-403 < GB:L/7117; NID:g2826348; FIDN:AAB98918.1; PID:g1591587; T.C.Senetics:
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                                                                                                                                                                                                                                                              Length 401;
                                                                                                                                                                                                                                                     Query Match
14.9%; Score 60; DB 2; Length 401
Best Local Similarity 100.0%; Pred. No. 6.7e-51;
Matches 60; Conservative 0; Mismatches 0; Indels
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Q ŏ

A:Map position: REV845792-844581 C;Superfamily: pantothenate metabolism flavoprotein dfp C;Keywords: flavoprotein

Thu Jan 31 13:32:12

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F;91-165/Domain: HMG box homology <HMG2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%; S
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain OT3
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A;Accession: T36548
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-391 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 SDFRPKIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 SDFRPKIK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 TSKEKLIE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 TSKEKLIE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: E71125
                 A; Accession: S62355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T36548
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RESULT 7
D69455
pantothemate metabolism flavoprotein dfp homolog AF1645 - Archaeoglobus fulgidus
N;Alternate names: probable aspartate 1-decarboxylase activase
C;Species: Archaeoglobus fulgidus
C;Accession: D69455
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
C;Accession: R.A.; Zhou, L.; Owarbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Nature 390, 364-370
Nature 390
N
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$56235
high mobility group protein 1 - African clawed frog
high mobility group protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: 862355
R;Nightingale, K; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
EMBO J. 15, 548-561, 1996
A;Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in A;Reference number: 862355; MUID:96174815
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T23443

T23443

T23443

Hypothetical protein K08C9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T23443

R;Lennard, N.
Submitted to the EMBL Data Library, November 1996
A;Reference number: 219741
A;Recession: T23443
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T23443
A;Rocession: T23443
A;Rocession: L1244
A;Rocession: L1247
A;Rocession: City CML>
A;Rocession: City CML>
A;Rocession: City CML>
A;Rocession: City CML>
A;Cross-references: EMBL:281567; PIDN:CAB04589.1; GSPDB:GN00019; CESP:K08C9.6
A;Experimental source: clone K08C9
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A;Introns: 52/2; 69/1
C;Superfamily: Caenorhabditis elegans hypothetical protein K08C9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 404;
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Pred. No. 1.3;
0; Mismatches
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Pred. No.
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tive 0;
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100.0%;
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Best Local Similarity 100.00
-202 8; Conservative
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Best Local Similarity
Matches 9; Conserv
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FRIRKIKL 92
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R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: E71125

    Pyrococ

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submitted to the EMBL Data Library, May 1999
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A; Cross-references: EMBL:AL049754; PIDN:CAB42045.1; GSPDB:GN00070; SCOEDB:SCH10.36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable aromatic-amino-acid transaminase (EC 2.6.1.57) PH0771 [similarity]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
A;Status: preliminary; nucleic acid sequence not shown
A;Nolecule type: mRNA
A;Residues: 1-210 <NIG>
A;Residues: 1-210 <NIG>
A;Cross-references: EMBL:U21933; NID:g709958; PIDN:AAC59859.1; PID:g709959
A;Cross-references: EMBL:U1933; NID:g709958; PIDN:AAC59859.1; PID:g709959
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Pomain: HMG box homology <HMG1>
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C;Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
F;236/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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. 6.9;
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Pred. No. 12;
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100.0%; Pred. No. 6.9
ative 0; Mismatches
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Length 396;

2.0%; Score 8; DB 2; 100.0%; Pred. No. 12; tive 0; Mismatches

Query Match 2.0 Best Local Similarity 100. Matches 8; Conservative

197 VLVTAGAT 204

ò QQ

0; Indels

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cagisland protein - Helicobacter pylori (strain J99)
C; Species: Helicobacter pylori
C; Species: D: Pilori
C; Species: D: Pilori
C; Species: D: Pilori
C; Species: D: Pilori
C; Accession: D71927
River, C; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F
River, C; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F
River, C; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A; Reference number: A71800; MUID:99120557
A; Receiber DNA
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-481 CARNA
A; Residues: 1-481 CARNA
A; Respeciences: GB: ABC01481; GB: AEC01439; NID: g4155005; PIDN: AAD06054.1; PID: g415
A; Cronstreer
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R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, August 1999
A;Reference number: Z21618
A;Accession: T36972
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-794 <-OLI>
A;Residues: 1-794 <-OLI>
A;Residues: 1-794 <-OLI>
A;Cross-references: EMBL:AL109949; PIDN:CAB52886.1; GSPDB:GN00070; SCOEDB:SCJ11.01c
A;Experimental source: strain A3(2)
A;Genetics:
A;Genetics:
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Pred. No. 14;
); Mismatches
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100.0%; Pre
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Best Local Similarity 100
Matches 8; Conservative
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A;Gene: orf8
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phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat

C;Species: Triticum aestivum (common wheat)

C;Date: 31-Dec1991 *sequence_revision 31-Dec-1991 *text_change 11-Jun-1999

C;Date: 31-Dec1991 *sequence_revision 31-Dec-1991 *text_change 11-Jun-1999

C;Date: 31-Dec1991 *sequence_revision 31-Dec-1991 *text_change 11-Jun-1999

C;Date: 31-Dec1991 *sequence_revision 2096

R;Longstaff M.; Raines, C.A.; McMorrow, E.M.; Bradbeer, J.W.; Dyer, T.A.

Nucleic Acids Res. 17, 6569-6580, 1989

A;Title: Wheat phosphoglycerate kinase: evidence for recombination between the genes for

A;Reference number: S05966; MUID:89385983

A;Title: Wheat phosphoglycerate kinase

C;Genetics:

A;Map position: 1

C;Superfamily: phosphoglycerate kinase

C;Keywords: ATP; Calvin Gycle; chloroplast; phosphotransferase

F;1-72/Domain: transit peptide (chloroplast; phosphotransferase

F;277,399/Binding site: ATP (Lys, Glu) *status predicted cMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13

Gag pathogenicity island protein cag3 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori
C;Accesion: B64585
R;Tomb, J.F; White, O.; Kerlavge, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S;: Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.B.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L.A.; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A.; Altle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: B64585
A;Accession: B64585
A;Accession: B64585
A;Setuus: preliminary; nucleic acid sequence not shown; translation not shown
A;Melcule type: DNA
A;Residues: 14481 CTOM>
A;Residues: 14481 CTOM>
A;Cross-references: GB:AE0000566; GB:AE000511; NID:g2313628; PIDN:AAD07589:1; PID:g231363
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Length 480;

Ouery Match 2.0%; Score 8; DB 1; Best Local Similarity 100.0%; Pred. No. 14; Matches 8; Conservative 0; Mismatches

192 LEGKRVLV 199

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0; Indels

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Search completed: January 31, 2002, 13:20:05
Job time: 106 sec
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Gaps

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Indels

. 0

Length 481;

DB 2;

2.0%; Score b; 100.0%; Pred. No. 14;

Query Match 2.0 Best Local Similarity 100. Matches 8; Conservative

SKEKLIEE 343 SKEKLIEE 288

336

g ò

RESMLT

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us-08-957-709-19.rsp

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:39:10 ; Search time 46.78 Seconds (without alignments) 315.860 Million cell updates/sec Run on:

US-08-957-709-19 403 1 MLHHVKLIYATKSRKLVGKK......KMKKRELAERIWDEIEKXLS 403 Title: Perfect score: Sequence:

Scoring table:

OLIGO . Gapop 60.0 , Gapext 60.0

100059 seqs, 36664827 residues Searched:

0 Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		. ap			SUMMARIES	
Result		Query				
No.	Score Match Length DB ID	Match	Length	DB	ΙD	Description
		1 1 1 1 1		1		*****************************
-	-	7	7.03	-	11 2 7 A 02 1 DE METTA	OE0372 mothans

Description	OCE 0200		P12782 triticum ae	Q9uvx3 aspergillus		Q9fbm4 streptomyce	m		Q9uyr6 pyrococcus		4	m	dictyost	Q9pgg2 xyleila fas		chlamyd	vibrio fis		Q9a211 caulobacter	methanos	-	P47145 saccharomyc	_	40134	88		P09029 escherichia		752	2	199	67749 aquifex	014018 schizosacch
T QI	DED MERTA	AAT DVPHO	PGKH_WHEAT	NMT_ASPFU	PGMU_BROIN	EX7S_STRCO	Y022_ARCFU	Y659_METJA	IF2B_PYRAB	IF2B_PYRHO	RL11_RICPR	PTP2_NPVOP	RM06_DICDI	- 1	- 1	CLP1_CHLPN	LUXG_VIBFI	Y060_METJA	- 1	YOR3_METBA	HIS1_CANAL	YJ77_YEAST	ETFA_MEGEL	RA51_LYCES	RADA_HALVO	DDL_HELPY	- 1	YII3_YEAST	FP	₹*	F-4	ď	SYSC_SCHPO
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Length	403	105	480	492	581	88	91	138	140	140	145	160	170	173	191	191	236	252	257	282	298	328	338	342	343	347	355	365	390	410	425	433	450
% Query Match	2.7.		5.0	•	٠	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	٠	•	1.7	1.7	1.7
Score	11	į	ω	80	80	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	,
sult No.	-	۰,	m	4	Ŋ	9	7	۵	6	10	11	13	13	14	15	16	17	18	13	20	21	22	23	74	25	56	27	28	59	30	31	32	5.

P08293 azotobacter P10577 rhizobium m P28972 equine herp P26041 mus musculu P32372 schizosacch P04410 rattus norv P04411 mus musculu P04065 saccharomyc P29760 saccharomyc P16084 butyrivibri Q10327 schizosacch P09505 barley yell
NIFE_AZOVI NTRC_RHIME UL21_HSVEB MOES_MOUSE RAD4_SCHPO KPC1_RAT RPC2_MOUSE AWY1_SACDI AMY1_SACDI AMY1_SACDI SGL_SUTFI YD72_SCHPO RRPO_BYDVP
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4444 4844 530 648 671 671 767 768 830 851
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66888888888888888888888888888888888888

## ALIGNMENTS

Query Match 2.7%; Score 11; DB 1; Length 403; Best Local Similarity 100.0%; Pred. No. 0.0046; Matches 11; Conservative 0; Mismatches 0; Indels

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Gaps ó

1111111111 219 SSGKMGVALAE 229 218 SSGKMGVALAE 228 οy Dp

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NMT_ASPFU
Q9UVX3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00155; aminotran_1; 1.
PROSITE; PS00105; AA_TRANSFR_CIASS_1; 1.
Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
BINDING 236 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 391 AA, 44565 MW; C335FD73BD08FEAC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98344137; PubMed=9679194;
MEDLINE-9834137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakal M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Obfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazawa H., Takamida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-0CT-1999 (Rel. 12, Last sequence update)
01-0CT-1999 (Rel. 134, Last annotation update)
PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR (EC 2.7.2.3).
Triticum aestivum (Wheat).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticum.
                                                                                                                                                                                                                                                                               Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-i- SIMILARITY: BELLONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
                                                                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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100.0%; Pred: No. 4.6;
ative 0; Mismatches
                                                       PRT; 391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP000003; BAA29863.1; -. HSSP; Q56232; 1BKG.
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Best Local Similarity luv..
کم 8; Conservative
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                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                      20-AUG-2001 (Rel
ASPARTATE AMINOT
ASPC OR PH0771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticeae, Triti
NCBI_TaxID-4565,
                                                AAT_PYRHO
058489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGKH_WHEAT
P12782:
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AC PGKHEW

AC P12782

DT 01-0CT

DT 01-0CT

DT 01-0CT

DT 01-0CT

CC SPETM

                 AAT_PYRHO
ACCOMPANA
AAT_PYRHO
ACCOMPANA
BACCOMPANA
AANA
BACCOMPANA
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N-TETRADECANOYL-CHEPTIDE.
-1 - SUBCELLULAR LOCATION: CYTOPLASMIC.
-1 - SIMILARITY: BELONGS TO THE NMT FAMILY.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLYCYLPEPTIDE N-TETRADECANCYLTRANSFERASE (EC 2.3.1.97) (PEPTIDE N-MYRISTOYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sakata K., Hashido K., Aoki Y., Arisawa M.;
Sakata K., Hashido K., Aoki Y., Arisawa M.;
"n-myristoyl transferase.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ADDS WYRISTOYL GROUP TO N-TERMINAL GLYCINE RESIDUE OF CERTAIN CELLULAR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspērgillus fumigatus (Sartorya fumigata).
Sakaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
STRAIN=CV. MARDLER; TISSUE=Leaf;
MEDLINE=89385983; PubMed=2780287;
Longstaff M., Raines C.A., McMorrow E.M., Bradbeer J.W., Dyer T.A.;
Longstaff M., Raines C.A., McMorrow E.M., Bradbeer J.W., Dyer T.A.;
"Wheat phosphoglycerate Kinase: evidence for recombination between
the genes for the chloroplastic and cytosolic enzymes.";
the genes for the chloroplastic and cytosolic enzymes.";
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP +
3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP: P19912: 1PHP.
InterPro: IRP001576; PGK.
Pfam: PF00162; PGK: 1.
PRINTS: PR00477; PHGLYCKINASE.
PROSITE: PS00411; PGLYCERATE_KINASE; 1.
Transferase; Kinase; Multigene family; Calvin cycle; Chloroplast;
Transferase: Transferase; Multigene family; Calvin cycle; Chloroplast;
Transferase; Multigene family; Calvin cycle; Chloroplast;
Transferase; Multigene family; Calvin cycle; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                            -i- PATHWAY: CALVIN CYCLE.
-i- SUBGNIT: MONOWER.
-i- SUBCELLULAR LOCATION: CHLOROPLAST.
-i- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 480;
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PHOSPHOGLYCERATE KINAȘE.
3EBA1F378DAB16CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%; Score 8; DB 1;
100.0%; Pred. No. 5.5;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 LEGKRVLV 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOGLUCOMUTASE, CYTOPLASMIC (EC 5.4.2.2) (GLUCOSE PHOSPHOMUTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Stréptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOMERASE; Phosphorylation; Magnesium.
ACT_SITE 123 123 FORMS THE PHOSPHOSERINE INTERMEDIATE
(BY SIMILARITY).
SROUENCE 581 AA; 62672 MW; 2EDES4521A0F027D CRC64;
                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
                                                                                                                                                                                                                                        Length 492;
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                           Score 8; DB 1;
Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                       581 AA.
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bromus inermis (Smooth brome grass).
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                        2.v.,
100.0%; Pic
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PROSITE; PS00710; PGM_PMM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001485; PGM_PMM.
                                                                                       EMBL; AB035414; BAA87865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF197925; AAF04862.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00408; PGM_PMM; 1.
                                                                                                     HSSP; P14743; 2NMT.
InterPro; IPR000903; NMT.
                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sritubtim S., Lee S.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                             183 ATKSRKLV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=15371;
                                                                                                                                                                                                                                                                                                10 ATKSRKLV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bromeae; Bromus
                                                                                                                                                                                                                                                                                                                                                                                                       PGMU_BROIN
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
PGMU_BROIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ( PGM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rajandream M.A.;
Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
-!- CATALYTIC ACITYLTY: EXONUCLEOLYTIC CLEAVAGE IN EITHER 5'-TO 3'-OR
3'-TO 5'-DIRECTION TO YIELD 5'-PHOSPHOMONOUCLEOTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Seeger K.J., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
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                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE EXODEOXYRIBONUCLEASE VII SMALL SUBUNIT (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
               Length 581;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - STRIARITY .
- SUBCELLULAR .
- SUBCELLULAR .
- SIMILARITY: BELONGS TO THE XSEB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Nuclease; Exonuclease.
SEQUENCE 88 AA; 9376 MW; 3886E0F0CD7EF4FC CRC64;
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               DB 1;
. 6.5;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN AF0022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7%; Score 7; DB 1;
               Score 8; DB 1
Pred. No. 6.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AA.
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     2.0%; Scc.
100.0%; Pre
0; 7
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                                                                                                                                                                                                                                                                                         EXONUCLEASE VII SMALL SUBUNIT).
                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus.
Ouery Match
Best Local Similarity
'...hoc 8; Conservē
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                             319 IKEIQPNV 326
                                                                                                 225 ALAEEAD .231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
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                                                                                                                                                                                           EX7S_STRCO
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                                                                                                                                                                                                        09FBM4;
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STRAIN-ORSAY;
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Q9UYR6:
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IF2B_PYRAB
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Transcription of the methanogenic archaeon, Methanocccus

Transcription of the methanogenic archaeoccus

Transcription of the methanogenic archaeon, Methanocccus

Transcription of the methanoccus

Transcript
                                                                                                  STRAIN-VC-16, DSW 4304 / ATCC 49558;

STRAIN-VC-16, DSW 4304 / ATCC 49558;

MEDLINE-98049343; PubMed-9389475;

Rich H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,

Richardson D.L., Rerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Rithness E.F., Dougherty B.A., Morsenney K., Adams M.D., Loffurs B.L.,

Peterson S., Reich C.I., Moreil L.K., Badger J.H., Glodek A., Zhou L.,

Coverbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Sadow P.W., D'Andrea R.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, sulphate-teducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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Y659_METJA
TO 9-METJA
TO 9-METJA
TO 9-METJA
TO 10-NOV-1997 (Rel. 35, Last sequence update)
TO 10-NOV-1997 (Rel. 35, Last sequence update)
TO 10-NOV-1997 (Rel. 35, Last sequence update)
TO 10-NOV-1997 (Rel. 36, Last annotation update)
TO 10-NOV-1997 (Rel. 40, Last annotatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7%; Score 7; DB 1; Length 91;
100.0%; Pred. No. 14;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 91 AA; 10099 MW; E4A2250C4593DAE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001105; AAB91213.1; -.
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Best Local Similarity 100...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ENGABLE TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA).
PYGOCOCCUS abyssi.
PYGOCOCCUS abyssi.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NGBL_TAXID-29292;
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InterPro; IPR002735; eIF5_eIF2B.
Pfam; PF01873; eIF5_eIF2B; 1.
Protom; PD004078; eIF5_eIF2B; 1.
Initiation factor; Protein blosynthesis; Complete proteome.
SEQUENCE 140 AAA; 16247 MW; 9D40F2C55GBB559A CRC64;
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TICR; MJ0659; -.
Hypothetical protein; Complete proteome.
SEQUENCE 138 AA; 15470 MW; 96A8AE06757D563C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.7%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 19; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.7%; Score 7; DB 1;
100.0%; Pred. No. 20;
ive 0; Mismatches
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Best Local Similarity الاست.
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76 TLEGKRV 82
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PTP2_NPVOP
010273;
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                                                                                                                                                                                                                                                                  Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                      Res. 5:55-76(1998).
FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                         Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID-53953;
                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA).
EIF2B OR PH0605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initiation factor; Protein blosynthesis; Complete proteome.
SEQUENCE 140 AA; 16247 MW; 9D40F2C1428A129A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE EIF-2-BETA / EIF-5 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 1;
Pred. No. 20;
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30-WAY-2000 (Rel. 39, Last sequence update)
20-WG-2001 (Rel. 40, Last annotation update)
50S RIBOSOWAL PROTEIN L11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AA
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100.0%; Pred
0; N
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Pfam; PF01873; eIF5_eIF2B; 1.
ProDom; PD004078; eIF5_eIF2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP000003; BAA29694.1; -
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                                                        STANDARD;
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                                                                                                                                                               Pyrococcus horikoshii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q9ZE24;
                                                      IF2B_PYRHO
058312;
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RL11_RICPR
1D RL11_R
AC 092E24
DT 30-MAY
DT 20-MAY
DT 20-MAY
DF 50S RI
GN RPLK 0
GN RICKET
OC Bacter
OC RICKET
NOBLET
                                        IF2B_PYRHO
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                              Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Elksson A.-S., Winkler H.H., Kurland C.G., mithe genome sequence of Rickettsia prowazekii and the origin of mitochondria.
                                                                                                                                                                                                                                         -! - SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                           -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orgyia pseudotsugata multicapsid pólyhedrosis virus (OpMNPV).
Viruses; dSDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 - PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,.
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein; RNA-binding; Complete proteome. SEQUENCE 145 AA; 15312 MW; C327E41CED9F69B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE 2 (EC 3.1.3.48).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.7%; Score 7; L
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000911; Ribosomal_L11.
Pfam; PF00298; Ribosomal_L11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001367; Ribosomal_L11; 1. PROSITE; PS00359; RIBOSOMAL_L11; 1.
STRAIN=MADRID E;
MEDLINE=99039499; Pubmed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ235270; CAA14604.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                    Nature 396:133-140(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
                                                                                                                                                                                                               (BY SIMILARITY).
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Best Local Similarity
Tr Conserve
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STRAIN=AX3;
MEDLINE=20279206; PubMed=10821186;
MEDLINE=20279206; PubMed=10821186;
MEDLINE=20279206; PubMed=10821186;
MEDLINE=20279206; PubMed=1082186;
MATSHO K., Morito T., Urushihara H., Yanaqisawa K., Tanaka Y.;
Matsho K., Morito T., Urushihara H., Yanaqisawa K., Tanaka Y.;
The mitochondrial DNA of Dictyostellum discoideum: complete sequence, gene content and genome organization.";
Mol. Gen. Genet. 263:514-519(200)
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE LEP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-AX3;

STRAIN-AX3;

BUDDLINE-SQB22827.2 Pubmed-9560439;

IWABHOLD M., Pi M., Kurlhara M., Morio T., Tanaka Y.;

"A ribosomal protein gene cluster is encoded in the mitochondrial Did Dictyostellum discoldeum: UGA termination codons and similarity gene order to Acanthamoba castellanii.";

Curr. Genet. 33:304-310(1998).
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                  Length 160;
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                       BY SIMILARITY.
51DDA804A554301B CRC64;
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NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update).
20-AUG-2001 (Rel. 40, Last annotation update)
MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L6.
                                                                                                                                                                                                                                                                                               Score 7; DB 1;
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 170 AA.
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PRINTS; PR00059; RIBOSOMALL6.
ProDom: PD002236; Ribosomal_L6; 1.
PROSITE; PS00525; RIBOSOMAL_L6_1; FALSE_NEG.
EMBL; U75930; AACS9008.1; -
InterPro; IPR000340; DS_phosphatase.
InterPro: IPR000347; TYR_phosphatase.
Pfam: PF00782; DSPC; 1.
SMART: SM00195; DSPC; 1.
SMART: PS003183; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50054; TYR_PHOSPHATASE_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
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InterPro; IPR000702; Ribosomal_L6.
InterPro; IPR002358; Ribosomal_L6_1.
                                                                                                                                                                                                                                                                                               Query Match 1.7%; Scc
Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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                                                                                                                                                                                  Hydrolase.
ACT_SITE 96 96 B
SEQUENCE 160 AA; 17979 MW;
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RMO6_DICDI
DE RMO6_DICDI
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DEC-1998
CO AUG-2001
DE MITCCHONDRIA
OS DICTYOSTELIU
OS MITCCHONDRIA
NCBI_TAXID-4X3;
RX MEDLINE-9822
RX MEDLINE-9822
RX MEDLINE-8027
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REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=10910347;
REDLINE—20055717; Pubbadd=1091034, Bainen W.R.S., Bainen W.R.S., Gomen G.R., Carlard D.M., Redline M., Furlan L.R., Remper E.L., Kitajima J.P., Reraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Remper E.L., Hoheised J.D., Junqueira M.H.S., Gomes S.L., Gituber A.P., R. Krigger J.E., Hoheised J.D., Junqueira M.H., Remper E.L., Kitajima J.P., R. Krigger J.E., Hoheised J.D., Junqueira M.H., Marino C.L., Martino E.M.F., Martino C.L., Martino C.L., Monen D.H., Nagai M.A., Nascimento A.L. T.O., Netto L.E.S., A do Jiveira M.C., de Oliveira R.C., Palmieri D.A., Paris A. Deliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A. Deliveira M.C., de Sa R.G., Santelli R.N., Sawasaki H.E., A de Silveira A.C.R., Salveira M.A., Terenzi M.F., Salveira M.A., Satz M., Meidanis J., Seuubal J.C., Teubal M. J., Teubal M.A., Zatz M., Meidanis J., Seuubal J.C., Terenzi M.F., Terenzi M.F., Terenzi M.F., Selveira M.A., Zatz M., Meidanis J., Selveira M.A., Zatz M., Meid
                                                                                                                                                                                                                                                            Gaps
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--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (BY SIMILARITY).
---- SIMILARITY: BELONGS TO THE DSBB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSBB OR XF0340.
Xylella fastidiosa.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DISULFIDE BOND FORMATION PROTEIN B (DISULFIDE OXIDOREDUCTASE).
                                                                                                                                                                     Length 170;
                                                                                                                                                                                                                                                       0; Indels
Ribosomal protein; Mitochondrion.
SEQUENCE 170 AA; 19083 MW; F2C4622EFBEEB97D CRC64;
                                                                                                                                                          Query Match 1.7%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                    218 SSGKMGV 224
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27 SSGKMGV 33
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Q9PGG2;
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DSBB_XYLFA
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NUCLEIC ACIDS RES. 28:1397-1406(2000).

NUCLEIC ACIDS RES. 28:1397-1406(2000).

THAT REQUIRES APP HYDROLYSIS. CLP MAY BE RESPONSIBLE FOR A FAIRLY GENERAL AND CENTRAL HOUSEKEPING FUNCTION RAPHER THAN FOR THE DEGRADATION OF SPECIFIC SUBSTRATES (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS TO SMALL PEPTIDES IN THE PRESENCE OF ATP AND WAGNESIUM. ALPHA-CASETN IS THE USUBLITES SUBSTRATE. IN THE ABSENCE OF ATP. ONLY OLIGOPEPTIDES SHORTER THAN FIVE RESIDUES ARE CLEAVED (SUCH AS SUCCINYL-LEU-TYR-I-NHWEC; AND LYR-I-TRP-BOND ALSO OCCURS).

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S14; ALSO KNOWN AS CLEPP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MOPN N.A.
STRAIN-MOPN / Nigg;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                              Gaps
                                               Oxidoreductase; Redox-active center; Electron transport; Chaperone; Transmembrane; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 (EC 3.4.21.92)
(ENDOPEPTIDASE CLP 1).
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                                                                                                                                               REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
626DF05E3FB3A49C CRC64;
                                                                                                                                                                                                                              Length 173;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
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5. 23;
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Pred. No.
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100.0%; Pre
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Pfam; PF00574; CLP_protease; 1.
EMBL; AE003886; AAF83150.1; -.
                                                                                                                                                                               19231 MW;
               InterPro; IPR003752; DsbB. Pfam; PF02600; DsbB; 1.
                                                                                                                                                                                                                           Query Match 1.7
Best Local Similarity 100.
Matches 7; Conservative
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131
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160 LVGFKAE 166
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TRANSMEM
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CLP1_CHLMU
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DR PRINTS; PR00127; CLPPROTEASEP.
DR PROSITE; PS00381; CLP_PROTEASE_SER; FALSE_NEG.
DR PROSITE; PS00381; CLP_PROTEASE_HIS; 1.

KW Hydrolase; Serine protease; Complete proteome.
FT INIT_MET 0 0 BY SIMILARITY.
FT ACT_SITE 91 91 PROBABLE.
FT ACT_SITE 116 116 PROBABLE.
SQ SEQUENCE 191 AA; 20946 MW; 30196D0814C2339E CRC64;
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Ouery Match 1.7%; Score 7; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Qy 117 PVTTVVT 123
Db 80 PVTTVY 86

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Gaps

Search completed: January 31, 2002, 13:39:12 Job time: 72 sec

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pasteurella mycobacteri

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

09977 xylella fas 09424 caulobacter 092103 helicobacte 025512 helicobacte 052596 bradyrhizob 09pal campylobact 099210 streptococc 09075 lactococcus 09chz6 lactococcus 09chz6 lactococcus 09chz6 lactococcus 09chz6 lactococcus 09558 fowlpox vir 091580 fowlpox vir 091580 fowlpox vir 09x4q1 streptomyce 09d376 mus musculu 09hab homo sapien 09fdm9 streptococc 09rp16 streptococc 09f02 streptococc 09ho17 homo sapien 09hc17 homo sapien Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida M., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998)

EMBL: Ap000006; BAA30551.1;
InterPro: IPR003382; Flavoprotein. Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus. NCBL_TaxID=53953; Query Match 83.5%; Score 1667.5; DB 1; Length 401; Best Local Similarity 83.4%; Pred. No. 3e-82; Matches 337; Conservative 33; Mismatches 29; Indels 5; 09ccq5 09clr0 26CBC5F523AE02C8 CRC64; Last sequence update)
Last annotation update) 401 AA ALIGNMENTS 07, Created) 07, Last seq 025512 052596 099PA1 099Z10 099Z10 09CHZ6 09CHZ6 09UT17 09J5E0 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TREMBLrel. 07, Last seq 01-JUN-2001 (TrEMBLrel. 17, Last ann 401AA LONG HYPOTHETICAL PROTEIN DFP. Q9X4Q1 Q9D376 Q9F0G2 Q9HC17 Q9LZM3 PRT; Q9HAB8 29FDM9 29RPL6 292L03 STRAIN-OT3; MEDLINE-98344137; PubMed-9679194; 401 AA; 44624 MW; PRELIMINARY; 178 183 625 289 Pyrococcus horikoshii, Complete proteome. SEQUENCE 401 AA; [1] SEQUENCE FROM N.A. 447 4425.5 4485.5 4485.5 4485.5 448.5 351 351 351 351 223 224.5 170 170 160 160 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161.5 161. 059114 RESULT 059114 (without alignments) 1680.381 Million cell updates/sec aquifex aeo aeropyrum p bacillus ha vibrio chol listeria mo pseudomonas archaeoglob methanobact methanobact halobacteri 059114 pyrococcus Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1 MLHHVKLIYATKSRKLVGKK......KMKKRELAERIWDEIEKXLS 403 ; Search time 35.08 Seconds Description 09hrs1 066997 006897 099810 09894 098741 098741 098713 0987213 035033 035033 099788 09hh70 027284 028628 473505 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Total number of hits satisfying chosen parameters: 473505 seqs, 146272329 residues SUMMARIES January 31, 2002, 13:12:34 Listing first 45 summaries OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 059114 098053 098053 091470 091781 066997 097810 098017 098017 098017 098017 098017 098017 098017 098017 sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* Post-processing: Minimum Match 0% Maximum Match 100% sp_vertebrate: sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-08-957-709-19 sp_rodent:* sp_virus:* sp_plant:* DB SPTREMBL_17:* sp_fung1:* sp_mhc:* Length Query Match 833.5 336.8 336.8 336.8 336.8 337.2 224.7 223.7 223.7 223.7 223.7 223.7 223.7 223.7 

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                                                                                                                                                                                                                                                                                      357
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Archaea: Euryarchaeota: Thermococcales: Thermococcaceae; Pyrococcus.
NCBI_TaxID=29292;
                                                                                                    HPYAMEFATGNPVITEITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVT
                                                        1 MLHHVKLIYATKSRKLVGKKIVXXXPGSIAALD-VKACEGLIRHGAEVHAVMSEAATKII
                                   TVVTTAFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Pyrococcus abyssi genome sequence: insights into archaeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.6%; Score 1649.5; DB 1; Length
82.9%; Pred. No. 2.8e-81;
ive 31; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ248285; CAB49630.1;
InterPro; IRR00382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
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                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN (DFP).
PAB1897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 AA.
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Best Local Similarity 82.94
Matches 335; Conservative
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SEQUENCE FROM N.A.
SERVAIN-C-16, DSW 4304 / ATCC 49558;
MEDLINE=98040343; Pubbed=989475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk M.-P., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., Mockenney K., Adams M.D., Loffurs B.,
Peterson S., Reich C.I., Moreli L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Gaps
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KSGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADLVVG
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Mature 390:364-370(1997).
EMBL; AE000989; AAB89597.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
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Pfam. PF02441; Flavoprotein. 1
Hypothetical protein; Complete proteome.
SEQUENCE 404 AA; 44885 MW; E5A2B899G3E6A66F CRC64;
                                                                                                                        NTLEAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXL 402
                                                                                                                                                       01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PANTOTHENATE METABOLISM FLANOPROTEIN (DFP).
                                                                                                                                                                                                                                                                                                                                    AA.
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62 EIEHVKYAG-----ADLILVAPATANIIGKLAYRLADNPISSLLLTASGMGTPIVWVPSM 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 XNPKIIDRIKEIQPNVFLVGFKAE--TSKEKLIEEGKRQIERAKADLVVGN--TLEAFGS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 -NPKVIGIAREINPEAFIVGFKAEYDVDNEALVESARKQIRESGVDMVVANDVSVEGFGS 343
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                                                                                                                                                                                          Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois Addredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Midani N., Caruso A., Bush D., Safer H., Petwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comperative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 386;
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Archaea; Buryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PANTOTHENITE MITABOLISM FLAVOPROTEIN.
DFP OR VNG0572G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.6%; Score 731; DB 1; L. Best Local Similarity 44.9%; Pred. No. 5.7e-32; Matches 176; Conservative 62; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANTOTHENATE METABOLISM FLAVOPROTEIN
                                          Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                EMBL, AE000889; AABB5705.1;
InterPro: IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Complete proteome.
SEQUENCE 386 AA; 42010 MW; 5638
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MEDLINE=98037514; PubMed=9371463;
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SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=145262;
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301 APELVLKL-KESPKIIKEVRKIYSG-HIIGFKAETGMSDDELLKVASEKMADDNLNMVVA 358
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                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145261;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Luo Y., Pfister P., Leisinger T., Wasserfallen A.;
"The genome of archaeal prophage psiM100 encodes the lytic eresponsible for autolysis of Methanothermobacter wolfeii.";
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45.5%; Pred. No. 5.6e-32;
11ve 65; Mismatches 126; Indels
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SEOUENCE 382 Aa; 41207 MW; 8E792042DFDFA3AB CRC64;
                                                      359 NTL--EAFGSEENQVVLIGRDFTKELPKMK-----KRELAERI 394
                                                                                            NDVLERGMGTEDTRVLIL-----TPKROEWVEGLKOHVAERI 395
                                                                                                                                                                                                                              Created)
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(TrEMBLrel. 05, I
(TrEMBLrel. 17, I
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Best Local Similarity 45.5%
Matches 178; Conservative
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01-MAR-2001 (
01-JUN-2001 (
MTW1216.
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RESULT 027284 ID 02 AC 02 AC 02 DT 01 DT 01

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354 LITKDQIVELPKGSKLENARFI 375
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                                      Nature 392:353-358(1998).
EMBL; AE000708; AAC06944.1; -.
HSSP; Q9SWE5; 1E20.
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NCBI_TaxID=56636;
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         MEDLINE FROM N.A.

MEDLINE2-20504483; PubMed-11016950;

MG W.V., Kennedy S.P., Mahalras G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Welf D., Hall J., Dahl T.A., Welltl R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

"Genome sequence of Halobacterium species NRC-1.",

"Genome Sequence Of Halo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 APAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIVYRVIKKLHKKTLE 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 EPTR-KLVGAVRDDNPDLPIVGFKAETPADDGTAGDDSMVAAARSLLQRDGLAFVVANDA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIRTK---GSVKAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                  31.3%; Score 626; DB 1; Length 392
38.1%; Pred. No. 2.6e-26;
ive 73; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                           392 AA; 40521 MW; 11FC417D17C926AA CRC64;
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01-506-1998 (TrEMBLrel. 07, Last sequence update)
01-507-1998 (TrEMBLrel. 07, Last sequence update)
01-507-1998 (TrEMBLrel. 17, Last annotation update)
PANTOTHEATE METABOLISM FLAVOPROTEIN.
DFP OR AQ. 815.
Aquifex aeolicus.
Bacteria, Aquificales; Aquificaceae; Aquifex.
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InterPro; IPR003382; Flavoprotein.
Pfam, PF02441; Flavoprotein; 1.
Complete proteome.
SEQUENCE 392 AA: 40521 ....
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Best Local Similarity 38.1'
Matches 151; Conservative
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313 PKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADLVVGNTLEAFGSEENQVV 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 KRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGAVTLIRTKGSVKAFRIRKIK
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EMBL; APO00063; BAA80969-1; --
InterPro; IPRO1382; Flavoprocein.
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1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
437AA LONG HYPOTHETICAL DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN.
complete genome of the hyperthermophilic bacterium Aquifex
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                               Length 388;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
26.8%; Score 535.5; DB 2; Length
Best Local Similarity 37.2%; Pred. No. 1.8e-21;
Matches 142; Conservative 74; Mismatches 137; Indels
                                                                                                                                                                  Interpro; 1PR003382; Flavoprotein.
Pfam: PF02441; Flavoprotein; 1.
Complete protecome.
SEQUENCE 388 AA; 43539 MW; 682BA44B64524D0B CRC64;
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STRAIN=EL TOR NIG961 / SEROTYPE 01;
MEDLINE=20466833; PubMed=10952301;
MEDLINE=20466833; PubMed=10952301;
Medloberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ITEI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVV--TTA 125
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                                                                                                                                                                                                                                                                                                                               EI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHI
                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 GNTL----EAFGSEENQV-VLIGRDFTKELPKMKKRELAER----IWDEIEK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 ANNVTEEGAGFQTDTNRVTVYFKQGDVKPLPLMTKDEVAHRLIMMISEQLEK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 AA ...
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Pfam; PF02441; Flavoprotein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000).
EMBL; AE004111; AAF93391.1;
HSSP; Q9SWE5; 1E20.
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SEOUENCE 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APAMHETMYRHPIVRENIERLKKLGVEFIGPRIEEGRAKVASIDEIVYRVIKKLHK--KT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 XNPKIIDRIKEIQPNVFLVGFKAE--TSKEKLIEEGKRQIERAKADLVVGNTLEAFG--- 365
                                                                                                                                                                                                                                                                                                                                                                                                   47 GKTIVLGVTASVALYRSLDL--ARWLLRRGARVITVMTPEAAKLVSPEMFHWASGGPVYT 104
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                   GKKIVXXXPGSIA---ALDVKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
EMBL; BAP001515; BAB06229.1; -.
ESSP; Q9SWE5; 1E20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LVGKKIVXXXPGSIAALDVKA-CEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVIT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIRTKGSVKAFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 RKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKIKSGRSITIELVP
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STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
MASAMI H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                           40;
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                                                                                                                                                       26.8%; Score 535; DB 1; Length 437; 36.8%; Pred. No. 2.3e-21; ive 66; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 ASPLIDVIMIDKSGEAVIKG-SFHKEI------VAAVIADEIAKLLS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXLS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterium
                                     46842 MW; 91463879F31F1618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 AA; 44044 MW; 47FF382F2AEB9E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
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NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR003382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 33.5% Matches 138; Conservative
                                                                                                                                                                                                                                   Matches 150; Conservative
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                                          437 AA;
                                                                                                                                                                                                 Similarity
    Complete proteome
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                                     SEQUENCE
                                                                                                                                                           Query Match
Best Local 3
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Q9K9Y4; **09K9Y4** 

RESULT Q9K9Y4

366

15;

39; Gaps

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Page

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PRT;
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HSSP; Q987E5; LE20.
Interpro; IROR03382; Flavoprotein.
Pfam; PF02441; Flavoprotein; 1.
Complete proteome.
SEQUENCE 402 AA; 43133 MW; 5F10
                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                                                IKKSRDNDTLTIEMV-KNPDIVASVAALTENRPFTVGFAAETQDVETYARSK--LVRKNL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 IKSGR---SITIELVPXNPKIIDRIKEIQPN-VFLVGFKAETSKEKLIEEGKRQIERAKA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEE------GRAKVASIDEIVYRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 IK--KLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIR 240
SDSLLDPAAEASMGHIELA----KWADLVLLAPATADLIARMAAGMGNDLLTTLILATSA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKGS-----VKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKNILLAVSGGIAVYKAVALTSKLTQAGANVKVMMTAHAQEFVPPLSFQVLSKNDVYTDT 62
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                                                                   STRAIN=EGD;
Milohanic E., Pron B., Boumaila C., Berche P., Gaillard J.L.;
Misolation and characterization of Listeria monocytogenes mutants
altered for adherence to eucaryotic cells."
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104226; AAF04653.1;
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                                                                                                                                                                                                            IRTKGSVK-AFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGK
                                                                                                                                                                                                                                         VYRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTL
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                                                                                                                                                                                                                                                                                                                                                                                                           DLVVGNTL----EAFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 399;
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34.8%; Pred. No. 9.8e-19;
ive 69; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, Q9SWE5; 1E20.
InterPro; IPROD3382; Flavoprotein.
Pfam; PFC441; Flavoprotein; 1.
SEQUENCE 399 AA; 43395 MW; 566E98FF6F07F7EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.
DFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 34.8%
Matches 144; Conservative
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09R0H7
1D 09R0H7
DT 01-MAY
DT 01-MAY
DT 01-WAY
DT 01-WAY
DT 01-WAX
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SEQUENCE FROM N.A.

STRAIN-PAO1;

MEDLINE-2043/337; PubMed-10984043;

MEDLINE-2043/337; PubMed-109840043;

MEDLINE-2043/337; PubMed-109840043;

MEDLINE-2043/337; PubMed-109840043;

MEDLINE-2043/37; Pan X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger R.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulisen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen."

Nature 406:595-964(2000).
                                            : | | | | : :: : : DQKIKKQPGDFTIAMKRTKDILLEIGQHKTSEQVVIGFAAET--ENVEANARKKLTSKNA 343
EGKI-KSGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 AFPHIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRI-----EEGRAKVASIDE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIRTĶGSV---KAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPVITEI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 RKLVGKKIVXXXPGSIAALDVKACEGLIR----HGAEVHAVMSEAATKIIHPYAWNLPTG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKADLVVGNTLE----AFGSEENQVVLIGRD-----FTKELPKMKKRELAERIWDEIEK 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVYRVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VT
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                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DNA/PRNTOTHENATE METABOLISM FLAVOPROTEIN.
DPP OR PA5220.
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas.
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406 AA.

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RAK KUNST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G.; Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G.; Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Pabret C., Ferrari E., Foulger D.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

Glim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Doris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Sato T., Scanlan E., Schleich S., Schroeke M., Sadaie Y.,

RA Takeuchi M., Tacconi E., Takagi T., Tarahashi H., Tarkemaru K.,

RA Takeuchi M., Tamakoshi A., Tarayan T.,

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RA Takeuchi M., Tamawoshi A., Tarayan T.,

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RA Takeuchi M., Wambutt R., Wedler E., Wedler R., Wasarotti A.,

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RA Takeuchi M., Pamawoshi A., Tanamanco K., Yataka K.,

RA Takeuchi M., Pamamoco H., Yamane K., Yasumoto K., Yatak K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Tosato V., Uchiyawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

RH, T. F. Complete Genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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                                          05, Created)
05, Last sequence update)
17, Last annotation update)
                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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Pfam; PF02441; Flavoprotein; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foulger D., Errington J.;
Submitted (AUG-1997) to the EM
EMBL; Z99112, CAB13443.1;
EMBL; Y13937; CAA74260.1; -.
HSSP; Q9SWE5; 1E20.
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                 Bacillus subtilis.
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Best Local Simi.
Matches 143;
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Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ITGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFPHIPI 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ILVPTMNYRMYSNKLFQENLEKLKNNGWFVVEP - - EEGHLACGEVGKGRYPENEKIVEAV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 TSLKPPYYVDEFVKVESAEEMYEEVMK -- RFEDTDIVIMNAAVGDYRPKKVFEGKLKKTE 289
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20 KIVXXXPGSIA---ALDVKACEGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPVITE- 75
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Pred. No. 1.3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBCC811C151ECFCA CRC64;
                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                             DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN.
TM1687.
                                                                                                                               394
                                                                                                                                                                                                                                                                                               Bacteria; Thermotogales; Thermotoga.
NCBI_TaxID=2336;
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
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Pfam; PF02441; Flavoprotein; 1.
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HSSP; Q9SWE5; 1E20.
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                                                                                                                               PRELIMINARY;
                                                                                                                                                                   01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEOUENCE 394 AA
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                                                                                     RESULT 13
Q9X213
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17;
                                                                                                                                                          16 LVGKKIVXXXPGSIAALDVKAC---EGLIRHGAEVHAVMSEAATKIIHPYAWNLPTGNPV 72
                                                                                                                                                                                    2 LNNRNVLLCVSGGIAV--YKACALIJSKLVQAGANVKVIMTESACRFVSPLTFQALSRHEV 59
                                                                                                           61;
                                                                   Length 406;
                                                                                                              Indels
406 AA; 43977 MW; 10EC58AD6EEE3FF3 CRC64;
                                                                   DB 2;
                                                               23.7%; Score 473.5; DB 2; 34.1%; Pred. No. 4.2e-18; tive 73; Mismatches 142;
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RESULT 035033

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15;
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STRAILMEACS F. SERGGROUP B;
MEDLINE-20175755; PubMed-10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Doddson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Clecko A., Parksey D.S., Blair E., Clittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Smith H.O., Fraser C.M., Masignani V., Pitza M., Grandi G., Sun I.,
Smith H.O., Fraser C.M., Maxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                               232 VILISGPVSLDQPKGLAEF-----IPVQSAADMREAVLSVYDAS--DIVIKTAAVADF 282
                                                                                                                                                                                                                                                                       289 RPKIKAEGKI-KSGRSITIELVPXNPKIIDRIKEI---QPNVFLVGFKAETSKEKLIEEG 344
ITEI-----TGFIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
01-MN-2001 (TrEMBLrel. 17, Last annotation update)
NMB1658.
NB1858FIA meningitidis (serogroup B).
NB258FIA meningitidis (serogroup B).
NBCTETIA: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                           345 KRQIERAKADLVVGNTLEA----FGSEENQVVLIGRD-FTKELPKMKKRELAERIWDEI 398
                                                                                                                                                                                                                                                                                                                                                               -----VTLIRTKGSVKAFRIRKIKLKVETVEEMLSAIENELRSKKYDVVIMAAAVSDF
                                                             HIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRIEE------GRAKVASIDEI
                                                                                                                                   VYRVIKKLHKKT---LEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
SEQUENCE 394 AA; 42212 MW; B427D1901932AB91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Pfam; PF02441; Flavoprotein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:1809-1815(2000).
EMBL; AE002516; AAF42007.1;
HSSP; Q9SWE5; 1E20.
TIGR; NNB1658; -.
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Best Local Similarity
Matches 143; Conser
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09JYB7;
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73 ITEITG-----FIEHVELAGEHENKADLILVCPATANTISKIACGIDDTPVTTVVTTAFP 127 

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17 VGKKIVXXXPGSIAALDVKACEGLIR----HGAEVHAVMSEAATKIIHPYAWNLPTGNPV 72

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241 TKGSVKAFRIRKIKLKVETV--EEMLSAIENELRSKKYDVVIMAAAVSDFRPKIKAEGKI 298
                                                                                                                                                                     ---KSGRSITIELVPXNPKIIDRIKEIQPNVFLVGFKAETSKEKLIEEGKRQIERAKADL 355
                                                                                                                                                                                     HIPIMIAPAMHETMYRHPIVRENIERLKKLGVEFIGPRI-----EEGRAKVASIDEIVY 181
                                                                                                                                       --GQLQTALPFGISDTVQAVSAENMHRAVHRLI--DKQDAFISVAAVSDYRVKNRSTQKF 287
                                                      RVIKKLHKKTLEGKRVLVTAGATREYIDPIRFITNASSGKMGVALAEEADFRGA-VTLIR
                                                                                                                                                                                                                                             356 VVGNTLE-AFGSEENQVVLIGRDFTKELPKMKKRELAERIWDEIEKXLS 403
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GenCore version 4.5
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OM protein – protein search, using sw model

January 31, 2002, 13:08:39; Search time 21.39 Seconds (without alignments) 555.551 Million cell updates/sec Run on:

US-08-957-709-71 Perfect score:

1 MLLPDWKIRKEILIEPFSEE.......PYRGNYQGSTRLAFSKRKKL 156 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		đ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	. dı	Description
н	768	95.3	156	7	E71216	dCTP deaminase (EC
7	703	87.2	154	7	G75030	deaminase (
m	243	30.1	180	7	A70439	ble dCTP d
4	242.5	30.1	177	7	н83695	dine.
S	4	30.0	173	7	S26382	
9	232.5	28.8	181	7	D72724	dCTP
7	216	26.8	191	7	T36613	dCTP
æ	199	24.7	200	7	A69114	┍
6			190	7	B70526	dCTP deaminase (EC
10	89.	-:	186	ď	A81272	probable dCTP deam
11	184.5	22.9	195	~	G84184	deoxycytidine trip
12	181	22.5	190	Н	D64566	w
13	180	22.3	188	~	E71860	e e
14	174		206	7	C84942	dCTP deaminase (EC
15	172		188	~	A83210	probable deoxycyti
16	165	20.5	193	~	C85833	2'-deoxycytidine 5
17	164.5		191	7	G82765	deoxycytidine trip
18	163	20.3	193	Н	A42940	dCTP deaminase (EC
19	159	6	163	7	H72759	probable dCTP deam
20	155	19.2	188	7	D81149	deoxycytidine trip
21	154	9.	204	7	F64353	dCTP deaminase (EC
22	153	٥.	150	7	D69081	
23	150.5	18.7	190	7	D81717	deoxycytidine trip
24	149.5		190	~	B71565	
25	149.5	18.5	195	Н	10	dCTP deaminase (EC
56	145	18.0	188	7	E71715	probable dCTP deam
27	138	17.1	190	7	F86539	a
28	138	17.1	190	~	F72084	dCTP deaminase (EC
29	137	17.0	172	7	T44356	70

dCTP deaminase (EC	polyprotein -	polyprotein (c	pol polyprotein -	pol polyprotein -	· probable dCTP deam	nucleoside-triphos	pol polyprotein -	dUTP pyrophosphata	dUTP pyrophosphata	pol polyprotein -	pol polyprotein -	Pol protein - Maed	deoxycytidine trip	probable duTP pyro
375588 59388	JEV	LJEW	NLJ22	145345	564437	C7565	46335	16256	2777	NLJVS	45390	21162	84406	326429
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1 57	1 GNI	1 GN	1	н П	2 E	3	1 B	2 A4	9 7	1 G	1 B	7	2	7
193 1 87	,	7	-	-	7	m	-	7	7	7	-	~	2	178 2 8
-10	1145 1 (	1146 1 (	1146 1 (	1109 1	161 2 1	188 3	1086 1	141 2 1	164 2 (	1101 1 (	1101 1	1087 2	165 2 1	
193 1 8	15.6 1145 1 (	15.6 1146 1 0	15.6 1146 1 (	14.6 1109 1 1	14.6 161 2 1	14.3 188 3	13.8 1086 1 1	13.8 141 2 1	13.8 164 2 (	13.8 1101 1 (	13.8 1101 1 I	13.5 1087 2	12.8 165 2 H	12.7

### ALIGNMENTS

E71216 GCTP deaminase (EC 3.5.4.13) PH1997 [similarity] - Pyrococcus horikoshii

C.Species: Pyrococcus horikoshii C.Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C; Accession: E71216

R. Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A.; Title: Complete sequence and gene organization of the genome of a hyper-thermophili A.; Reference number: A71000; MUID:98344137
A.Accession: E71216
A.; Accession: E71216
A.; Molecule type: DNA
A.; Residues: 1-156 < KAM>A.; Residues: 1-156 < Kampania interim accession for a sequence replaced by GenBa A.; Residues: PH1997
C.; Superfamily: GCTP deaminase
C.; Reywords: hydrolase

Gaps .; 0 Length 156; Indels Score 768; DB 2; Lv Pred. No. 1.1e-64; 4; Mismatches 6; Query Match 95.3%; Best Local Similarity 93.6%; Matches 146; Conservative

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1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALI

g

61 LTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGE 120 δ qq

121 RFVQIAFIRLEGPARNPYRGNYQGSTRLAESKRKKL 156

121 RFVQIVFIRLEDPPRNPYSGNYQGSTRLVFSKRKKL 156 Db

RESULT

G75030
GCTP deaminase (EC 3.5.4.13) PAB1164 [similarity] - Pyrococcus abyssi (strain Orsay)
GCTP deaminase (EC 3.5.4.13) PAB1164 [similarity] - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Accesion: G75030
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A;Reference number: A75001
A;Accession: G75030

9

q ò qq ŏ Ωp

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RESULT 5
526382
probable dCTP deaminase (EC 3.5.4.13) [similarity] - Desulfurolobus ambivalens
NA1ternate names: hypothetical protein 3 lig-region
C.Species: Desulfurolobus ambivalens
C.Species: Desulfurolobus
C.Species: Desulfurolobus
C.Species: 22-Nov-1993
R.Kletzin, A.
Nucleic Acia Res. 20, 5389-5396, 1992
A.Title: Molecular characterisation of a DNA ligase gene of the extremely thermophili
A.Reference number: S26382, MUID:93065206
A.Status: preliminary, nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-173 < KLE>
A.Cross-references: EMBL:X63438; NID:940784; PIDN:CAA45033.1; PID:940785
A.Cross-references: EMBL:X63438; NID:940784; PIDN:CAA45033.1; PID:940785
C.Superfamily: dCTP deaminase
C.Keywords: hydrolase
C; Accession: H83695
R; Takani, H; Nakasone, K; Takaki, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A; Reference number: A83650; MUID: 20263314
A; Accession: H83695
A; Status: preliminary
A; Noceule type: DNA
A; Residues: 1-177 <STO>
A; Residues: 28: APOO1508; GB: BA000004; NID: g10172890; PIDN: BAB04087.1; GSPDB: GA; Experimental source: strain C-125
A; Gene: BH0368
C; Superfamily: dCTP deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 REYALILTLERIKLPDDVMGDMKIRSSLAREGV-IGSFAWVDPGWDGWLTLMLYNASNEP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 LILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EGKVVIPP 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 173;
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Similarity 35.9%; Pred. No. 1.76-15. Indels
56; Conservative 30; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.1%; Score 242.5; DB 2; ilarity 37.2%; Pred. No. 1.6e-15; Conservative 30; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 KEILIEPFSEESLQPAGYDLRVGREAFV----KGKLIDVEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 VELRYGERFVQIAFIRLEGPARNPYRGNY --- QGST 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 IELPIGRRICQLVFAEVTGEVA-PYQGKYLFQKGAT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRK 154
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es 58; Conserv
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Best Local S
Matches 56
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Best Local S
Matches 58
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C:Specites: Aquifex aeolicus
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C:Specites: Aquifex aeolicus
C:Specites: Aquifex aeolicus
C:Accession: A/0439
B*Deckert, G: Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Wature 392, 353-358, 1998
A*Atures: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A*Reference number: A/0300, MUID:9819666
A*Accession: A/0439
A*Accession:
A;Status: preliminary
A;Anlecule type: DNA
A;Molecule type: DNA
A;Residues: 1-154 <RAN>
A;Residues: 1-154 <RAN>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAB50685.1; PID:9545919
A;Experimental source: strain Orsay
C;Genetics:
C;Genetics:
A;Gene: Gdd; PABIL164
C;Keywords: hydrolase
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#83695
decaycytidine triphosphate deaminase BH0368 [imported] - Bacillus halodurans (strain C-G); Species: Bacillus halodurans
C; Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 -----IPPREYALILTLERIKLPDDVMGDMKIRSSLAREGV-IGSFAWVDPGWDGNL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 1; Score 703; DB 2;
1; Pred. No. 1.3e-58;
13; Mismatches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKR 153
                                                                                                                                                                                                                                                                                                                                                                                             87.2%;
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Best Local Similarity 85.65
Matches 131; Conservative
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Query Match Best Loca Matches

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121 GFSGHVTLELSNLATLPIKLWPGMKIGQLCLFRLTSPAEHPYGSERYGS 169

g

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GCTP deaminase (EC 3.5.4.13) MTH1847 [similarity] - Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: (9.5 Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Mar-2000 C; Accession: A6914
R; Smith, D.R.; Doucette-Stamm L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicalite, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A; Reference number: A69000; MUID: 98037514
A; Accession: A69114
A; Accession: A69114
A; Residues: 1-200 
A; Experimental source: strain Delta H
C; Genetics:
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:296800; GB:AL123456; NID:g3261800; PIDN:CAB09605.1; PID:g21939
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-190 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 WVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY-----RGNYQGSTR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVE-----KEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LLPDWKIRKE----ILIEPFS--EESLQPAGYDLRVGREAFVKGKLI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
24.7%; Score 199; DB 2;
Best Local Similarity 31.6%; Pred. No. 2.1e-11;
Matches 59; Conservative 29; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dCTP deaminase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: MTH1847
C;Superfamily: dCTP de
C;Keywords: hydrolase
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PQTSRIK 190
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probable dCTP deaminase (EC 3.5.4.13) APE0333 [similarity] - Aeropyrum pernix (strain KI C; Species: Aeropyrum pernix (c; Species: Aeropyrum pernix (c; Species: 20-404-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 R; Accession: D7274 R; Awarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah Ases. 6, 83-101, 1999 Aseference of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Accession: D7274 Asecssion: D7274 Asecsion: D7274 Asecsion: D72754 Ase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable dCTP deaminase (EC 3.5.4.13) SCH35.46 [similarity] - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C; Accession: T36613 Eschiver, K; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999 A; Reference number: 221610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T36613
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-191 <OLI>
A;Residues: 1-191 <OLI>
A;Residues: BMBL:AL078610; PIDN:CAB44381.1; GSPDB:GN00070; SCOEDB:SCH35.46
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLPDWKIRK----EILIEPFSEESLQPAGYDLRVGREAFVK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.8%; Score 232.5; DB 2; 31.8%; Pred. No. 1.4e-14; Live 38; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 216; DB 2;
; Pred. No. 5.2e-13;
32; Mismatches 60
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31.4%;
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Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: APE0333
C;Superfamily: dCTP deaminase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SCOEDB:SCH35.46
C;Superfamily: dCTP deaminase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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7;

Gaps

36;

Indels

63;

Length 200;

63

7;

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"GGTP deaminase (EC 3.5.4.13) HP0372 [similarity] - Helicobacter pylori (strain 26695)

C) Species: Helicobacter pylori
C) Species: Helicobacter pylori
C) Species: Helicobacter pylori
C) Species: Helicobacter pylori
C) Date: 10.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C) Accession: D64566
R) Tomb, JF: White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.A.; Khalak, H.G.; Glodek, A.; McKe
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A.Althe: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Reference number: A64520; MuID:97394467
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-190 <TOM>
A.Cossion: GB:AE000554; GB:AE000511; NID:g2313475; PIDN:AAD07441.1; PID:g231
C) Genetics:
A.Start codon: GCP
C) Superfamily: dCTP deaminase
C; Keywords: hydrolase
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    <STO>
< GB:AE004437; NID:g10579885; PIDN:AAG18843.1; GSPDB:GN00138</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VDEYVTETVVEDGDEFILHPGDFVLGTTKERVEVPRDLVAQVEGRSSLGRLAVVVHATAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 ID-----VEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFA 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 WVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLLPDWKIRK-----EILIEPFSEESL--QPAGYDLRVGRE--AFVKGKL-
                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                            Query Match 22.9%; Score 184.5; DB 2 Best Local Similarity 31.2%; Pred. No. 4.6e-10; Matches 54; Conservative 31; Mismatches 59
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A, Residues: 1-195 <STO>
A, Cross references: GB:AE00445
C, Genetics:
A, Gene: dtd
C, Superfamily: dCTP deaminase
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A181272
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Compylobacter jejuni (strain N C;Species: Campylobacter jejuni (strain N C;Species: Campylobacter jejuni (strain N C;Species: Jan.Aar.-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C;Accession: A81272
C;W: Quail, M:; Rajandream, M.A.; Rutherford, K.M.; Churcher, C.; Basham, D.; Chillin N C; Accession: A81272
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf A;Reference number: A81250; MUID:20150912
A;Restence number: A81250; MUID:20150912
A;Status: preliminary
A;Molecule type: DNA
A;Restences: GB:AAL199078; GB:AAL11168; NID:g6968723; PIDN:CAB73719.1; PID:g696872
A;Experimental source: serotype 02, strain NCTC 11168
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deoxycytidine triphosphate deaminase [imported] - Halobacterium sp. NRC-1

c; Species: Halobacterium species NRC-1

Jung, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, R.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li Archinors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li Arcession: G84184

A; Status: preliminary

A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                           39 GKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFAWVDP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 VKGKLIDVEKEGKV-VIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVD 95
                                                                                         24;
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Similarity 30.2%; Score 198; DB 2; Length 190; Similarity 30.2%; Pred. No. 2.5e-11; 11; Conservative 3; Mismatches 61; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 GWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 DWKIRKEIL----IEPFSEES-----LQPAGYDLRVGRE------
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                                                                                                                                                           1 MLLPDWKIRKEIL----IEPFSEESLQPAGYDLRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: dcd; Cj1292
C;Superfamily: dCTP deaminase
C;Keywords: hydrolase
Query Match
Best Local S
Matches 51
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probable deoxycytidine triphosphate deaminase PA3480 [imported] – Pseudomonas aerugin
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Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: PA3480
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i Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A.Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A.Reference number: A71800; MUID:99120557
A.Accession: E71860
A.Accession: E71860
A.Roccasion: Barain J99
A.Roccasion: E71860
C.Genetics: A.Generianiase
C.Superfamily: dcTP deaminase
C.Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTP deaminase (EC 3.5.4.13) [imported] - Buchnera sp. (strain APS)
N;Alternate names: deoxycytidine triphosphate deaminase
C;Species: Buchnera sp.
C;Date: 02-War-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: C84942
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Aitle: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173
A;Retares preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Cross-references: Strain APS
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 IMSNEIIFSKEQPCFLQPGSLVLCSTFESIKMPNNLVGWLDGRSSLARLGLMIHATAHRI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 IEEWLERKELIIEPYPNKTLINGITVDIHLGNKFRFFFFFFFFFFSCIDLSNSKIIGGLSLTE 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 NASNEPVELRYGERFVQIAFIRLEGPARNPYR---GNYQGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LIEPFSEE----SLOPAGYDLRVGRE----AFVKGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LPDWKIRKEILIEPFSEESL-QPAGYDLRVGRE--AFVK--GKLIDV-
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.0%
Matches 47; Conservative
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C;Keywords: hydrolase
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A;Status: preliminary
A;Molecule type: DNA
Residues: 1-188 <STO>
A;Cross-references: GB:AE004769; GB:AE004091; NID:99949624; PIDN:AAG06868.1; GSPDB:GN
                                                                                                                                                                    C; Accession: A83210
R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Search completed: January 31, 2002, 13:08:39 Job time: 46 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:09:23; Search time 14.53 Seconds (without alignments) 393.649 Million cell updates/sec Run on:

US-08-957-709-71 806 1 MLLPDWKIRKEILIEPFSEE......PYRGNYQGSTRLAFSKRKL 156 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ργ				~	Q9yfa8 aeropyrum p	streptomy	027875 methanobact	_	_	Q9zkd0 helicobacte		-	Q9zhd8 buchnera ap	_		-				_		ednine	eduine	P32542 equine infe		_	316 homo s	Visna	visna	6 visna	· 1	09p6q5 schizosacch
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SUMMARIES	ŢΩ	DCD_PYRHO	DCD_PYRAB	DCD_THEAC	DCD_AQUAE	DCD_ACIAM	DCD_AERPE	DCD_STRCO	DCD_METTH	DCD_MYCTU	DCD_HELPY	DCD_HELPJ	DCD_BUCAI	DCD_ECOLI	DCD_BUCAP	DCD_METJA	DCD_CHLAMU	DCD_CHLTR	DCD_HAEIN	DCD_PASMU	DCD_RICPR	DCD_CHLPN	DCD_CLOHI	POL_EIAVY	POL_EIAV9	POL_EIAVC	POL_CAEVC	POL_OMVVS	DOT_HUMAN	POL_VILVK	POL_VILV	POL_VILV1	- 1	DUT_SCHPO
	DB										<del></del> 1				-						<del>- 1</del>								Н				Η,	-
	Length	156	154	183	180	173	181	191	197	190	188	188	193	193	193	204	190	190	195	194	188	190	172	1145	1146	1146	1109	1086	252	1101	1105	1105	1105	140
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	Score	76	703	257.5	243	242	232.5	216	199	198	181	180	174	163	161.5	154	150.5	149.5	4	146.5	145	138	137	125.5	125.5	125.5	118	111.5	111	111	111	111	111	105.5
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Q89662 avian adeno P70583 rattus norv	P57914 pasteurella P43792 haemophilus	Q9yysO avian adeno	P33826 variola vir O83855 treponema p	P31822 feline immu 068992 chlorobium	O41033 paramecium P17374 vaccinia vi
DUT_ADEG1 DUT_RAT	DUT_PASMU DUT_HAEIN	DUT_ADEG8	DUT_VARV DUT_TREPA	POL_FIVT2 DUT_CHLTE	DUT_CHVP1 DUT_VACCV
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178 205	151 151	163	147	1124 152	141 144
12.7	12.5	12.1	11.5	11.4	11.2
102 101	100.5	97.5	92.5	92 91.5	90.5
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DE	PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
E C	DEAMINGS
Z (	DCD OK PHISSON
2 5	s nortkosnii.
3 8	Archaea; Euryarchaeora; inermococcates; inermococcatea; rylococcus. NCBI TayTDEA3063.
RN	
RP	SEQUENCE FROM N.A.
RC	STRAIN=0T3;
RX	MEDLINE=98344137; PubMed=9679194;
RA	awa H., Haikawa Y., Hino Y.
RA	Yamamoto S., Sekine M., Baba SI., Kosugi H., Hosoyama A., Nagai Y.,
RA	:.
KA	Yamazaki J., Kushida N.,
£ 6	
¥ &	magacai i., saladya n., araudaa Toomoleate sequence and gene organization of the genome of a hyper-
E E	ic archaebacterium. Pyrococcus horikoshii OT3.":
Z.	DNA Res. 5:55-76(1998)
ပ္ပ	-1 CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
8	-! - SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
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ည	use by non-profit institutions as long as its content is in no way
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DR	EMBL; AP000007; BAA31124.1;
DR	InterPro; IPR003232; dCTP_deaminse.
DR	InterPro; IPR001428; dUTPase.
DR	
DR	
ΚW	e; Complete proteome.
čs	SEQUENCE 156 AA; 17871 MW; 96B2C2C50393A985 CRC64;
ã	95.3%;
ğ ğ	Best Local Similarity 93.6%; Pred. No. 4.9e-66; Matches 146; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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δλ	1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALI 60
QQ	1 Milpdwkirkeilieppeseeslopagydlrvgreafysgklidvekegkvyippreyali 60
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Thermoplasma acidophilum.
Archaea; Buryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
NCBL_TaxID-2303;
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4; Conservative
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Aquifex aeolicus.
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Best Local Sim
Matches 64;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-! - CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-! - SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
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  LTLERVKLPDDVMGDMKIRSSLAREGILGSFAWVDPGWDGNLTLMLYNASNEPVELKYGE 120
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09HKK0;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DEAMINASE).
DCD OR TA0598.
                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi.
Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=1919192;
                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last amoctation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
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87.2%; Score 703; DB 1; Length 154;
Best Local Similarity 85.6%; Pred. No. 7e-60;
Matches 131; Conservative 13; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRKKL 156
                                                                     AA.
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InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
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ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                          STANDARD;
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Q9UXS8;
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TO DT 20-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 PREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEP 113
                                                                                                      Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H. W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLLPDWKIRKEI-----LIEPFSEESLQPAGYDLRVGREAFVKGKLIDVE--KEGKVVIP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 MILNDSTIMRMVSDGLLISENFDRGCLTPNGYDLRV------DAIDVEGRQYSEFEIG 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.9%; Score 257.5; DB 1; Length 183;
41.3%; Pred. No. 1.5e-17;
tive 22; Mismatches 50; Indels 19
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20-70-2001 (Rel. 40, Last sequence update)
20-705-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL445064; CAC11737.1; -.
InterPro; IPR001322; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
Pfam: PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteony
SEQUENCE 183 AA; 20245 MW; 41D1992A99CD6682 CRC64;
                                                                                                                                                                                                                                              114 VELRYGERFVQIAFIRLEGPARNPYR---GNYQGS 145
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SEQUENCE FROM N.A.
STRAIN-DSM 1728;
MEDLINE-20479972; PubMed=11029001;
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or send an email to license@lsb-sib.ch).
                           or send an email to license@isb-sib.ch).
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                                                                                                                    Interpro; IPR003232; dCTP_deaminse.
Interpro; IPR001428; dUTPase.
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InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
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                                                                       EMBL; X63438; CAA45033.1; -.
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Matches 56; Conservative
                                                                                                                                                                   Pfam; PF00692; dUTPase; 1.
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                                                                                                PIR; S26382; S26382.
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                                                                                                                                                                                                                                        SEQUENCE
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LEFEEYFDIMPKQFLLATTLEYISLPPYVTAFVEGRSSLGRLGLFIENAGWVDAGFEGQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IPPREYALILTLERIKLPDDVMGDMKIRSSLAREGV-IGSFAWVDPGWDGNL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLLPDWKIRK-----EILIEPFSEESLQPAGYDLRVGRE-AFVKGK-LIDVEKEGKVV-- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
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Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Acidianus.
NCBL_TaxID=2283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular characterisation of a DNA ligase gene of the extra thermophilit archaeon Desulfurolobus ambivalens shows close phylogenetic relationship to eukaryotic ligases."; Nucleic Acids Res. 20:5389-5396(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Complete proteome.
SEQUENCE 180 AA; 20544 MW; B2710421A2FA48D6 CRC64;
  CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3). SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 TLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TLELFNANDRPIRLYRGMRICQLVFARLDRPPERVYSGKYKG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.1%; Score 243; DB 1; 37.7%; Pred. No. 3.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Mismatches
                                                                                                                                                                                                                                                                                                                                                          ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                         EMBL; AE000747; AAC07499.1; -.
Interpro; IPR003232; dCTP_deaminse.
Interpro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Lei 10 / DSM 3772;
MEDLINE-93065206; PubMed=1437556;
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00692; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 37.7%
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kletzin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCD_ACIAM
002103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
DCD_ACIAM
DCD_ACIAM
DCD ACIO
OC 1-APP
DT 01-APP
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                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 LILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fikui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nomura N., Sako Y., Kikuchi H.; Rubota K., "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                   12 ILIEPFSESSLQPAGYDLRVG-----REAFVKGK----LIDVEKEGKVVIPPREYA 58
                                                                                                                                                                                                                                                                                                                                                                                                   17 IVISPLTQDTIRENGVDLRVGGEIARFKKTDEIYEDGKDPRSFYEIEKGDEFIIYPNEHV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
173 AA; 19858 MW; B4D922503CD4B25A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix K1.";
DNA Res. 6.83-101(1999).
-!- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                             30.0%; Score 242; DB 1; 35.9%; Pred. No. 4.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 GERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRK 154
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Query Match
Best Local Similarity 31.6%
Matches 59; Conservative
                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-145262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQTSRIK 187
                                                                                                                                                                                                                                                                                                               DCD OR MTH1847.
                                                                                                                                                       DCD_METTH
027875:
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                              1 MLLPDWKIRK-----EILIEPFSEESLQPAGYDLRVGREAFVK------G 39
                                                                                                                                                                                                          40 KLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 GKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFAWVDP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EAFVK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coellcolor.

Bacteria: Actinobacteria: Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomyces.

NGBL_TaxID=1902;
                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 GNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query March 26.8%; Score 216; DB 1; Length 191; Best Local Similarity 31.4%; Pred. No. 1.4e-13; Matches 53; Conservative 32; Mismatches 60; Indels
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLPDWKIRKEI-----LIEPFSEESLQPAGYDLRVGR--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOMYCTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DEAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 AA; 21496 MW; 6352A496990F910C CRC64;
                         D8B6CBDC1722EFE9 CRC64;
                                                                                      / Match 28.8%; Score 232.5; DB 1; Local Similarity 31.8%; Pred. No. 3.5e-15; Conservative 38; Mismatches 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL078610; CAB44381.1; -. InterPro; IPR003232; dCTP_deaminse. InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 181 AA; 19894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCD_STRCO
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                                                                                        Query Match
                                                                                                               Best Loca
Matches
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10CD_STRCO
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                                                                                                                                                                                                                                                                                                                                                                                                             93 WVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY-----RGNYQGSTR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 DVE-----KEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFA
                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last amoctation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Archaea: Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 197;
97 GWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGS 145
                        InterPro; IPRUU14.v.,
Dfam; PF00692; dUTPase; 1.
Probom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
PronnRCE 197 AA; 22426 MW; 96A019F9DBA3528F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.7%; Score 199; DB 1;
31.6%; Pred. No. 5.7e-12;
ive 29; Mismatches 63.
                                                                                                                                              197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000937; AAB86313.1; ALT_INIT.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                 PRT;
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39 GKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFAWVDP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      durpase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.5%
Best Local Similarity 28.0%
Matches 47; Conservative
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                             DCD OR HP0372.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.
                                                                                                                                                                                                                      DCD_HELPY
025136;
                                                                                                                                                                                                                                                                                                                                              DEAMINASE)
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                                                                                                                                                                                                                                                                                                                                                    Davies 9. Seeper K., Seelton S., Harris D., Garnier T., Churcher C., Harris D., Gordon S.V., Elgianeier K., Gas S., Barry C.E., Ili, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Hurphy L., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Bectphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J. Bodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GREAFVK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.6%; Score 198; DB 1; Length 190; 30.2%; Pred. No. 6.9e-12; ive 33; Mismatches 61; Indels
                                                                                                                 20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Complete proteome.
SEQUENCE 190 AA; 20869 MW; F409329810B64781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLLPDWKIRKEIL----IEPFSEESLQPAGYDLRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 OR RV0321 OR MT0336 OR MTCY63.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculist; Rv0321; -.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 296800; CAB09605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006940; AAK44559.1;
                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 393:537-544(1998).
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                                                                                              (Rel. 40,
(Rel. 40,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P16088; 1DUT.
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          STRAIN-H37RV
                                                                                              20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                      DCD_MYCTU
007247;
                                                                                                                                                                                DEAMINASE)
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MEDLINE=97394467. PubMed=9252185;
MEDLINE=97394467. PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
MCKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 MISPFCEKQVGKNVISYGLSSYGYDIRVGSEFMLFDNKNALIDPKNFDPNNATKIDASKE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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                                                                                                   97 GWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGS 145
                                                                                                                                               108 NASNEPVELRYGERFVQIAFIRLEGPARNPYR---GNYQGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCXTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
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SEQUENCE 188 AA; 20904 MW; F45AEE3C3F040876 CRC64;
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-!- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
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InterPro; IPR001428; dUTPase.
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                                                         Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 IMSNEIIFSKEQPCFLQPGSLVLCSTFESIKMPNNLVGWLDGRSSLARLGLMIHATAHRI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LPDWKIRKEILIEPFSEESL-QPAGYDLRVGRE--AFVK--GKLIDV------------44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12; WEDDINE-1324907; WEDLINE-2380941; PubMed-1324907; Wang L., Weiss B.; "dcd (dCTP deaminase) gene of Escherichia coll: mapping, cloning, sequencing, and identification as a locus of suppressors of lethal
                                                                                                                                                             STRAIN-TOWN N.A.
STRAIN-TOWN VO. 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watenabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. Aps.";
Nature 407:81-86(2000).
-:- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-:- SIMILARITY: BELONGS TO THE DCTP DEAMINSE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 -----EKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFAWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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21.6%; Score 174; DB 1; Length 193;
Best Local Similarity 29.3%; Pred No. 1.3e-09;
Matches 48; Conservative 30; Mismatches 58; Indels
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01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interest IPRULIAL,
Pfam; PF00692; dUTPase; 1.
Probom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
Hydrolase; 193 AA; 21951 MW; DE7DD7FD961FC9FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 DPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 DPGWNGNIVLEMFNAGKLTLVLRPKMRIAALSFEVLSQPVLRPY 171
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SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
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InterPro; IPR001232; GCTP_deaminse.
InterPro; IPR001428; dUTPase.
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DCD OR DUS OR PAXA OR B2065.
Escherichia coli.
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                 DEAMINASE).
DCD OR BU108.
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P28248;
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DCD_ECOLI
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DCD ON JHP1009.
Helicobacter pylori J99 (Campylobacter pylori J99),
Helicobacter pylori spillon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| | :: | | : | | : | | 138 NTTNLPAKVYANEGIAQVVFLQGDEMCEQSYKDRGGKYQGQVGITLPK 185
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InterPro; IPR001323; GCTP_deaminse.
InterPro; IPR001428; GUTPase.
Pfam; PF00692; GUTPase; 1.
ProDom; PD004900; GCTP_deaminse; 1.
Hydrolase; Complete proteoner
SEQUENCE 188 AA; 20883 MW; FB58311156742276 CRC64;
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                                                                                                                          188
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Best Local Similarity 28.0
Matches 47; Conservative
                                                                                                                          STANDARD;
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Clark M.A., Baumann L., Baumann P.;
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InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
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                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98440331; Pubmed=9767718;
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Matches 47; Conservative
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                                                               DEAMINASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
DCD_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 REYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFA--WVDPGWDGNLTLMLYNASNE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 ERINGATVDVRLGNKFRTFRGHTAAFIDLSGPKDEVSAALDRVMSDEIVLDEGEAFYLHP 85
                                                      SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                         MEDLINE-97251358; PubMed=9097040;

Hitch T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Maki H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Maki T., Mazobuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; A 460-kb DNA sequence of the Escherichia coli K-12 genome Corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.2%; Score 163; DB 1; Length 193; 29.9%; Pred. No. 1.5e-08; Pred. No ative 23; Mismatches 60; Indels
                                                                                                                                                                                     Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 PVELRYGERFVQIAFIRLEGPARNPYR-----GNYQGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 PLALRPGMLIGALSFEPLSGPAVRPYNRREDAKYRNQQGAVASRIDK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Complete proteome.
SEQUENCE 193 AA; 21249 MW; B0044051ADE7F919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA RES. 3:379-392(1996).
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-!- SUBUNIT: HOMOTETRAMER (PROBABLE).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A42940; A42940.

EcoGene; EG11418; dcd.

InterPro; IPR001332; dcTP_deaminse.

InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
. (dUTPase) mutations.";
Bacteriol. 174:5647-5653(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000296; AAC75126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M90069; AAA23669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90844; BAA15918.1; -. EMBL; D90845; BAA15923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dUTPase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00692;
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Q9ZHD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
DCD_BUCAP
ID DCD_BU(
AC Q9ZHD8
DT 20-AUG
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20-AUG-2001 (Rel. 40, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 DPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LPDWKIRKEILIEPFSEESL-QPAGYDLRVGRE--------AFVKGK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCD_METJA STANDARD, PRT; 204 AA.
057872;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LIDVE----KEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFA--WV
                                                                                                                                                                                                                                                                                                                                    "Buchnera aphidicola (Aphid endosymbiont) contains genes encoding enzymes of histidine biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 IEEWLSKKKLVIOPYPKKOLINGITVDIHLGNKFRFFYDHTTSCIDLSGSKEKIALDLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 AA; 21871 MW; 8E19D4580C7C55E8 CRC64;
                                                                                                                                        Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                        Curr. Microbiol. 37:356-358(1998).
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.0%; Score 161.5; DB 1; 26.0%; Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2190;
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MEDLINE-96337999; pubMed-8688087; Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Firzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness B.F., Weinststock K.G., Merrick J.W., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klomk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.1%; Score 154; DB 1; Length 204; 25.7%; Pred. No. 1.1e-07; Live 37; Mismatches 61; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00692; durpase; 1. Procedum: PD004900; durpase; 1. ProCom: PD004900; dcrp_deaminse; 1. Pydrolase; Complete protecome. SEQUENCE 204 AA; 23432 MW; 1218368057723371 CRC64;
                                                                                                                                                                                                                                                            Januschil.;
Science 273:1058-1073(1996).
-1- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-1- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003232; dCTP_deaminse.
Interpro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67494; AAB98415.1; -. TIGR; MJ0430; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.7%.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MJ0430
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9

Gaps

61; Indels 38;

90 SFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGSTRLA 149 

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Search completed: January 31, 2002, 13:09:23 Job time: 39 sec

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: | 187 YQK 189 150 FSK 152

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:13:34; Search time 35.08 Seconds (without alignments) 650.470 Million cell updates/sec Run on:

US-08-957-709-71 806 1 MLLPDWKIRKEILIEPFSEE......pyrgonyqgstrlafskrkkl 156 Title: Perfect score: Sequence:

Scoring table:

473505 segs, 146272329 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammani:* 11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:* sp_mhc:* sp_organelle:* sp_phage:* sp_plant:*
sp_rodent:*
sp_virus:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	O9kfv3 bacillus ha	071028 archaeal vi	Q9cb17 mycobacteri	Q9pn07 campylobact	Q9hsg3 halobacteri	Oghyc9 pseudomonas	O9pfb6 xylella fas	Q9yq32 aeropyrum p	Q9jre8 neisseria m	027642 methanobact	P74073 synechocyst	Q9e6g1 equine infe	029157 archaeoglob	Q9whf3 agrotis seg	Q9w7u6 equine infe	O89468 equine infe	089472 equine infe		09ep46 equine infe
	GI	Q9KFV3	071028	Q9CB17	Q9PN07	Q9HSG3	Q9HYC9	Q9PFB6	Q9YG32	Q9JRE8	027642	P74073	Q9E6G1	029157	Q9WHF3	907W6Q	089468	089472	066733	Q9EP46
	DB	5	12	7	7	1	7	0	-	7	٦	7	12	П	12	12	12	12	12	12
	Query Match Length DB	177	158	190	186	195	188	191	163	188	150	193	1146	168	170	1138	1146	1146	422	1148
dР	Query Match	30.1	29.4	24.5	23.5	22.9	21.3	20.4	19.7	19.2	19.0	16.8	15.7	15.6	15.6	15.6	15.6	15.6	15.3	15.3
	Score	242.5	237	197.5	189.5	184.5	172	164.5	159	155	153	135.5	126.5	126	125.5	125.5	125.5	125.5	123.5	123.5
	Result No.		7	3	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Ogrmfl zymomonas m Ogg2j6 equine infe Ogg41 equine infe Ogg8502 methanococc Ogg82k2 equine infe	Q9dkv8 caprine art Q9v3il drosophila Q9hmf3 halobacteri Q9alk2 streptococc	09jj44 mus musculu Q9cq43 mus musculu Q9cu90 mus musculu O72165 orf virus.		_	O91ff1 vaccinia vi Q66933 feline immu P90246 feline immu Q9a253 caulobacter O10287 orgyia pseu
Q9RMF1 Q992J6 Q9EP41 Q58502 Q992K2	Q9DKV8 Q9V3I1 Q9HMF3 Q9A1K2	09JJ44 09CQ43 09CU90 072165	Q84809 Q9STG6 Q9WMY7 Q98W23	Q9J5G5 Q9J880 Q9Q8S9 P87630	Q9JFF1 Q66933 P90246 Q9A253 O10287
12 12 12 13	17 17 17	17 11 11 11 11 11 11 11 11 11 11 11 11 1	175	122	12 12 12 13
199 1134 1148 161 1134	1107 188 165 148	162 162 204 160	1086 166 430 430	145 143 148	147 1123 1150 155 317
15.3 15.0 14.8 14.6	14.5 14.3 12.8 12.7	12.5 12.5 12.5 12.5	12.3	11.5	11.1 10.9 10.9 10.8
123 120.5 119.5 117.5	116.5 115.5 103 102	101 101 101 100.5	99 96.59 96.59	93.5 93.5 89.5	89.5 87.5 87.5 86.5
20 21 22 23 24	25 26 27 28	29 30 31	33 35 36 36	37 38 39 40	4443 4443

## ALIGNMENTS

6;

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4

29; Gaps

g ò g 071028 071028;

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Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Peltwell T., Fraser A., Hamin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.
"Massive gene decay in the leprosy bacillus.";
Nature 409:007-1011(2001).
InterPro; IPR001232; dGrp_deaminse.
InterPro; IPR001232; dGrp_deaminse.
Probom, PD004900; dGrP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLPDWKIRKEIL----IEPFSEESLQPAGYDLRV------GREAFVK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 GKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFAWVDP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCD OR CJ1292.
Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 GWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY-----RGNYQG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OU-2001 (TrEMBLrel. 17, Last annotation update)
POSSIBLE DEOXYCYIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 190 AA; 20820 MW; 1CA936700500B6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL139078; CAB73719.1; -
InterPro; IPR003232; dCTP_deaminse.
Probom; PD004900; dCTP_deaminse; 1.
Complete Proteome.
SEQUENCE 186 AA; 20699 MW; 68DC660FB28FD33C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.5%; Score 197.5; DB 2; 30.6%; Pred. No. 4.5e-10; tive 32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.5%; Score 189.5; DB 2; Best Local Similarity 29.4%; Pred. No. 23e-09; Matches 53; Conservative 34; Mismatches 58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWKIRKEIL ---IEPFSEES --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
24.5%
Best Local Similarity 30.6%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=197;
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MEDINE-98165772; PubMed-9497317;
Prangishvili D., Klenk H.P., Jakobs G., Schmiechen A., Hanselmann C., HOLZ I., Zillig W.;
Bacchemical and phylogenetic characterization of the dUTPase from the archaeal virus SIRV.;
J. Biol. Chem. 273:6024-6029(1998).
J. Biol. Chem. 273:6024-6029(1998).
J. GATALYITC ACTIVITY: DUTP + H(2)0 = DUMP + PYROPHOSPHATE.
EMBL, AROAZ221; AAG15873.i.;
InterPro: IPRO01428; dUTPase.

InterPro: IPRO01428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 HTFLLATTMETVKLPNHLTAFVEGRSSVGRLGLFIQNAGWVDPGFNGQITLELFNANRLP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 EYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLLPDWKIR-----KEILIEPFSEESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| | |: ::| | |: ::| | ||::| | ||:| | | |: | | ||:| | | | |: | | | ||:| | | | ||: | | | ||: | | | ||: | | | ||: | | | ||: | | ||: | | | ||: | | ||: | | | ||: | | ||: | | ||: | ||: | ||: | ||: | ||: | ||: | ||: | ||: | ||: | ||: | ||: | ||: ||: | ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID-1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-TN;
MEDLINE-2112313; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.4%; Score 237; DB 12; Length 158; 34.4%; Pred. No. 1.1e-13; Live 36; Mismatches 61; Indels 6
                                                                                                                                                                                                                                                                                                                                01-505-1998 (TrEMBLrel. 07, Created)
01-505-1998 (TrEMBLrel. 07, Last sequence update)
01-30N-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DUTPASE (EC 3-6.1.23) (DUTP PYROPHOSPHATASE) (DEOXYURIDINE-TRIPHOSPHATASE).
Archaeal virus SIRV.
VIRUSES: unclassified viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA; 17906 MW; 5BA47765E0889190 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09CB17 PRELIMINARY; PRT; 190 AA. 09CB17; 00.01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE. ML2507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 LRYGERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSK 152
                                                               114 VELRYGERFVQIAFIRLEGPARNPYRGNY---QGST 146
                                                                                                                134 IELPIGRRICQLVFAEVTGEVA-PYQGKYLFQKGAT 168
                                                                                                                                                                                                                                                                                  158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pram; Prubbyz; durrase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.4%
Best Local Similarity 34.4%
Matches 54; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE

120

Q ò q à g RESULT 100 CB 113 CB

7;

Gaps ----AF 36

35;

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3acteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequ
                                                                                                                                                                                                                                                                                          EMBL, AE004769, AAG06868.1; -.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.3%
Best Local Similarity 26.3%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00692; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 188 AA:
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                    NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20504483; PubMed=11016950;
NA WY, Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
NG W.V., Kennedy S.P., Mahairas G.G., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
R. Bhardt H., Lowe T.M., Lidng P., Riley M., Hood L., DasSarma S.;
R. Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
REMBL, AEORGH88; AGAIB8431; -.
RILEFPO: IPR001322; GCTP_deaminse.
                                                                                                           PGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY---RGNYGGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 VKGKLIDVEKEGKV-VIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 ID-----VEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFA 92
                                                       66 VEENVVDF--EGDVCIVPANSFALARTIEYFKMPDNVLAICLGKSTYARCGIIVNVTPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NW-IRKMALEHKMIEPFCEANIGKGVVSYGLSSYGYDIRVGREFKIFTNVNSTVVDPKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FIDPGFNGRVTLELSNLGKVPVALTPEMRISQLVFTELTSPADRPY-GDERGS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 WVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQGS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.9%; Score 184.5; DB 1; Length 195; 31.2%; Pred. No. 6.7e-09; ive 31; Mismatches 59; Indels 29
                                                                                                                                                                                                                                                                                                                                                                     Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLLPDWKIRK-----EILIEPFSEESL--QPAGYDLRVGRE--AFVKGKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 AA; 21542 MW; 86CCDA4D48BC0C9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HYCG;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.2%,
Matches 54; Conservative
                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
SEQUENCE 195 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                   DTD OR VNG0245G.
                                                                                                                                                                                                                                                         Q9HSG3;
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RESULT 09HYC9 1D 09 AC 09 DT 01 DT 01 DT 01 DT 01 OF PR

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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto M.R.P., Canardo C., Costa F.F., Costa M.C.R., Costa Neto C.M., Coutinho L.L., Cristofani M., Dias.Neto E., Docena C., El-Dorry H., Fraga J.S., Franca S.C., Franco M.C., Ferreira V.C.A., Ferro J.A., Farga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., And P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., A Lemos M.Y.F., Lopes C.R., Machado J.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 EKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTL 104
MEDLINE-20437337: PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";
Nature 406:959-964(2000)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 MIEPFVEROVRGADDSRVISYGVSSYGYDVRCAAEFKVFTNIHSAVVDPKNFDEKSFVDI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 MLYNASNEPVELRYGERFVQIAFIRLEGPARNPYR---GNYQGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA; 21154 MW; 9A811B5F17B2A996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LIEPFSEESLQPA------GYDLRVGRE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%; Score 172; DB 2; 26.3%; Pred. No. 8.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 DVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Hino Y., Horikowa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-i., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagat Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Makamura Y., Nomura N., Sako Y., Kikuchi H.,
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyum pernix Kl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GYDLRVGRE------AFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeropyrum pernix.
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AA; 21531 MW; D7B23653F94B3649 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-1999 (TrEMBLrel. 17, Last annotation update)
163AA LONG HYPOTHETICAL DEOXYCYTIDINE TRIPHOSPHATE L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.4%; Score 164.5; DB 3
30.5%; Pred. No. 3.9e-07;
Live 25; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003917; AAF83572.1; InterPro; IPR003232; dCTP_deaminse. ProDom; PD004900; dCTP_deaminse; 1.
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InterPro: IPR00323; dCTP_deaminse.
InterPro: IPR001428; dTPasse.
Pfam: PF00652; dUTPase: 1.
ProDom; PD004900; dCTP_deaminse; 1.
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MEDLINE-99310339; PubMed-10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 --EGPARNPYR---GNYQGST 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 DPDDVCQTSYRDRNGKYQGQT 184
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Best Local Similarity 30.5%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
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095 GOLT

096 GOLT

097 GOLT
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STRAIN-MC58 / SEROGROUP B;
MEDLINE-201755; PubMed-10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Heisen W.C., Gwinn M.L., DeBDY R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisserla meningitidis serogroup B strain MC58.";
                                                                                                                                                                                                                                                                                         59 LILTLERIKLPDDVMGDMKIRSSLAREG-VIGSFAWVDPGWDGNLTLMLYNASNEPVELR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis (serogroup A), and
Neisseria meningidis (serogroup B).
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699, 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                               62; Indels 18; Gaps
                                                                                                                          ------EAFVKGKLIDVEKEGKVVIPPREYA 58
                                                                                                                                                                                     17 VVKGHSNGAIQPAGVDLSVGEIESLADAGFLGEEDKIMPKGDRIQCE-YGVCELEPGAYR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CH-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN NMA1060 (DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATAIN—22491 / SEROGROUP A / SEROTYPE 4A;

MEDLINE=202556; PUDMG=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Rate S.R., Morelli G., Basham D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.,

Complete DNA sequence of a serogroup A strain of Neisseria

menigitidis Z3491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
   Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.2%; Score 155; DB 2; Length 18
24.1%; Pred. No. 2.7e-06;
Live 32; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.7%; Score 159; DB 1; 32.7%; Pred. No. 9.8e-07; iive 19; Mismatches 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AA
                                                                                                                                                                                                                                                                                                                                                                                   118 YGERFVOIAFIRLEGPARNPYRGNYOG 144
                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : |:||| : |:|||
134 MGSRIAQLVVARVEGPLTSLYKGDYQG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                          13 LIEPFSEESLQPAGYDLRVGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:1809-1815(2000).
EMBL, AL162755; CAB84324.1; -
EMBL, AE002438; AAF41260.1; -
TIGR: NMB0849; -
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity.
Matches 41; Conserva
Query Match
Best Local Similarity
Matches 48; Conserv
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MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 REGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGP----ARNPYR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLPDWKIRKEI---LIEPFSEESL----QPA-----GYDLRVGREAF----VKG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 KLIDV------EKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLA 83
                                                                                                                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Equine infectious anaemia virus proteins with epitopes most frequently recognized by cytotoxic T lymphocytes from infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
McGuire T.C., Leib S.R., Lonning S.M., Zhang W., Byrne K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McGuire T.C., Leib S.R., Lonning S.M., Zhang W., Byrne K.M.
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-!- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE
TRANSCRIPTASE).
                                                                                                                                                                                                                                                                                                                               EMBL; D90912; BAA18149.1; -.
InterPro; IPR003232; dCTP_deaminse.
Probon; PD004900; dCTP_deaminse; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 193 AA; 21378 MW; BA8DF70AD4348330 CRC64;
                                                      Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POL PROTEIN (FRAGMENT).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 21.4 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
16.8%; Score 135.5; DB 2
Best Local Similarity 26.1%; Pred. No. 0.00015;
Matches 48; Conservative 29; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gen. Virol. 81:2735-2739(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=1148;
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                                                                                         KEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLM 105
                                                                                                              -----ALILTLER-IKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 EPPIYRLEPGKAYLASVDRMIEIPEGYAMLYLPRSTLLRSFVSVQTAVGDPGFRGTLQFL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVGR--EAFVKGKLIDVEKEGKVVIPPREY- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.R., Douette-Stamn L.A., DeLoughery C., Lee H.-M., DuBois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Hartison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Juwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
                                          Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
                                                                                                                                                                106 LYNASNEPVELRYGERFVQIAFIRLEGPARNPYR---GNYQGSTRLAFSK 152
                                                                                                                                                                                                     138 FSNTTPLPAKIYAGEGVAQVLFFESDEICETSYKDRNGKYMGQTGVTLPK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%; Score 153; DB 1; Length 150; 32.3%; Pred. No. 3e-06; Live 24; Mismatches 59; Indels
                     ----GYDLRVGRE----AFVKGKLIDVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LtaH: functional analysis and comparative genomics.";
Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 AA; 16996 MW; AFA09D55FB371648 CRC64;
                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYCYTIDINE-TRIPHOSPHATE DEAMINASE RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 LYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQ 143
                                                                                                                                                                                                                                                                                                150 AA.
                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: ACENO22: AABB6078.1; -
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P74073 PRELIMINARY;
P74073;
01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 32.39 tes 51; Conservative
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00692; dUTPase;
                   13 LIEPFSEESLOPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deltaH: functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=145262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
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01-JAN-1998 (
01-JUN-2001 (
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Best Local S:
Matches 51;
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RESULT 11

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q ŏ QQ P74073

25 P P

7;

Length 193;

Indels

64; DB 2;

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SEQUENCE FROM N.A.

STRAIN-VC-16, DEM 4304 / ATCC 49558;

MEDLINE-98040343; PubMed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gvinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Jeaham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zho,

Overbeek R., Gocayne J.D., Weldman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Wason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
C. -i- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

EMBL; AF247394; AAG02702.1; -FAMILY.

InterPro; IPR001969; ASP_protease.

InterPro; IPR001969; ASP_protertrov.

InterPro; IPR001969; May_prot_retrov.

InterPro; IPR001969; RaseH.

IPR001969; RaseH.

IPR001969; RaseH.

IPR001969; RaseH.

IPR001969; RaseH.

IPR01969; RaseH.

IRR01969; RaseH.

IRR01969; RaseH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 KIRKEILI----EPFSEESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Mature 390:364-370(1997).
EMBL; AE001027; ABB90130.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1146;
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Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
WCBI_TaxID-2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.7%; Score 126.5; DB 12; Length Best Local Similarity 23.0%; Pred. No. 0.0097; Matches 32; Conservative 38; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYCYIDINE TRIPHOSPHATE DEAMINASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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52 IPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LPKGVYRAKLN-EVVRLGNDIMAIARPRSTLIRCGANVLTAVWDAGYEGRSEVSIVVHND 131
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                                                                                                                                                                                                                                                                                                                                                                                                                               8 IRKEILIEPF--SEESLQPAGYDLRV-----GREAFVKGK-----LIDVEKEGKVV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 LRVGREAFVKGKL----IDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLA- 83
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 18.5 KDA PROTEIN.
Agrotis seqetum granulosis virus (AsGV) (Agrotis segetum granulovirus).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
NCBL_TAXID=10464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.6%; Score 126; DB 1; Length 168; Best Local Similarity 29.4%; Pred. No. 0.00088; Matches 45; Conservative 25; Mismatches 65; Indels 18;
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InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 168 AA; 19227 MW; D99EE0FB943869D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1138 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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141 TDRAEGGF-GSTGIASQQQEEI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Q9WHF3;
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Q9W7U6;
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Petropoulos C.J.; "Development and characterization of an in vivo pathogenic molecular clone of equine infectious anemia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98105784; PubMed-9445039; Cook R.F., Leroux C., Cook S.J., Berger S.L., Lichtenstein D.L., Ghabrial N., Montelaro R.C., Issel C.J.; "Development and characterization of an in vivo pathogenic molecular clone of equine infectious anemia virus."; J. Virol. 72:1383-1393(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANGCRIPTASE).

-! SIMILARITY: TO RETROVIRAL INTEGRASE, C-TERMINUS.
-! SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO KNOWN AS THE RETROPESEIN FAMILY.

EMBL; AF033820; AAC82600.1; -.

EMBL; AF016316; AAC03761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD000946; dufpase; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_ROT_RETROY. 1.
Aspartyl protease; DNA-binding; Endonuclease; Hydrolase;
Nucleotidyltransferase; Polyprotein; RNA-directed DNA polymerase.
SEQUENCE 1138 AA; 128709 MW; BD0F7AA5BAA2734D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

GOOK R.F., Leroux C., COOK S.J., Berger S.L., Lichtenstein D.L.,
Ghabrial N.N., Montelaro R.C., Issel C.J.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

-1 FTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROT

-1 SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE

TRANSCRIPTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (In) Coffin J.M. (eds.);
Retroviruses, pp 757-757, Cold Spring Harbor Laboratory Press.
New York (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chappey C.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POL POLYPROTEIN.
GAG-POL OR POL.
GAG-POL OR POL.
VINUAGE: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001969; Asp_protease.
InterPro; IPR001995; Asp_prot_retrov.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_zn.
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-98105784; PubMed=9445039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
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SEQUENCE FROM N.A.
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Pfam; PF00552;
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7 KIRKEILI----EPFSEESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILT 62

Query Match 15.6%; Score 125.5; DB 12; Length 1138; Best Local Similarity 23.0%; Pred. No. 0.012; Matches 32; Conservative 38; Mismatches 50; Indels 19;

Search completed: January 31, 2002, 13:13:34 Job time: 60 sec

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Zea mays protein Protein involved

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Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR;
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AAY36904
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                      Misc-difference
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21-MAR-1997;
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                      Compugen Ltd
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                                                                                 January 31, 2002, 13:15:19
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AAW72870
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This is the amino acid sequence of the P45 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638.

The sequence is predicted from a DNA sequence (see AAW73844) are the from genomic DNA by PCR. P45 and P30 (see AAW72844) are the predominant components of PEF, which acts to enhance the activity of P. Furiosus DNA polymerase. P45 functions as a durpase, and can be reactions. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies. Also polymerases, as well as DNA constructs and antibodies. Also included are methods for identifying compositions with PEF activity, for purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity.

Mucleic acid polymerase reactions can be enhanced (claimed) by mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acids sequencing or amplification
                                 Polymerase enhancing factor proteins, extracts and complexes - improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication
                                                                                                           Claim 17; Page 43; 161pp; English
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                                                                                                  This peptide comprises an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 8638. It has been obtained from isolated P45; a full-length sequence is provided in AAM72847. PEF, the predominant components of which are P45 and P50 (see AAM72844) proteins, enhances the activity of P. furiosus DNA Polymerase, thereby providing activity of P. furiosus DNA Polymerase, thereby providing propling and possesses polymerase enhancing activity. The invention provides novel extracts, proteins and complexes that improve the provides novel extracts, proteins and complexes that improve the polymerisation activity of nucled activity. These peptide. Also included proteins including the P45 N-terminal peptide. Also included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that include proteins including the P45 N-terminal peptide. Also included are methods for identifying and using these compositions, and specific extracts, proteins and compositions compositions at least 1 polymerase activity. Nucleic acid polymerase compositions at least 1 polymerase activity. Nucleic acid polymerase composition activity. Rits are provided for replicating nucleic acid enhancing activity. Rits are provided for replicating nucleic acid enhancing activity. Rits are provided for replicating nucleic acid acids. The Kits are provided for replicating nucleic acid acids. The Kits are provided for replicating nucleic acid acids. The Kits are provided for replicating nucleic acid acids. The Kits are provided for replicating activity.
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Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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primers"
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                                                                     Claim 17; Page 33; 161pp; English.
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase enhancing factor P45 component N-terminal peptide.
Ouery Match 82.4%; Score 14; DB 19; Length 156; Best Local Similarity 100.0%; Pred No. 4.1e-07; Matches 14; Conservative 0; Mismatches 0; Indels
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Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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100.0%; Pred. No. 0.61;
iive 0; Mismatches
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                                                                                            This peptide comprises an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. It has been obtained from isolated P45. PCR primers (see AAV63861-64) based on the peptide were used to amplify P45 DNA (see AAV63860). A full-length P45 sequence is provided in AAW72847. PEF, a predominant component of which is P45 protein, enhances the activity of P. furiosus DNA Polymerase, thereby providing replication products of greater length and purity. P45 is a duTPase and possesses polymerase enhancing activity. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These complexes may included are methods for identifying compositions peptide. Also included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase compositions can be enhanced (claimed) by mixing a nucleic acid cumpanial template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acid control acid composition having polymerase entains and acids. The kits are provided for replicating nucleic acids controls acids of the beach and accomposition having polymerase entains and composition having polymerase entains and composition having polymerase entains and composition having polymerase entains acids and accomposition having polymerase entains and acids and accomposition having polymerase entains accomposition accompositio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequencing or amplification (preferably PCR or RT-PCR).
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                              Claim 17; Page 33; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW72870 standard; Peptide; 15 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Leu, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US05497.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STRA-) STRATAGENE.
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21-MAR-1997;
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Gaps

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito K,
Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                        Human protein sequence SEQ ID NO:12168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sogai T, Nishikawa T, Hay
Sugiyama T, Wakamatsu A,
AAB93202 standard; Protein; 782 AA
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                    26-JUN-2001 (first entry)
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to the complementary strand of a polynuclectide which comprises one of the S602 nuclectide sequences defined in the specification, where the oligonuclectide comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to the sequence and an oligonuclectide comprising a sequence, where the oligonuclectide which comprises a 3'-end sequence, where the oligonuclectide which comprises a 3'-end sequence, where the oligonuclectide comprises a 1'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the firedually! Full-length comprises a 1'-end be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosts of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length AHH3632 to AAH3632 to AAH363 to AAH36
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41.2%; Score 7; DB 22; Length 782;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels
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990S-0123180.
990S-0123518
990S-012578
990S-0126785.
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990S-01308714.
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05 MAR-1999;
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01 APR-1999;
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PR 06 - MAY - 1999; 99U5 - 0132486.

PR 17 - MAY - 1999; 99U5 - 0134287.

PR 14 - MAY - 1999; 99U5 - 0134281.

PR 14 - MAY - 1999; 99U5 - 0134218.

PR 14 - MAY - 1999; 99U5 - 0134211.

PR 15 - MAY - 1999; 99U5 - 0134211.

PR 21 - MAY - 1999; 99U5 - 013421.

PR 22 - MAY - 1999; 99U5 - 013421.

PR 23 - MAY - 1999; 99U5 - 013421.

PR 24 - MAY - 1999; 99U5 - 013421.

PR 25 - MAY - 1999; 99U5 - 013421.

PR 26 - MAY - 1999; 99U5 - 013421.

PR 27 - MAY - 1999; 99U5 - 013421.

PR 27 - MAY - 1999; 99U5 - 013421.

PR 28 - MAY - 1999; 99U5 - 013421.

PR 16 - JUN - 1999; 99U5 - 013421.

PR 16 - JUN - 1999; 99U5 - 013421.

PR 16 - JUN - 1999; 99U5 - 013442.

PR 16 - JUN - 1999; 99U5 - 013442.

PR 18 - JUN - 1999; 99U5 - 013442.

PR 18 - JUN - 1999; 99U5 - 013442.

PR 18 - JUN - 1999; 99U5 - 013442.

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PR 18 - JUN - 1999; 99U5 - 013442.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 18 - JUN - 1999; 99U5 - 014239.

PR 19 - JUL - 1999; 99U5 - 014331.

PR 19 - JUL - 1999; 99U5 - 014331.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 19 - JUL - 1999; 99U5 - 0144333.

PR 20 - JUL - 1999; 99U5 - 0144333.

PR 20 - JUL - 1999; 99U5 - 0144333.

PR 20 - JUL - 1999; 99U5 - 0144433.

PR 21 - JUL -
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99US-0145089.
99US-0145192.
99US-0145145.
99US-0145214.
99US-0145214.
99US-0145913.
99US-0145913.
99US-0145919.
99US-0145919.
99US-0146389.
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99US-0147038.
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990S-0148171.
990S-0148319.
990S-014855.
990S-0148684.
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                                                                                                                                Score 6; DB 21;
Pred. No. 33;
0; Mismatches 0
                                                                                                                            35.3%; Scc.
100.0%; Pre
0; }
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99US-0160814.
99US-0160815.
99US-0160980.
99US-0160981.
99US-0161404.
99US-0161406.
99US-0161360.
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99US-0161361.
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99US-0123180.
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                                                                                                                                                   Conservative
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                                                                                                                                         Similarity 6; Conserv
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          21-0CT-1999;
22-0CT-1999;
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29-MAR-1999;
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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 72467.
                                                 AAG56382 standard; Protein; 110 AA
                                                                                                                                                                                                                          990S-0121825
990S-0123548
990S-0125788
990S-0125788
990S-0126785
990S-0128746
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990S-0128744
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990S-0120487
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                                                                                    18-OCT-2000 (first entry)
                                                                                                                                                       Arabidopsis thaliana
35 illpdw 40
                                                                                                                                                                        EP1033405-A2.
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                                                                  AAG56382;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                        Arabidopsis thaliana protein fragment SEQ ID NO: 79597.
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                                                                                          Arabidopsis thaliana
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Pred. No.
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100.0%; Pre
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Matches 6; Conservative
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AAG61372
ID AAG6137
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AAG61372 standard; Protein; 110 AA.

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        18 - JUN-1999;
        99US-0133462

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        99US-0133763

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        99US-0133763

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        99US-0144335

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PR 26 AUG-1999; 9908-015066.

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PR 27 AUG-1999; 9908-015066.

PR 27 AUG-1999; 9908-0151066.

PR 27 AUG-1999; 9908-0151066.

PR 27 AUG-1999; 9908-015108.

PR 27 AUG-1999; 9908-015108.

PR 27 SEP-1999; 9908-015108.

PR 28 SEP-1999; 9908-015108.

PR 28 SEP-1999; 9908-015108.

PR 29 SEP-1999; 9908-015108.

PR 29 SEP-1999; 9908-015108.

PR 20 SEP-1999; 9908-015108.

PR 2
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AAG16696 standard; Protein; 154 AA.

RESULT 1

17-OCT-2000 (first entry)

AAG16696;

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AAC AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; catipsoriatic; antiparkinsonian; noctropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidianematory; antibacterial; antiviral; antifungal; antirheumatic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidianematory; antibacterial; antiviral; antichension of predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the pathological conditions associated with an ORFX-associated disorder. The nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, colliferative disorders, neurodegenerative disorders, osteoarthritis, hypertension, hypothyroidism, cholesterol ester storrage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, auticimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nectural heemoglobinuria, antiinfilammatory disease; to enhance companied impublic thrombosis; and as a contraceptive.
            Vulnetary; antipopoiatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; fundobytic; nequilart; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidiabetic; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiantenterial; antifungal; antirheumatic; antithyroid; antiantenterive disorder; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; hypothyroidism; SCID; AIDS; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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02-APR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                              Arabidopsis thaliana protein fragment SEQ ID NO: 17441.
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Query Match 35.3%; Score 6; DB 21; Length 151; Best Local Similarity 100.0%; Pred. No. 50; Matches 6; Conservative 0; Mismatches 0; Indels

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Best Local Similarity 100.0%;
Matches 6; Conservative (
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AAB93696

us-08-957-709-11.rag

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Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                           Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                   Eucalyptus grandis cell signalling involved protein SEQ ID NO:542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 241-242; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2000; 2000WO-US00724.
                                                                   27-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                      Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                WO200042171-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2000
                      AAB25223;
full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to the sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence; selected from those defined in the specification. The primer sets can be used in antisense therapy and the primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow sequences; AAB92446 to AAH13633 to AAH13633 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632. The present invarious and sequences; and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K,
, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID 13267; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T, Nishikawa T, Hayashi K, S
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                 Human protein sequence SEQ ID NO:13267
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100.0%; Prev
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-0116126.
                 (first entry)
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6; Conservative
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                                                                                                                Human; primer;
                                                                                                                                                                                                           EP1074617-A2.
                                                                                                                                                             Homo sapiens
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                 26-JUN-2001
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99US-0162866.

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pine (Pinus radiata also known as Monterey pine). The protein sequences isolated from encalyptus (Bucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to'decrease branching frequency in forest tree species giving long stretches of valuable knot free clear wood which can be used in solid timber furniture and veneers.
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to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
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Mismatches
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DB 22; Length 182; 0; Indels

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AAB25223 standard; Protein; 200 AA.

RESULT 15 AAB25223

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014495 homo sapien Q9vyt2 drosophila Q9fgg4 arabidopsis P72969 synechocyst

Q9kqm8 vibrio chol Q9an62 bradyrhizob Q9uhn0 homo sapien Q9v282 pyrococcus O9svx6 arabidopsis O84773 chlamydia t O9plf5 chlamydia m O02297 caenorhabdi

09fg12 arabidopsis 09sva7 arabidopsis 067052 aquifex aeo

Q9fvv6 arabidopsis Q9y4q6 homo sapien Q99ulh9 laulfurispha Q9ulh9 homo sapien O87984 bordetella

Word size :

Searched:

sequence:

Title:

Q9askl oryza sativ Q9aj63 rickettsia Q9aj36 rickettsia P76465 escherichia

OM protein

Run on:

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Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AB046816; BAB13422.1; -.
NON_TER 1
SEQUENCE 1151 AA; 130000 MW; ED6120D527699C04 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
KIAALS96 PROTEIN (FRAGMENT).
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Last annotation update)
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ilarity 100.0%; Pred. No. 55;
Conservative 0; Mismatches
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095X52
09LHE7
014495
014495
09VYTZ
09FGG4
09FG08
099AN62
09CHNO
09V282
09FG12
09FG12
09SVA7
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Q9Y4Q6
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SEQUENCE FROM N.A.
PubMed=10997877;
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Matches 7; Conserv
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09unj2 homo sapien
09unj2 homo sapien
09x18 pyrococcus
075314 homo sapien
09x44 aeropyrum p
09x171 thermotoga
021778 reclinomona
02619 methanobact
029219 archaeoglob
070356 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91ahl acetobacter
Q9vb61 drosophila
Q9xtil caenorhabdi
Q42912 malus domes
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                                                                         ; Search time 130.99 Seconds
(without alignments)
18.983 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                473505 seqs, 146272329 residues
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                                                                          January 31, 2002, 13:34:55
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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Q9L7U5
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0901B8
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sp_invertebrate:*
sp_mammal:*
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sp_phage:*
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Length 1151;

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-WISB8 / DSM 3109;
SETAIN-WISB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDson K.E., Clayton R.A., Gill S.R., Jinher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;
Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
Mature 399:333-3291999)
EMBL; AB001770; AAD36203.1; -.
TIOR, YM1127, -.
                                                                                                                     Gaps
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SEQUENCE FROM N.A.

SEQUENCE FROM N.C.;

"Convergent Adaptive Radiations in Madagascan and Asian Ranid Frogs
Reveal Co-variation between Larval and Adult Traits.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF249179; AAG49822.1;

NON_TER 17 17

SEQUENCE 177 AA; 20423 MW; 28A72B222A031854 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
17YROSINASE PRECHRSOR (FRAGMENT).
Limonectes kuhlil.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
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                                                 Length 132;
                                                                                                                 0; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UND-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 19.9 KDA PROTEIN.
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                                                     Score 6; DB 2;
Pred. No. 87;
0; Mismatches
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Bacteria; Thermotogales; Thermotoga.
NCBI_TaxID=2336;
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SEQUENCE FROM N.A.

SEQUENCE Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,

Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Theologis A., Ecker J.,

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC023279; AAF79252.1; - 333CEEC1816A74D5 CRC64;
                                                                                                                                                                                                                           Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Sperantophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae; eurosids II; Brassicales: Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic sequence for Arabidopsis thaliana BAC F12K21 from chromosome
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SEQUENCE FROM N.A.

MCClain J.R., Rollo D., Bauer C.E., Rushing B.R., Jiang Z.;

McClain J.R., Rollo D., Bauer C.E., Rushing B.R., Jiang Z.;

"Gene duplication and lateral transfer events giving rise to components.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

BEBL; AF220002; AAF35844.1;

NON_TER 132 132 13601 MW; ESEEOC543E479CD1 CRC64;
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Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Rhodospirillum.
NCBI_TaxID=34018;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
FLAGELLAR M RING PROTEIN FLIF (FRAGMENT).
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RESULT Q9NUJ2

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SEQUENCE FROM N.A.
MEDLINE=98158729; PubMed=9490638;
Post P., Bokoch G., Mooseker M.;
"Human myosin-IXb is a mechanochemically active motor and a GAP for
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wirth J.A., Jensen K.A., Post P.L., Bement W.M., Mooseker M.S.; "Human myosin.Tib, an unconventional myosin with a chimerin-like rho/rac GTPase-activating protein domain in its tail."; J. Cell Sci. 109:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-IXB SPLICE VARIANT (FRAGMENT).
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1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
101-MAX-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 28.2 KDA PROTEIN.
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                                                           Mismatches
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                       Score 6; I
Pred. No.
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STRAIN-MADRID E;
MEDLINE-99039499; PubMed-9823893;
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                         35.55,
100.0%; Pre-
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EMBL; AF020267; AAC26597.1; -.
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                                                             Conservative
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                   Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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KEILIE 30
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ11339 FIS, CLONE PLACE1010743, WEAKLY SIMILAR TO HOMO SAPIENS
MYOSIN-IXB SPLICE VARIANT MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ248284; CAB49431.1; .
                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSBE-PLACENTA;
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
2-KETOGLUTARATE FERREDOXIN OXIDOREDUCTASE, SUBUNIT GAMMA (KORG-2).
KORG-2 OR PAB0348.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                         Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO02201; BAA92132.1; -
SEQUENCE 182 AA; 20562 MW; 4311D85F0B587E20 CRC64;
178 AA; 19894 MW; F6665DA03B4F4C0D CRC64;
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                                                       35.3%; Score 6; DB 2; Len 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0;
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                                                       Query Match 35.3
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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69 IRKEIL 74
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SEQUENCE FROM N.A.
STRAIN-MSB8 / DSB 3109;
MEDLINE-99287316; PubMed-10360571;
MEISON K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Peterson J.D., Nelson W.C., Ketchum K.A.,
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
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35.3%; Score 6; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.56+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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Nature 396:133-140(1998).
EMBL: AJ25272; CAA14951.1; -.
Hypothetical protic Complete proteome.
SEQUENCE 247 AA: 28210 MW; 606D03AC2B030392 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09YA74;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 26.7 KDA PROTEIN APE1860.
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Last sequence update)
Last annotation update)
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01.NOV-1999 (TrEMBLrel. 12, Last seque
01-JUN-2001 (TrEMBLrel. 17, Last annot
LIPASE, PUTATIVE.
TM350.
THETMOCOGA MARITIMA.
BACTERIA: Thermotogales; Thermotoga.
NCBL_TAXID-2336;
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NCBI_TaxID-56636;
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80 IRKEIL 85
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09X171;
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09YAT4
AC 09YAT4
AC 09YAT4
DT 01-NOV
DT 01-NOV
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McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M., Fraser C.M., Fraser C.M., Fraser C.M., Fraser C.M., Fraser C.M., Malte G.C., Praser C.M., Fraser C.M., Malter J. Smith H.O., Venter J.C., Fraser C.M., Fraser C.M., Fraser C.M., Fraser C.M., Malter J. Smith H.O., Venter J.C., Fraser C.M., Fra
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STRAIN=ATCCS0334;
MEDILINE=97311393; PubMed=9168110;
Lang B.F., Burger G., O'Kelly C.J., Cedergren R., Golding G.B.,
Lemieux C., Sankoff D., Turmel M., Gray M.W.;
"An ancestral mitochondrial DNA resembling a eubacterial genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Nature 387:493-497(1997).

SEQUENCE FROM N.A.
STRAIN-ATCC50394.
Lang B.F., Burger G.;
Submitted (2017-1997).

InterPro: JPR002641; Cytc_asm.
InterPro: JPR003557; Cytc_biog_ccmC.
Pfam: PP01578; Cytc_asm.
InterPro: JPR013586; CCMCBIOGNSIS.
Mitochondrion.
SEQUENCE 262 AA; 30542 MW; 69623E67457547C5 CRC64;
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.5e+02;
s 0; Indels
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SEQUENCE 259 AA; 29603 MW; 426CCE1F16A9EC97 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SUBUNIT OF ABC TRANSPORTER FOR CYTOCHROME C1.
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Best Local Similarity 100.0%; Pred. No. 1.5
Best Chest 6; Conservative 0; Mismatches
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NCBI_TaxID=48483;
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Matches 6; Conserv
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245 KIRKEI 250
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SEQUENCE
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; Pubmed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Mendenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Wetdman J.F., McDonald L., Utterback T.,

Coctton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DELTA H;

KEDLINE-8007514; PubMed=9371463;

A MEDLINE-80157514; PubMed=9371463;

A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

A Harison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Juwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

R. MBL; AE000795; AAB84510.II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee H.-M., DuBois J.,
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                                                                                                                                                                                                                                                                                                      Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
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                                                                                                                                                                      Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBirel. 05, Last sequence update)
01-JUN-2000 (TrEMBirel. 14, Last annotation update)
HYPOTHETICAL 30.7 KDA PROTEIN.
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100.0%; Pred. No. 1.6e-
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                                                                   268 AA.
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Best Local Similarity 100.
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                                                                   PRELIMINARY;
                                                                                                                                   01-JAN-1998 (TrEMBLrel.
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                                                                                                                                                                                                                                      CONSERVED PROTEIN MTH1.
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| 149 KEILIE 154
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01-JUN-2001
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ROWEN L., Qin S., Loretz C., Mix L., Lasky S., Madan A., Hood L.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-! - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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                                                                                                                                                                     35.3%; Score 6; DB 1; Length 269; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                    Indels
Nature 390:364-370(1997).

EMBL; AEGO1031; AAB90208.1; -.
TIGR; AF1043; -.
Hypothetical protein; Complete proteome.
SEQUENCE 269 AA; 30670 MW; 6A41E02B25FBC0E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30334 MW; E745E84220343663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-500-1998 (TrEMBLrel. 07, Created)
01-806-1998 (TrEMBLrel. 07, Last sequence update)
01-501-1008-1001 (TrEMBLrel. 17, Last annotation update)
BUTYROPHILIN-LIKE (FRAGMENT).
BTNL2 OR NG10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.3%; Score 6; 'DB 11; Le 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    272 AA
                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 31, 2002, 13:37:30 Job time: 155 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1859549; Btn12.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF050157; AAC05289.1;
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
The 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 AA;
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# This Page Blank (uspto)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:38:00 ; Search time 46.78 Seconds (without alignments) 13.324 Million cell updates/sec

US-08-957-709-11 17 1 GAILLPDWKIRKEILIE 17

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | di   |        |               | SUMMARIES   |                    |
|---------------|-------|------|--------|---------------|-------------|--------------------|
| Result<br>No. | Score |      | Length | DB            |             | ip.                |
| 1             | 14    | 82.4 | 156    | . ⊣           | DCD PYRHO   | 057706 pyrococus   |
| 2             | 13    | 76.5 | 154    | Н             | DCD_PYRAB   | pyrococcu          |
| m             | 9     | 35.3 | 202    | Н             | SODM_STRMU  | _                  |
| 4             | 9     | 35.3 | 220    | Н             | Y132_METJA  | _                  |
| 'n            | 9     |      | 249    | ~1            | Y768_METJA  | Q58178 methanococc |
| 9             | 9     |      | 260    | 7             | YLBK_BACSU  | 034731 bacillus su |
| 7             | 9     | 35.3 | 284    | ٦             | CELA_ACEXY  | acetobact          |
| 80            | 9     | 35.3 | 285    | П             | YFIE_BACSU  | P54721 bacillus su |
| σ             | 9     | ů.   | 336    | 7             | Y883_METJA  |                    |
| 10            | 9     | S.   | 344    | Н             | STSY_RAUSE  |                    |
| 11            | 9     | ٠    | 478    | П             | HLYD_PASHA  |                    |
| 12            | 9     | S.   | 478    | Н             | HLYD_PASSP  |                    |
| 13            | 9     | 35.3 | 583    | Н             | T2F1_FLAOK  | P14870 flavobacter |
| 14            | 9     |      | 595    | Н             | P2X7_RAT    | Q64663 rattus norv |
| 15            | ø     | δ.   | 799    | Н             | YJV2_YEAST  |                    |
| 16            | 9     | ď.   | 829    | -             | GUTR_BACSU  |                    |
| 17            | 9     | 'n.  | 854    | -             | CLPC_CHLTR  |                    |
| 18            | 9     | ď.   | 870    | <del></del> 1 | CLPC_CHLMU  | Q9pka8 chlamydia m |
| 19            | 9     | ď.   | 992    | 1             | SCA4_RICTY  | Q9aj63 rickettsia  |
| 50            | 9     | •    | 1022   | -             | SCA4_RICPR  | Q9zd49 rickettsia  |
| 21            | 9     | S    | 1181   | Н             | YY02_METJA  | Q60301 methanococc |
| 22            | 9     | δ.   | 1391   | П             | N157_YEAST  | sacch              |
| 23            | 9     | 35.3 | 1756   | 7             | PEPL_HUMAN  | homod              |
| 24            | 9     | S    | 2032   | 7             | CTOG_HUMAN  | рошо               |
| 25            | 9     | 35.3 | 2158   | П             | MY 9B_HUMAN | homod              |
| 56            | 2     | 29.4 | 52     | ٦             | Y567_PSEAE  | bsend              |
| 27            | 2     | 29.4 |        | 7             | RC2A_ARATH  | Q9zng7 arabidopsis |
| 28            | S     | 29.4 |        | <b>~</b>      | YB69_SYNY3  |                    |
| 29            | 5     | 29.4 | 58     | Н             | VPU_HV12H   |                    |
| 30            | S     | 29.4 | 73     | -             | RC23_ARATH  |                    |
| 31            | 2     | 29.4 |        | -             | RC24_ARATH  | _                  |
| 32            | 2     | 29.4 | . 75   | 1             |             | 082232 arabidopsis |
| 33            | 2     | 29.4 | 92     | ٦             | FERN AZOVI  |                    |

RESULT

| 050322 synechococc 005971 synechocyst Q37761 cyanophora P77354 escherichia P76170 escherichia Q47874 alligator m Q36456 ornithorhyn P44956 haemophilus P16436 box taurus P49773 homo sapien P70349 mus musculu P80912 oryctolagus                                                                        | Thermococcaceae; Pyrococcus.  Thermococcaceae; Pyrococcus.  Haikawa Y., Hino Y.,  gi H., Hosyama A., Nagai Y.,  H., Tamaiya M., Ohfuku Y.,  aki J., Kushida N., Oguchi A.,  obb F.T., Horikoshi K.,  of the genome of a hyper- horikoshii OT3.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | DEAMINASE FAMILY.  It is produced through a collaboration informatics and the EMBL outstation te. There are no restrictions on its slong as its content is in no way removed. Usage by and for commercial of (See http://www.isb-sib.ch/announce/ch).                                                                                                                                                                                           | 85 CRC64;                                            | ; Length 156;08; 0; Indels 0; Gaps 0;                                                                                                         |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| 34 5 29.4 102 1 CH10_SYNVU 35 5 29.4 102 1 CH10_SYNV3 36 5 29.4 103 1 CH10_CXAPA 37 5 29.4 112 1 YAFU ECOLI 38 5 29.4 113 1 YNFE_ECOLI 40 5 29.4 115 1 NU3M_ALLMI 41 5 29.4 115 1 NU3M_ORNAN 42 5 29.4 125 1 HINT_HUMAN 44 5 29.4 125 1 HINT_HUMAN 44 5 29.4 125 1 HINT_MOUSE 45 5 29.4 125 1 HINT_RABIT | THO  CLD_EYRHO  STANDARD; PRT; 156 57706; 0-AUG-2001 (Rel. 40, Created) 0-AUG-2001 (Rel. 40, Last sequence upda 0-AUG-2001 (Rel. 40, Last sequence upda 0-AUG-2001 (Rel. 40, Last sequence upda 0-AUG-2001 (Rel. 40, Last annotation up ROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE).  EMAINASE).  CLD OR PH1997.  YOCOCCUS HOLINGSHAIL.  FORDER ENDA N.A.  TRAIN-0-73; 1]  EQUENCE FROM N.A.  TRAIN-0-73;  AWATABAYA137; PUDMEd=9679194;  AWATABAYA177; PUDMEd=9679194;  AWATABAYA177; PUDMEd=9679194;  AWATABAYA177; PUDMED S.T., KOSU ARA M., HOTIKAWA H.,  COMPLE S., SSKAINE M., MACAZAWA  UNDARAMULA T., YOSAIZAWA T., NAKAZAWA  ORDILLY SOBIZAWA T., NAKAZAWA  ORDILLY SOBIZAWA T., KUGOH Y., YAMAZAWA  ORDILLY SOBIZAWA T., KUGOH Y., YAMAZAWA  ORDILLY SOBIZAWA T., KUGOH H., YAMAZAWA  NA RES. 5-55-76(1998). | In SIMILARITY: BELONGS TO THE DOTP DEAMINASE FAMILY.  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the like European Bioinformatics Institute. There are no resime by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb or send an email to license@isb-sib.ch). | MBL;<br>nter<br>nter<br>fam;<br>roDc<br>ydrc<br>EQUE | Query Match 82.4%; Score 14; DB 1; Best Local Similarity 100.0%; Pred. No. 4.1e- Matches 14; Conservative 0; Mismatches 4 LLPDWKIRKEILIE 17 1 |
|                                                                                                                                                                                                                                                                                                          | й С'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 38888888888                                                                                                                                                                                                                                                                                                                                                                                                                                     | 2                                                    | Qu.<br>Be.<br>Ma.<br>Qy<br>Db                                                                                                                 |

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3 3 1
202 AA; 22494 MW;
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26
80
162
166
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Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=2190;
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80
162
166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y132_METJA
Q57596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
  QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioliformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its modified ann-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                            "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
--- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-22.
MEDLINE-86250886; PubMed-3722201;
Martin M.E., Byers B.R., Olson M.O.J., Salin M.L., Arceneaux J.E.L.,
                                                                                                                                                                           Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
(NBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTATE COLUMN STANDARD; PRT; 202 AA.
P09738, 059791;
01-MAR-1989 (Rel. 10, Created)
01-MOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUPERCOXIDE DISMUTASE [MN-FE] (EC 1.15.1.1).
SODA OR SOD.
STREPLOCOCOUS matens.
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                 20-500-2001 (Rel. 40, Created)
20-500-2001 (Rel. 40, Last sequence update)
20-500-2001 (Rel. 40, Last sequence update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DCD OR PABL164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakayama K.;
Widtochide sequence of Streptococcus mutans superoxide dismutase
gene and isolation of insertion mutants.";
J. Bacteriol. 174:4928-4934(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.5%; Score 13; DB 1; Length 154; 100.0%; Pred. No. 4.6e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ248288; CAB50685.1; -.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR004238; dUTPase.
Pfam: PF00692; dUTPase; 1.
Pr050m; PD004900; dCTP_deaminse; 1.
Pydrolase; Complete protecome.
SEQUENCE 154 AA; 17758 MW; C031BEE419094DDB CRC64;
                      154 AA
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GS-5;
MEDLINE-92332426; PubMed-1321118;
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Best Local Similarity 100.
Matches 13; Conservative
                    STANDARD;
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                          STRAIN-ORSAY;
Heilig R.;
                    DCD_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
SODM_STRMU
ID SODM,STRMU
DT 01.4MN
SCHEPT
OC BACTER
OC BA
DCD_PYRAB
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                   SEQUENCE FROM N.A.
STRAILNU-JALL-I, DSM 2661 / ATCC 43067;
MEDLINE-JALL-I, DSM 2661 / ATCC 43067;
MEDLINE-JALL-I, DSM 2661 / ATCC 43067;
MEDLINE-JALL-I, DSM 2661 G.J., Zhou L., Fletschmann R.D.,
Buttc C.J., White O., Olsen G.J., Zhou L., Fletschmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinston J.-F., Adams M.D., Rody A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woose C.R., Venter J.C.,
Complete genome sequence of the methanogenic archaeon, Methanococcus
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Tolbert C.;
"A Streptococcus mutans superoxide dismutase that is active with either manganese or iron as a cofactor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Archaea; Buryarchaeota; Methanococcales; Methanococcaceae;
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MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
L -> T (IN REF 2).
W. COC853BE0032B51 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MJ0132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 220 AA.
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ilarity 100.0%; Pred. No. 13;
Conservative 0; Mismatches
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S ¥ ¥ ¥ ¥ \$ 0

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Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae; Gluconacetobacter.
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                                                                                                                                                                                                                                                               260 AA
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                                                                                  Mismatches
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                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                           35.3%; Score 6; I
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 298682; CAB11357.1; -. EMBL; 299111; CAB13377.1; -. SubtiList; BG13363; ylbK. InterPro; IPR001423; UPF0028.
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                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acetobacter xylinum.
                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
                                                                                                                                              ||||||
136 KIRKEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 KIRKEI 254
                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 KIRKEI 14
                                                                                                                       9 KIRKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                             YLBK_BACSU 034731;
                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELA_ACEXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
CELA_ACEXY
                                                                                                                                                                                                                                          YLBK_BACSU
                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                        RESULT
                                                                                                                                                            g
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                                                                                                                         δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-96337999; Pubmd-8688087;
Bult C.J., White O., Olsen G.J., Eleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Rlake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Scribeck R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts R.M., Hill H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
SIMILARITY: TO M.JANNASCHII MJ1220 AND MJECL42.
SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO THE N-TERMINAL OF M. TUBERCULOSIS MTCY71.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                       InterPro: IPR003356; N6_DNA_Mtase.
Pfam; PF02384; N6_Mtase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 220 AA; 25766 MW; 710DDAE4C7A47954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein; Complete proteome.
249 AA; 27147 MW; A6B66FF4B52C15A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            35.3%; Score 6; DB 1;
100.0%; Pred. No. 14;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MJ0768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 AA.
                                                                                                                                                                                                                                      EMBL; U67470; AAB98113.1; -. TIGR; MJ0132; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002847; DUF129.
Pfam; PF01996; DUF129; 1.
Hypothetical protein; Complet
SEQUENCE 249 AA; 27147 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67522; AAB98763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                         (M SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||
66 KIRKEI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 KIRKEI 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGR; MJ0768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y768_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         058178;
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01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UTP--GLUCOSE-1-PHOSPHATE URIDYLYLIRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHOTE
URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE).
                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 28.3 KDA PROTEIN IN CTAG-RPMF INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bertero M., Presecan E., Glaser P., Richou A., Danchin A., "Bacillus subtilis chromosomal region downstream nprE.", Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.
Length 249;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 260;
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Hypothetical protein; Complete proteome.
SEQUENCE 260 AA; 28258 MW; 363B6DDF017BE77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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0; Gaps

NCBI\_TaxID=28448;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-JAL1 / CBS 261 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

A Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., A Kerlavage A.R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Overbeek R., Kirkness E.F., Weinfand J.F., Merrick J.M., Glodek A., A Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Dorodovsky M., A Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschii!";

Science 273:1059-1073(1996).

L. Science 273:1059-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococcales; Methanococcaceae;
Methanococcus.
        Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%; Score 6; DB 1; Length 336; llarity 100.0%; Pred. No. 20; Conservative 0; Mismatches 0; Indels
                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003402; Met_10.
Interpro; IPR000051; SAM_bind.
Pfam; PF02475; Met_10. 1.
Hypotherical protein; Complete proteome.
SEQUENCE 336 AA; 39000 MW; 3E4811F0932EE95F CRC64;
        DB 1;
. 18;
                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN MJ0883.
                                                                                                                                                                                                                                                                         336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
STSY_RAUSE
1D STSY_RAUSE
AC P15324;
DJ 01-APR-1990 (Rel. 14, Last sequence update)
        Query Match 35.3%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No.18;
Best Cocal Similarity 100.0%; Mismatches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67532; AAB98887.1; -. TIGR; MJ0883; -.
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||
| 115 KIRKEI 120
                                                                                                                                    77 AILLPD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 KIRKEI 14
                                                                                                     2 AILLPD 7
                                                                                                                                                                                                                                                                         Y883_METJA
                                                                                                                                                                                                                                                                                             058293;
                                                                                                                                                                                                                         RESULT 9
Y883_METJA
                                                                                                                                                  q
                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96262713; PubMed=8704981;
Yamamnco H., Uchiyama S., Fajar A.N., Ogasawara N., Sekiguchi J.;
Yamamnto d. 1 Uchiyama S., Fajar A.N., Ogasawara N., Sekiguchi J.;
Determination of a 12 kb nucleotide sequence around the 76 degrees region of the Bacillus Subtilis chromosome.";
Microbiology 142:1417-1421(1996).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 299108; CABL1263.1; -.
EMBL; 299108; CABL1263.1; -.
Subtilist; BG11852; yfis.
Pfam; PF00903; Glyoxalase; 2.
Hypothetical protein; Complete proteome.
SEQUENCE 285 AA: 31521 MW; 79E47242334825E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A41382; A41382.
InterPro; IPR001825; NTP_transferase.
Pfam: PF00483; NTP_transferase; 1.
Transferase; Kinase; Nucleotidyltransferase.
SEQUENCE 284 AA; 30992 MW; 6C809AFFBBA1791B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFIE_BACSU STANDARD; PRT; 285 AA.
YFIE_BACSU STANDARD; PRT; 285 AA.
P54721;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AGC-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 31.5 KDA PROTEIN IN GLVBC 3'REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 35.3%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 18; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M76548; AAA21888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Gaps

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LEUKOTOXIN SECRETION PROTEIN D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B32051; B32051.
                                                                                                                                                                         STRAIN-SEROTYPE A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A
                                                      NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 WKIRKE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11111
23 WKIRKE 28
                                             Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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HLYD_PASSP
   g
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                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                               Kutchan T.M., Hampp N., Lottspeich F., Beyreuther K., Zenk M.H.; "The cDNA clone for strictosidine synthase from Rauvolfia serpentina. DNA sequence determination and expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Gentianales, Apocynaceae, Rauvolfioideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
STRICTOSIDINE SYNTHASE.
N-LINKED (GLCNAC. .) (POTENTIAL).
7CD38882621F768A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: 3-ALPHA(S)-STRICTOSIDINE - TRYPTAMINE
                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: VACUOLAR.
SIMILARITY: BELONGS TO THE STRICTOSIDINE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                 Rauvolfia serpentina (Serpentwood) (Devilpepper), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyase; Glycoprotein; Alkaloid metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%; Score 6; DB 1;
100.0%; Pred. No. 21;
Live 0; Mismatches
15-JUL-1998 (Rel. 36, Last annotation update) STRICTOSIDINE SYNTHASE PRECURSOR (EC 4.3.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 AA
                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                       PATHWAY: ALKALOID BIOSYNTHESIS. SUBUNIT: MONOMER.
                                                                                                                                SPECIES=R.serpentina;
MEDLINE=89005637; PubMed=3049153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 N
38162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y00756; CAA68725.1; -. EMBL; X62334; CAA44208.1; -. EMBL; X63431; CAA45025.1; -.
                                                                                                                                                                                    FEBS Lett. 237:40-44(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                    Vinceae; Rauvolfia.
NCBI_TaxID=4060, 4062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S01325; S01325.
PIR; S21868; S21868.
PIR; S21718; S21718.
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Best Local Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 AA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                          Rauvolfia mannii
                                                                                                                                                                                                                                                                                                                              SECOLOGANIN
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32 KEILIE 37
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P16534;
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HLYD_PASHA
ID HLYD_P
AC P16534
DT 01-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89123172; PubMed-2914876; Strathdee C.A., Lo R.Y.C.; "Cloning, nucleotide sequence, and characterization of genes encoding the secretion function of the Pasteurella haemolytica leukotoxin determinant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA 8:15-28(1989).
-!- FUNCTION: INVOLVED IN THE TRANSPORT OF THE LEUKOTOXIN.
-!- SUBCELLULAR LOCATION: INNER MEMBRANE-BOUND (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE HLYD FAMILY OF SECRETION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Transmembrane; Inner membrane.
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STRAIN-SEROTYPE A1 / PH1101;
MEDLINE-89210283; Pubmed=2707120;
Highlander S.K., Chidambaram M., Engler M.J., Weinstock G.M.;
"DNA sequence of the Pasteurella haemolytica leukotoxin gene
Pasteurella haemolytica.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                    "Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica Al."; Infect. Immun. 55:1987-1996(1987).
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E2B8B5FF5AF988C1 CRC64;
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D -> E (IN REF. 3).
N -> T (IN REF. 3).
F -> L (IN REF. 3).
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100.0%; Pred. No. 28;
iive 0; Mismatches
                                                                                                                                                                                           STRAIN=SERCTYPE 41;
MEDLINE=87306837; PubMed=3040588;
LO R.Y.C., Strathdee C.A., Shewen P.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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Pfam; PF00529; H1yD; 1.
PROSITE; PS00543; HLXD_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 171:916-928(1989).
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SUBUNIT
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92239320; Pubwed=8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin gene from a Pasteurella haemolytica-like organism, encoding a new member of the RTX toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR'1990 (Rel. 14, Created)
01-APR'1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYPE IIS RESTRICTION ENZYME FOXI (EC 3.1.21.4) (ENDONUCLEASE FOXI)
FOXIR OR RFOXI.
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STAINA-RACC 33414 / IFO 12536;
MEDLINE-89174630; PubMed-2784436;
Kita K., Kotani H., Sugisaki H., Takanami M.;
Kita K., Kotani H., Sugisaki H., Takanami M.;
Nita K., Rotani H., Sugisaki H., Takanami M.;
Nita K., Kotani H., Sugisaki H., Takanami M.;
Nita K., Kotani H., Sugisaki H., Takanami M.;
Nita Fastriction and modification and muleocide sequences of the restriction and modification genes.";
J. Biol. Chem. 264:5751-5756(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEREL: L12148; AAA16440...,
InterPro; IPR002215; HlyD.
InterPro; IPR002215; HlyD.
PROSITE; PS00543; HLYD_FAMILY; 1.
TRANSMEM 79 POTENTIAL.

99 478 PERIPLASMIC (POTENTIAL);

74 478 PERIPLASMIC (POTENTIAL);

75 7650 MW; 221461A69482913A CRC64;
    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
LEUKOTOXIN SECRETION PROTEIN D.
LKTD.
Pasteurella haemolytica-like sp. (strain 5943B).
Bacteria: proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.3%; Score 6; DB 1; Length 478; llarity 100.0%; Pred. No. 28; Conservative. 0; Mismatches 0; Indels
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Bacteria: Flrmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Planomicrobium.
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  STANDARD;
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6; Conserv
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23 WKIRKE 28
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P14870;
HLYD_PASSP
P55125;
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Best Local S
Matches 6
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12F1_ELAOK
10 72F1_E
AC P14870
AC D1-APR
DT 01-APR
DT 20-AUG
DE (R.FOK
GN FOKIR
GN FOKIR
CO Bacter
CO Bact
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                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

X-RAIN-ARCC 33414 / IFO 12535;

MEDLINE-97357159; Pubmed-9214510;

Wah D.A., Hirsch J.A., Dorner L.F., Schildkraut I., Aggarwal A.K.;

"Structure of the multimodular endonuclease Fok! bound to DNA.";

Nature 388:97-100(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REBASE; 1056; Fokt.
Hydrolase; Endonuclease; Nuclease; Restriction system; Magnesium;
3D-structure.
SEQUENCE 583 AA: 66710 111
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MEDLINE=98393685; PubMed=9724744;
MEDLINE=99393685; PubMed=9724744;
MEDLINE=91, Wah D.A., Aggarwal A.K., Schildkraut I.;
Fox I dimerization is required for DNA cleavage.";
Proc. Natl. Acad. Sci. U.S.A. 95:10570-10575 (1998).
-1- CATALYTIC ACTIVITY: RECGINIZES THE DOUBLE-STRANDED SEQUENCES GAGG AND CATCC AND CLEAVES RESPECTIVELY 14 BASES AFTER G-1 AND 13 BASES BEFORE C-1.
-1- COFACTOR: REQUIRES MAGNESIUM.
-1- SUBUNIT: MONOMER. HOMODIMER WHEN BOUND OT DNA.
[2]
SEQUENCE FROM N.A.
MEDILINE=90060769; Pubwed=2684765;
Looney M.C., Moran L.S., Jack W.E., Feehery G.R., Benner J.S.,
Slatko B.E., Willson G.G.,
"Nucleotide sequence of the
separaté strand-specificity domains in the methyltransferase.";
Gene 80:103-208(1989).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR)
P2X77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
35.3%; Score 6; DB 1; Length 583;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
STRAIN-ATCC 33414 / IFO 12536;
MEDLINE-98393684; PubMed-9724743;
Wah D.A., Bitinaite J., Schildkraut I., Aggarwal A.K.;
"Structure of Foxl has implications for DNA cleavage.";
Proc. Natl. Acad. Scl. U.S.A. 95:10564-10569(1998).
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EMBL; M28828; AAA24934.1; ALT_INIT.
PITS, A32861.
PDB; IFOK; 03-DEC-97.
PDB; ZFOK; 17-JUN-98.
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P2X7_RAT
ID P2X7_RAT
C04463;
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Search completed: January 31, 2002, 13:39:10
Job time: 70 sec
                               MEDLINE=95242842; PubMed=7725802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                              STRAIN-M33;
MEDLINE-96202420; PubMed=8614837;
Surprenant A., Rassendren F., Kawashima E., North R.A., Buell G.N.;
"The cytolytic P2z receptor for extracellular ATP identified as a P2X
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                          Science 272:73-738(1996).

- FOUCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION CHANNEL. RESPONSIBLE FOR ATP-DEPENDENT LYSIS OF MACROPHAGES THROUGH THE FORMATION OF MEMBRANE PORES PERMEABLE TO LARGE MOLECULES. COULD FUNCTION IN BOTH FAST SYNAPTIC TRANSMISSION AND THE ATP-MEDIATED LYSIS OF ANTIGEN-PRESENTING CELLS.
-!--SUBUNIT: HONG- OR HETEROPOLYMERS (BY SIMILARITY).
-!-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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25 CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).

2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Eukaryota; Fungi; Ascomycota; Saccharomycoties
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01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
YJL212C OR J0236 OR HRD799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 595;
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NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.3%; Score 6; DB 1;
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Pfam: PP00864; P2X_receptor: 1.
PRINTS; PR01307; P2XRECEPTOR.
PRNSTS; PR01314; P2XXRECEPTOR.
PROSITE; PS01212; P2X_RECEPTOR.
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Matches 6; Conservative
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                                                                                                         SEQUENCE FROM N.A.
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                                                       NCBI_TaxID=10116;
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| 575 WKIRKE 580
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YJV2_YEAST
TO YJV2_YEAST
TO YJV2_YEB
DT 01-FEB
DT 01-FEB
DT 01-CFB
DT 01-CFB
DT 01-CFB
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                "Sequence analysis of a 40.2 kb DNA fragment located near the left telonere of yeast chromosome X.";
Yeast 10:1657-1662(1994).
-!- SIMILARITY: STRONG, TO S.POMBE ISP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
Vandenbol M., Durand P., Bolle P.-A., Dion C., Portetelle D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .l protein.
799 AA; 91615 MW; AF81676CC9B30759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.3%; Score 6; DB 1;
100.0%; Pred. No. 43;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z34098; CAA83999.1; -. EMBL; Z49487; CAA89509.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; $45161; $45161.
SGD; $0003748; YJL212C.
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Best Local Similarity
6, Conserve
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SEQUENCE 79
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:18:19 ; Search time 78.64 Seconds (without alignments) 16.467 Million cell updates/sec Run on:

US-08-957-709-11 17 Title: Perfect score: Sequence:

GAILLPDWKIRKEILIE 17

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

0 Word size :

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES Description | dCTP deam  | dCTP deaminase ( | hypot  |        | superoxide dismu |        |        | hypothetical | hypothetical | hypothetical | conserved hyp | probable t | conserved. |        |                  |        |        | hypothetical | probable phos |        | strictosidine | strictosidine | hypothetical prote | benzoate tran | probable |        | cytochrome P450 ho | 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1 |
|-----------------------|------------|------------------|--------|--------|------------------|--------|--------|--------------|--------------|--------------|---------------|------------|------------|--------|------------------|--------|--------|--------------|---------------|--------|---------------|---------------|--------------------|---------------|----------|--------|--------------------|------------------------------------------|
| SUM                   | <br>E71216 | G75030           | D72293 | H75168 | A42710           | D64316 | E71653 | H64395       | C72572       | F72264       | H69874        | S78172     | A69000     | C69380 | A41382           | н69802 | T20141 | H96539       | T17012        | C64410 | S29894        | S01325        | S74947             | D82134        | E75208   | D30169 | T09367             | A70378                                   |
| DB                    | 7          | 7                | ?      | 7      | ~                | 7      | 7      | -            | 7            | ~            | 7             | 7          | Н          | 7      | <del>, - 1</del> | ~      | 7      | 7            | ~             | 7      | ~             | 7             | 7                  | 7             | 7        | ~      | 7                  | ç                                        |
| Length                | 156        | 154              | 178    | 185    | 203              | 220    | 247    | 249          | 251          | 259          | 260           | 262        | 268        | 269    | 284              | 285    | 299    | 303          | 303           | 336    | 342           | 344           | 382                | 387           | 410      | 478    | 508                | 513                                      |
| %<br>Query<br>Match   | 82.4       | 76.5             | 35.3   | 35.3   | 5.               | 35.3   | 35.3   | Š.           | δ.           | δ.           | ď.            | 5.         | 35.3       |        | ď.               | 'n.    |        | 5.           | Ŋ.            | വ      | S             | വ             | 35.3               | 35.3          | •        | 35.3   | 35.3               | 35                                       |
| Score                 | 14         | 13               | 9      | 9      | 9                | ø      | 9      | 9            | 9            | 9            | 9             | 9          | 9          | 9      | 9                | 9      | 9      | 9            | 9             | 9      | 9             | 9             | 9                  | ø             | 9        | 9      | 9                  | ۷                                        |
| Result<br>No.         | г          | 7                | က      | 4      | 2                | 9      | 7      | 80           | 6            | 10           | 11            | 12         | 13         | 14     | 15               | 16     | 17     | 18           | 19            | 20     | 21            | 22            | 23                 | 24            | 25       | 56     | 27                 | 28                                       |

| hypothetical prote | conserved hypothet | type II site-speci | hypothetical prote | ARE1-like protein, | hypothetical prote | hypothetical prote | DNA-directed DNA p | probable membrane | sorbitol dehydroge | endopeptidase Clp | ATP-dependent Clp | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| C71473             | E81735             | A32861             | T24456             | G96737             | T49456             | T12528             | JC7382             | S50773            | 140014             | C71533            | B81689            | B64516             | B64993             | S50608             | T00337             |
| 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                 | 7                  | Н                 | 7                 | 7                  | 7                  | 7                  | 7                  |
| 562                | 564                | 583                | 604                | 701                | 739                | 745                | 781                | 799               | 829                | 854               | 870               | 1181               | 1337               | 1391               | 1426               |
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| 35                 | 35                 | 35                 | 35                 | 35                 | 35                 | 35                 | 35                 | 35.3              | 35                 | 35                | 35                | 35                 | 35                 | 35                 | 35                 |
| 9                  | Q                  | 9                  | 9                  | 9                  | 9                  | 9                  | ø                  | 9                 | 9                  | 9                 | 9                 | 9                  | ø                  | 9                  | 9                  |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                | 39                 | 40                | 41                | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

dCTP deaminase (EC 3.5.4.13) PH1997 [similarity] - Pyrococcus horikoshii

C.Species: Pyrococcus horikoshii C.Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000

C; Accession: E71216

R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se R; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: E71216

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-156 <KAW>
A;Residues: 1-156 <KAW>
A;Cross-references: GB:AP000007; NID:93236134; PIDN:BAA31124.1; PID:93258441
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa

A,Gene: PH1997 C,Superfamily: dCTP deaminase C,Keywords: hydrolase

ö Gaps ; 0 Length 156; Score 14; DB 2; Length 100. Pred. No. 1e-07; 82.4%; Scc. 100.0%; Pred 0; N Conservative Query Match Best Local Similarity Matches 14; Conserva

4 LLPDWKIRKEILIE 17 δy

2 LLPDWKIRKEILIE 15 g

RESULT

dCTP deaminase (EC 3.5.4.13) PAB1164 [similarity] - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000
C;Accession: G75030

Rianonymous, Genoscope submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A; Reference number: A75001
A; Reference number: A75001
A; Accession: G75030
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-154 < KMA>
A; Cross-references: GB: AJ248288; GB: AL096836; NID: g5458960; PIDN: CAB50685.1; PID: g545
A; Experimental source: strain Orsay

C; Genetics:

A;Gene: dcd; PAB1164 C;Superfamily: dCTP deaminase

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restriction modification enzyme subunit MI homolog - Methanococcus jannaschii restriction modification enzyme subunit MI homolog - Methanococcus jannaschii C; Species: Methanococcus jannaschii C; Species: Methanococcus jannaschii Diate: 13:8ep-1996 #text_change 21-Jul-2000 C; Accession: D64316 F; Methol. C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak F; Beich, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak F; Beich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, I.Son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Reference number: A64300; MUID:96337999 A; Reference number: A64300; MUID:96337999 A; Reference number: A64300; MUID:96337999 A; Molecule type: DNA A; Residues: 1-220 ABU->
                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 174, 4928-4934, 1992
A;Title: Nucleotide sequence of Streptococcus mutans superoxide dismutase gene and is
A;Reference number: A42710; MUID:92332426
A;Contents: GS-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A42710
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Accession: A42710
Accession: A2770
Accession: A2770
Accession: A2782: GB:D01037; NID:q251294; PIDN:AAB22503.1; PID:q251295
Access-references: GB:S39782; GB:D01037; NID:q251294; PIDN:AAB22503.1; PID:g251295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: GB:U67470; GB:L77117; NID:92826247; PIDN:AAB98113.1; PID:91592267
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Streptococcus mutans
C;Species: Streptococcus mutans
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession: A42710; A24812
R;Nakayama, K.
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Pred. No. 31;
0; Mismatches
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Pred. No. 29;
); Mismatches
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100.0%; Pre
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Best Local Similarity 100.0%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: REV127472-126810
A; Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.3
Best Local Similarity 100.
Matches 6; Conservative
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2 AILLPD 7
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66 KIRKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3

hypotherical protein - Thermotoga maritima (strain MSB8)

C.Species: Thermotoga maritima

M.N.: Stewart, M.M.: Stewart, M.M.: Cotton, M.D.; Pratt, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.: Stewart, A.M.: Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Nature 399, 333-329, 1999

M.; Reference number: A72200; MUID:99287316

A.Scession: D72293

A.Scession: D72
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2-Ketoglutarate ferredoxin oxidoreductase, chain gamma (korg-2) PAB0348 - Pyrococcus abysinococcus abyssinococcus aby
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                                                                                                                                                            Length 154;
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C;Superfamily: Thermotoga maritima hypothetical protein TM1127
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1.1e-06;
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                                                                                                                   76.5%; St. 100.0%; Pred. No. ... 0; Mismatches
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Pred. No. 25
0; Mismatches
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C.Superfamily: pyruvate synthase gamma chain
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                                                                                                                                                Query Match 76.5
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                         C;Keywords: hydrolase
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Best Local S
Matches 6
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C; Accession: H60874

R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berr C; Bron, S.; Broulliet, S.; Eruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C. (Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Evine, A.; Liu, H.; Masuda, S.; Mau, Y. M.; Ogawa, K.; Ogiwara, A.; Odega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteter Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togato, V.; Uchiya T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Togato, V.; Uchiya A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida A; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Accession: H69874
                                A;Residues: 1-251 <KAM>
A;Cross-references: DDBJ:AP000062; NID:95105244; PIDN:BAA80864.1; PID:d1044650; PID:9
A;Experimental source: strain K1
C;Genetics:
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A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: F72264
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein TM1350 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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                                                                                                                                                                A;Gene: APE1860
C;Superfamily: Aeropyrum pernix hypothetical protein APE1860
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                                                                                                                                                                                                                                                                                            DB 2;
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Mismatches
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Pred. No.
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100.0%; Pre
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100.0%;
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C;Superfamily: peroxidase
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GAILLP 128
                   DNA
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E71653
Dypothetical protein RP499 - Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Species: Rickettsia prowazekii
C; Date: 21-Nov-1998 #text_change 03-Nov-2000
C; Accession: E71653
A; Anderesson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature 396, 133-140, 1998
A; Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A; Reference number: A71653
A; Accession: E71653
A; Accession: E71653
A; Accession: E71653
A; Accession: E71653
A; Accession: B71653
A; Residues: 1-247 < Anno
A; Residues: 1-247 < Anno
A; Cross-references: GB: AJ235272; GB: AJ235269; NID: q3861033; PIDN: CAA14951.1; PID: e134279
A; Genetics:
A; Genetics: A7499
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C. Species: Methanococcus jannaschii
C. Cate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C. Accession: H64395
R. Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R. Bult, C.J.; Worsbeek, R.; Kirkness, E.F.; Weinstock, R.G.; Merrick, J.M.; Glodek, A.; reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, R.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A. Aluthors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A.; Tille: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A. Reference number: A64300; MUID:96337999
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: C72572
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
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A;Reference number: A72450; MUID:99310339
A;Accession: C72572
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A;Residues: 1-249 <BUL>
A:Cross-references: GB:U67522; GB:L77117; NID:g2826315; PIDN:AAB98763.1; PID:g1499588;
C;Genetics:
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Map position: FOR689591-690340 C;Superfamily: hypothetical protein MJ0768

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ò g A;Status: preliminary

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A;Gene: MTH1 C;Superfamily: conserved hypothetical protein MTH1

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Dysothetical protein AF1043 - Archaeoglobus fulgidus
C;Specias: Archaeoglobus fulgidus
C;Specias: Archaeoglobus fulgidus
C;Specias: Archaeoglobus fulgidus
C;Specias: Archaeoglobus fulgidus
C;Baccession: C69380
C;Accession: C69380
A;Authors: Utterback, R.; Accession: C69380
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Recession: C69380
A;Accession: C69380
A;Acce
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Species: Acetobacter pasteurianus
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 31-Mar-2000
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 31-Mar-2000
C;Accession: Ad1382
S;Bredde, G; Fjaervik, E; Valla, S.
J. Bacteriol. 173, 7042-7045, 1991
A;Title: Nucleotide sequence and expression analysis of the Acetobacter xylinum uridi
A;Title: Nucleotide sequence and expression analysis of the Acetobacter xylinum uridi
A;Accession: A41382
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A;Reference number: A69000; MUID:98037514
A;Accession: A69000
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-268 cMTH>
A;Residues: 1-268 cMTH>
A;Residues: GB:AE000795; GB:AE000666; NID:92621036; PIDN:AAB84510.1; PID:92621036; C;Genetics:
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: 1-260 CKUN> A;Cross-references: 6B:299111; GB:AL009126; NID:g2633699; PIDN:CAB13377.1; PID:e1185094; A;Cross-reference: strain 168 C;Genetics: A;Gene: ylbk
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Human bcl2 proto-o

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Part of yeast proh

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Zea mays protein

Human secreted pro cormate dehydrogen Staphylococcus aur Zea mays protein f

Zea mays protein

Human ubiquitin co Human UCSP-2 prote Human ubiquitin co

Breast cancer asso Rat neuronal immed

Human zinc finger

Polymerase enhancing factor proteins, extracts and complexes -improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

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Human secreted pro

Human zinc finger

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Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR;
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AAW72847
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                                                           This peptide comprises an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638. It has been obtained from isolated P45. PCR primers DSM 3638. It has been obtained from isolated P45. PCR primers (see AAV63861-64) based on the peptide were used to amplify P45 DNA (see AAV63860). A full-length P45 sequence is provided in AAW72847. PEF, a predominant component of which is P45 protein, enhances the activity of P. furiosus DNA polymerase, thereby providing activity of P. furiosus DNA polymerase, thereby providing to activity of P. furiosus DNA polymerase enhancing activity. The invention provides novel extracts, proteins and complexes that improve the provides novel extracts, proteins and complexes that improve the complexes may include proteins including the P45 N-terminal peptide. Also included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that improve the information to enhance polymerase activity. Noteins and complexes that improve the reactions can be enhanced (claimed) by mixing a nucleic acid polymerase and a composition having polymerase combancing activity. Rise provided for replicating nucleic call mainty activity. Rise in the Rise of the sequencing or amplification (preferably PCR or RT-PCR).
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Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0;
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Claim 17; Page 33; 161pp; English
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97US-0822774
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21-MAR-1997;
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\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{X}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\overset{\circ}{\mathbf{A}}\over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This peptide comprises an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEP) of Pyrococcus furiosus DSM 3638. It has been obtained from isolated P45; a full-length sequence is provided in AAM72847. PEF, the predominant components of which are P45 and P50 (see AAM72844) proteins, enhances the cit withy of P. furiosus DNA polymerase, thereby providing activity of P. furiosus DNA polymerase, thereby providing activity of greater length and purity. P45 is a duTPase and possesses polymerase enhancing activity. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucletc acid polymerases. These complexes may include proteins including the P45 N-terminal peptide. Also included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that included are methods for identifying and using these compositions, and specific activity, for purifying and using these compositions and hance polymerase activity. Nucleic acid polymerase in template, at least 1 polymerase and a composition having polymerase compacting activity. Mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase conhancing activity. Mixing an ucleic acid acid acids. The kits can be used in site-directed mutagenesis, nucleic acids acid sequencing or amplification (preferably PCR or RT-PCR).
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100.0%; Score 8; DB 19; Length 15; Best Local Similarity 100.0%; Prect 0.0019; Matches 8; Conservative 0; Mismatches 0; Indels
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Claim 17; Page 33; 161pp; English.
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N-PSDB; AAV63860.
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The sequence is predicted from a DNA sequence (see AAW6386) obtained from a polymerase enhancing factor (FPF) of Pyrococcus furiosus DSA 3638.

The sequence is predicted from a DNA sequence (see AAW63860) obtained from genomic DNA by PCR. P45 and P50 (see AAW62844) are the corrections of PEF, which acts to enhance the activity of predominant components of PEF, which acts to enhance the activity of cused to enhance nucleic acid replication, polymerisation or PCR caexitons. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies. Also included are methods for identifying compositions with PFF activity, for purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Choicing a nucleic acid template, at least 1 polymerase and a mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acids, for site-directed mutagenesis.
improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication
                                                                                                                                        the amino acid sequence of the P45 component of
                                                                              Claim 17; Page 43; 161pp; English.
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Sequence

Gaps ö 100.0%; Score 8; DB 19; Length 156; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels Ouery Match
Best Local Similarity 100.

1 PDWKIRKE 8

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RESULT

AAG72102 standard; Protein; 339 AA. 31-JUL-2001 (first entry) AAG72102; 

Human olfactory receptor polypeptide, SEQ ID NO: 1783.

Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.

Homo sapiens

WO200127158-A2.

19-APR-2001.

06-OCT-2000; 2000WO-US27582.

(DIGI-) DIGISCENTS. (YEDA ) YEDA RES & DEV CO LTD. 08-OCT-1999; 99US-0158615. 24-FEB-2000; 2000US-0184809;

Glusman G, Fuchs T, Yanai I; Lancet D, Smith D, Bellenson J,

WPI; 2001-290713/30

New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists  $\,$ 

Claim 11; Page 1172-1173; 1857pp; English.

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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory aganists and antegnonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human P2X7 protein. The invention relates to the P2XM protein, which is significantly homologous to: (i) the P2X family of ATP receptors, and (ii) RP-2 protein which is expressed in thymocytes during apoptosis. Transcription of the genes is specifically regulated by the tumour-suppressor gene p53. The P2XM gene is specifically expressed in skeletal muscle and has been localised to chromosome 22q11, an area where mutation and sequence losses frequently occur in rhabdoid sarcomas. The genes may be used for diagnostic purposes (e.g. by detecting changes occurring in the gene in sarcomas), using probes and primers containing or derived from all or part of the genes. The genes may further be used in the development of new anticancer drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gene P2XM whose transcription is induced by p53 - useful, e.g. for diagnostic purposes and in development of new anticancer drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; p53 regulated protein; P2XM; ATP receptor; RP-2 protein; thymocyte; apoptosis; tumour-suppressor gene; rhabdoid sarcoma; anticancer drug.
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                                                                                                                                                                                                                                                                                                                                                                           Length 339;
                                                                                                                                                                                                                                                                                                                                                                         DB 22;
5. 6.5;
                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 6; DB 2
100.0%; Pred. No. 6.5
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW76441 standard; Protein; 595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human p53 regulated protein, P2X7.
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.0
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW76441;
                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is rat purinergic receptor P2X_7/P2Z. The coding sequence for this protein can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's diseases involving acute or chronic inflammation such as ribemmatch starthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the haematopoietic system and immune response such as autoimmune disorders, allergies and imphoperoliferative disorders, diseases involving apoptotic cell death, such as cardiac and cerebral ischaemia and microbial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors specific antibodies -
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                                                           DB 19; Length 595;
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                                                                         Pred. No. 11;
Mismatches
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                                                              Score 6;
                                                                                                                                                                                                                              AAB28243 standard; Protein; 595 AA
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                                                         Query Match
Best Local Similarity 100.0%; Pr
Matches 6; Conservative 0;
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N-PSDB; AAC63693.
              595 AA
                                                                                                                                                                                                                                                                                                                       Rat P2X_7/P2Z #1
                                                                                                                                            575 wkirke 580
                                                                                                                      3 WKIRKE 8
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                                                                                                                                                                                                                                                             AAB28243;
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              Sequence
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0; Indels

Query Match 75.0%; Score 6; DB 2. Best Local Similarity 100.0%; Pred. No. 11; Matches 6; Conservative 0; Mismatches

22; Length 595;

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Rat; P2X_7; neuroprotective; nootropic; antiinflammatory; antiantritic; antibacterial; antiviral, antiallergic; cytostatic; cardiant; cerebroprotective; immunosuppressive; P22; purinergic receptor; mervous system disorder; chronic inflammation; Alzehimer's disease; rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection; haematopoletic system disorder; immune response; autoimmune disorder; allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia; tuberculosis; antirhematic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is rat purinergic receptor P2X_7/P2Z. The coding sequence for this protein can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's disease, diseases involving acute or chronic inflammation such as rheumatois arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the haematopoietic system and immune response such as autoimmune disorders, allergies and lymphoproliferative disorders, diseases involving apoptotic cell death, barticularly tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthitic, respiratory disorders and neurodegenerative disorders, and to generate receptors specific antibodies.
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llarity 100.0%; Pred. No. 11;
Conservative 0; Mismatches
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                                                                                                             AAB28253 standard; Protein; 595 AA
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Best Local Similarity
Matches 6; Conserv
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575 wkirke 580
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| 575 wkirke
3 WKIRKE
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                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
                                                                                                                                             AAB28253;
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4 KIRKE 8
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1 kirke 5
  tuberculosis.
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                                             US6133434-A
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                       Rattus sp.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a peptide fragment of rat complement component C5a (the full-length sequence is given in AAB74051). The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or uninary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as anaphylatoxin.
                                                                                                                                                                                                                                                                                                                           Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a antibodies generated against C-terminal truncated C5a peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                      Rat; CSa; complement; antibody; bacterial infection; sinusitis; meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 5; DB 22; Length 20; 100.0%; Pred. No. 8.8; 1. ive 0; Mismatches 0; Indels
AAB74118 standard; Peptide; 20 AA
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                                                                                                                                                                                                                                                                      Sarma V;
                                                                                                                                                                                                                                                                                                                                                                       Claim 29; Page 27; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat P2X_7/P2Z C-terminal peptide.
                                                                                                                                                                                                  31-AUG-2000; 2000WO-US24219.
                                                                 Rat C5a peptide fragment #2
                                                                                                                                                                                                                          31-AUG-1999; 99US-0387671
                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.
5; Conservative
                                                                                                                                                                                                                                                                     Ward PA, Huber-Lang M,
                                                                                                                                                                                                                                                (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                           2001-226665/23
                                                                                                                                                                                                                                                                                           WPI; 2001-226665/
N-PSDB; AAF75799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
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6 kirke 10
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                                           16-MAY-2001
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                                                                                                                                 Rattus sp.
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Best Local S
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                      AAB74118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a C-terminal peptide of rat purinergic receptor P2X_7/P2Z. The coding sequence for P2X_7 protein (AAC63693) can be used to treat disorders of the nervous system, particularly diseases with a component of chronic inflammation, such as Alzheimer's disease, diseases involving acute or chronic inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral and other microbial infections, disorders of the haematopoietic system and immune response such as autoimmune disorders, allergies and lymphoproliferative disorders, diseases and microbial infections, particularly tuberculosis. The present sequence was used to produce a rabbit polyclonal antiserum, which was used in immunohistochemistry of rat P2X_7.
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                                                                                                                                                                                                                                                                                                                                                                 Mammalian purinergic receptor (P2X7) useful for screening for modulators which are useful for treating arthritic, respiratory disorders and neurodegenerative disorders, and to generate receptors specific antibodies -
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. 8.8;
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                                                                                                                                                                                                                      Surprenant A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Column 15; 40pp; English.
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97US-0842079.
                                                                 97US-0842079.
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                                                                                                                                                                                                                   Buell GN, Kawashima E,
                                                                                                                                             (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                        WPI; 2001-006153/01.
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Best Local Similarity
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The present invention relates to single exon nucleic acid probes (SENP: see AAI3115-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes multiple sclerosis; alcoholic liver disease; ubidiabetes mellitus type II; microtubule associated protein; Tau; Big Tau; neurofilament-F; presenilin I; presenilin II; cellular tumour antigen; gilal fibrillary acidic protein; GFAPP; pS3; semaphorin III; HUPF-1; bc-1: B-cell leukemia/Lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bcl2 proto-oncogene mutant protein fragment 69
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Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 37274; 654pp; English.
                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY21221 standard; Protein; 55 AA.
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Best Local Similarity 100.0%; Pr
Matches 5; Conservative 0;
                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                           26-MAY-2000; 2000US-0207455
30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-063366
21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0234687
04-OCT-2000; 2000US-0234687
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30-JAN-2001; 2001WO-US00663.
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                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48 AA;
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32 kirke 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KIRKE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY21221;
                                                                                                                                                                                                                                                                            Penn SG,
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Conjugation system (UCS) proteins, designated UCSP-1 and UCSP-2. The

CONJUGATION of a medical proteins are part of the UCS, a major pathway for the degradation

of cellular proteins in eukaryotic cells. The UCS mediates the

climination of abnormal proteins and regulates the half-lives of

important regulatory proteins that control cellular processes such as

gene transcription and cell Gycle progression. The UCS is implicated in

the degradation of mitotic cyclic kinases, oncoproteins, tumour

suppressor genes (e.g. p53), viral proteins, cell surface receptors

associated with signal transduction, transcriptional regulators and other

mutated or damaged proteins. Therefore, UCSP-1 proteins may be used to

treat disorders associated with the inappropriate expression or activity

of UCS proteins. For example, UCSP-1 may be administered to treat cancer

cell sarrocytomas, melanomas, lymphomas and cancers of the breast, brain

and prostate), immune disorders, smooth muscle disorders (e.g. angina,

and prostate), immune disorders, smooth muscle disorders (e.g. angina,

cell measles, gastrochereitis, Epstein-Barr virus infections and

hepatitis). The UCSP-1 proteins may also be used as antigens in the

production of antibodies or in assays to identify modulators of UCS

function. This sequence represents the bovine CEP protein which is used

in the description of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                 Isolated ubiquitin conjugation system protein useful for the treatment of cancer, immune disorders smooth muscle disorders and viral infections
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genetic disorder.
                                                                                                                                                                                                                              P, Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM37005 standard; Protein; 48 AA.
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                                                                98US-0134596.
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                                                                                                            97US-0861269
98US-0134596
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                                                                                                                                                                             (INCY-) INCYTE PHARM INC.
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Best Local Similarity
Matches 5; Conserv
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30 kirke 34
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                                                                13-AUG-1998;
                                                                                                            21-MAY-1997;
13-AUG-1998;
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                     13-JUL-1999.
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Length 48; 0; Indels

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99US-0129845.
99US-0130077.
99US-0130449.
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990S-0138847.
990S-0139119.
990S-0139453.
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990S-0139454.
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99US-0139750.
99US-0139750.
99US-0139817.
99US-0139899.
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99US-0140695.
99US-0140823.
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99US-0141287.
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99US-0142154.
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99US-0131449
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99US-0135629
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99US-0137502
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99US-0138094
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99US-0139459
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19-APR-1999;
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                                                                                                                                                                                                                                                                              This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, and litus type II

Can many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, allows a definitive diagnosis of Alzheimer's disease in living patients, allows a definitive diagnosis of Alzheimer's disease in living patients, can early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, con neurofilament-F, presentlin I, presentlin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-I, high mobility group protein-C (HMGP-C) and neuroenine specific protein A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                           Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                      Grosveld FG, Van Leeuwen FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays protein fragment SEQ ID NO: 39475.
(ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI (UYRO-) UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                    Disclosure; Figure 15; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG32683 standard; Protein; 74 AA
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99US-0123180.
99US-0123548.
99US-0125788.
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Matches 5; Conservative
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                                                                                                          N-PSDB; AAX75766
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30 kirke 34
                                                      Burbach JPH,
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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ID AAG33

AC AAG33

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XX B Prot.

KW Prot.

KW Prot.

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PR 19-ULL-1999 9915-0144315

PR 19-ULL-1999 9915-0144311

PR 19-ULL-1999 9915-0144312

PR 19-ULL-1999 9915-0144313

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PR 20-ULL-1999 9915-0144313

PR 21-ULL-1999 9915-0144313

PR 22-ULL-1999 9915-0144313

PR 22-ULL-1999 9915-0144884

PR 22-ULL-1999 9915-0144884

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PR 22-ULL-1999 9915-0144884

PR 22-ULL-1999 9915-0145085

PR 23-ULL-1999 9915-01499

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Gaps
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Pred. No. 27;
0; Mismatches 0; Indels
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                                                      990S-0159294
990S-0159295
990S-0159330
990S-0159331
990S-0159638
990S-0159638
990S-0160741
990S-0160767
990S-0160767
990S-0160767
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990S-0160914
990S-0160914
990S-0160915
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9905-0161406
9905-0161359
9905-0161360
9905-0161361
9905-0161923
9905-0161993
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             13 - OCT - 1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The invention relates to assays for measuring in-vivo levels of activated mannan-binding protein-associated serine protease (MASP-1 and MASP-2) activity. The assay comprises contacting a sample of blood or plasma comprising a metal ion chelator with a substrate of formula:

R-peptide-Y: wherein the peptide comprises at least 4 residues from the C-terminus of an anaphylatoxin selected from C3a, C4a and C5a; R is a peptide blocking, protecting or capping group; and Y is any group cleavable from the substrate by MASP and comprises a labelled tag. The substrate of the invention is also useful for monitoring in vitro and in vivo complement-activation (C-activation) by classical, alternative detecting or monitoring a condition associated with complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activation. The conditions include microbial infections caused by particularly cytomegalovirus (CMV), hepatitis virus and human immunodeficiancy virus (HTV), organ transplant rejection, tissue injury, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus (SLE)) and inflammatory responses (e.g. in Alzheimer's disease and bacterial diseases). The assay of MASP is also useful for assessing the toxicity or injury of therapeutic treatments or screening test compounds as agents for treatment of viral diseases, parasitic infections, tissue injury, organ transplant rejection, autoimmune diseases or inflammatory responses. The present sequence is mouse
Method for determining in-vivo levels of activated mannan binding protein-associated serine protease enzyme, and new peptide derivatives
                                                                                                               Claim 3; Column 51-52; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C5a anaphylatoxin
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77 AA; Sequence

Gaps ő DB 22; Length 77; . 28; 0; Indels 0; Mismatches Score 5; Pred. No 62.5%; £ Query Match 62.5 Best Local Similarity 100. Matches 5; Conservative

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|||||| 63 kirke 67 4 KIRKE 8 셤 ð

AAB74051 RESULT

AAB74051 standard; protein; 77 AA. AAB74051; 

(first entry) 16-MAY-2001

Rat C5a.

Rat; C5a; complement; antibody; bacterial infection; sinusitis; meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.

Rattus sp

WO200115731-A1.

08-MAR-2001.

31-AUG-2000; 2000WO-US24219.

99US-0387671 31-AUG-1999;

(UNMI ) UNIV MICHIGAN

Ward PA, Huber-Lang M,

Sarma V;

WPI; 2001-226665/23. N-PSDB; AAF75794.

Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a antibodies generated against C-terminal truncated C5a peptides

Example 1; Page 26; 84pp; English.

The present sequence is rat complement component C5a. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusatis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as anaphylatoxin. 

Sequence

Gaps .; 0 Length 77; 0; Indels 62.5%; Score 5; DB 22; 100.0%; Pred. No. 28; iive 0; Mismatches Query Match Best Local Similarity luv.. 5, Conservative

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4 KIRKE 8 ò

||||| 63 kirke 67 q Search completed: January 31, 2002, 13:18:04 Job time: 165 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:20:05 ; Search time 78.64 Seconds (without alignments) 7.749 Million cell updates/sec Run on:

US-08-957-709-69 8 1 PDWKIRKE 8 Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

219241 seqs, 76174552 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Listing first 45

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|     |       | d              |        |     | SUMMARIES |                  |
|-----|-------|----------------|--------|-----|-----------|------------------|
|     | Score | Query<br>Match | Length | DB  | ID        | Description      |
| : - |       | 100.0          | 154    | . 2 | G75030    | ) dCTP deaminase |
| 7   | · œ   |                | 156    | (7) | 121       |                  |
| m   | 9     | 75.0           | 478    | ~   | D30169    |                  |
| 4   | 9     | 75.0           | 1426   | 7   | T00337    | hypothetical pro |
| S   | 9     |                | 1972   | ~   | S68176    | •                |
| 9   | 2     |                | 46     | 7   | 147035    | uitin homo       |
| 7   | 5     | 62.5           | 144    | 7   | F69301    | hypothetical pro |
| 8   | 2     |                | 149    | ~   | F71240    | ₽                |
| 6   | S     |                | 167    | 7   | н81252    | NADH dehydrogena |
| 10  | 'n    |                | 192    | 7   | B75144    | hypothetical pro |
| 11  | 5     |                | 195    | 7   | A75171    | hypothetical pro |
| 12  | S     |                | 196    | Н   | 850709    | υ                |
| 13  | S     |                | 210    | ~   | A32618    | DNA-directed RNA |
| 14  | S     |                | 219    | ~   | F69435    | hypothetical pro |
| 15  | 5     |                | 220    | ď   | D64316    | ion π            |
| 16  | 2     |                | 230    | ~   | E81397    | probable 1-acylg |
| 17  | S     |                | 233    | -   | S30118    |                  |
| 18  | S     |                | 241    |     | A64454    | hypothetical pro |
| 19  | S     |                | 241    | ~   | C70178    |                  |
| 20  | S     |                | 243    | N   | T29635    |                  |
| 21  | S     |                | 249    |     | H64395    | hypothetical pro |
| 22  | 2     |                | 251    | ~   | S48227    | 3-isopropylmalat |
| 23  | S     |                | 257    | 7   | A70367    | transcription re |
| 24  | 2     |                | 260    | 7   | H69874    | conserved hypoth |
| 25  | Ŋ     |                | 269    | 7   | C69380    | hypothetical pro |
| 56  | ហ     |                | 287    | ~   | 64        | prohibitin PHB1  |
| 27  | ស     |                | 305    | 7   | 4         | hemolysin E - Es |
| 28  | ស     |                | 305    | ~   | E85696    | probable pore fo |
| 29  | S     |                | 306    | 7   | CI.       | conserved hypoth |

| prrD protein – Esc<br>plastoquinolplas | hypothetical prote<br>conserved hypothet | annexin II type 1<br>tryptophanyl tRNA | tryptophantRNA 1 | probable disulfide | disulfide bond iso | probable rRNA (ade | 3-isopropylmalate | hypothetical prote | 3-isopropylmalate | 3-isopropylmalate | 3-isopropylmalate | 3-isopropylmalate |
|----------------------------------------|------------------------------------------|----------------------------------------|------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|
| S09628<br>A26576                       | C64410<br>C70324                         | JQ1297<br>H86590                       | C72034           | G72016             | C86607             | T00442             | 832969            | A86841             | S25369            | S43454            | A47620            | DEBYI             |
| 7 7                                    | 0 0                                      | 7                                      | 7                | 7                  | 7                  | 7                  | 7                 | ~                  | Н                 | Н                 | Н                 | Н                 |
| 313<br>320                             | 336<br>338                               | 340<br>344                             | 344              | 348                | 348                | 353                | 359               | 361                | 362               | 362               | 363               | 364               |
| 62.5<br>62.5                           | 62.5<br>62.5                             | 62.5<br>62.5                           | 62.5             | 62.5               | 62.5               | 62.5               | 62.5              | 62.5               | 62.5              | 62.5              | 62.5              | 62.5              |
| ro ro                                  | വവ                                       | თ <b>ი</b>                             | Ŋ                | വ                  | D.                 | Ŋ                  | 'n                | Ŋ                  | Ŋ                 | 2                 | S                 | S                 |
| 30<br>31                               | 33<br>33                                 | 34<br>35                               | 36               | 37                 | 38                 | 39                 | 40                | 41                 | 42                | 43                | 44                | 45                |

## ALIGNMENTS

| ٦      |      |
|--------|------|
| RESULT | 7503 |

dCTP deaminase (EC 3.5.4.13) PAB1164 [similarity] - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug\_1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

C; Accession: G75030

Ryanonymous, Genoscope submitted to the EMBL Data Library, July 1999
A, Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A; Reference number: A75001
A, Accession: G75030
A; Status: preliminary
A, Molecule type: DNA
A, Residues: 1-154 < KAM>A, CROSS-references: GB: AJ248288; GB: AL096836; NID: g5458960; PIDN: CAB50685.1; PID: g545
A, Experimental source: strain Orsay

A; Gene: dcd; PAB1164 C; Superfamily: dCTP deaminase C; Keywords: hydrolase

ö Gaps ö 100.0%; Score 8; DB 2; Length 154; 100.0%; Pred. No. 0.012; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 8; Conservative

1 PDWKIRKE 8 δλ

g

dCTP deaminase (EC 3.5.4.13) PH1997 [similarity] - Pyrococcus horikoshii

C; Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000 C:Accession: E71216

R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: E71216

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A; Residues: 1-156 <KAW>

A; Cross-references: GB:AP000007; NID:93236134; PIDN:BAA31124.1; PID:93258441 A; Experimental source: strain OT3 A; Note: this accession replaces an interim accession for a sequence replaced by GenBa

sch orm

A,Gene: PH1997 C,Superfamily: dCTP deaminase

C; Keywords: hydrolase

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RESULT 6
147031
147032
147032
147032
15 pecies: Bos primigenius taurus (cattle)
C; Species: Dos primigenius taurus (cattle)
C; Species: O4-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 05-Nov-1999
C; Accession: 147035
R; Shima, D. T; Saunders, K. B.; Gougos, A.; D'Amore, P.A.
Differentiation 58, 217-226, 1995
A; Title: Alterations in gene expression associated with changes in the state of endot A; Recession: 147034; MUID:95220954
A; Accession: 147035
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Schaus: 1-46 cABIA
A; Residues: 1-46 cABIA
A; Residues: 1-46 cABIA
A; Cross-references: GB:S77733; NID:9998679; PIDN:AAB34029.1; PID:9998680
A;Cross-references: EMBL:AB011140; NID:93043659; PIDN:BAA25494.1; PID:93043660 A;Experimental source: brain; clone HH2280 C;Genetics: A?AA0568 A;Note: KIAA0568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Detics: Homo sapiens (man)
C:Detics: Homo sapiens (man)
C:Detics: Homo sapiens (man)
C:Detics: Blocher:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
F69301
hypothetical protein AF0414 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Decies: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
C;Accession: F69301
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 6; DB 2;
llarity 100.0%; Pred. No. 18;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                          Score 6; DB 2,
Pred. No. 14;
); Mismatches
                                                                                                                                                                                                                                                           Query Match
Pest Local Similarity 100.0%; P. Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
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| 874 WKIRKE 879
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| 563 WKIRKE 568
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S68176
TOG protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                    3 WKIRKE 8
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30 KIRKE 34
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Boulof

Cypecies: Pasteurella haemolytica
Cypecies: Pasteurella
Cypecies: Pasteurella
Cypecies: Pasteurella
Cypecies: Pasteurella
Ryllidiander, S.R.
Cydecasion: D30169: B32051: S29518
Ryllidiander: S.R.
Cypecies: Pasteurella
Ryllidiander: S.R.
Cypecies: Pasteurella
Ryllidiander: S.R.
Compared With conceptual translation
Aynolecule type: DAR
Aynolecule type: DA
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T00337
hypothetical protein KIAA0568 - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens
C:Accession: T00337
R:Nagase, T: Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
R:Nagase, T: Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
R:Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A; Mcference number: 214086; MUID:98290545
A; Accession: T00337
A; Accession: T00337
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mcsoides: L1426 < NAG>
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                                                                                                                                            Length 156;
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                                                                                                                                  Query Match 100.0%; Score 8; DB 2; Length 156
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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23 WKIRKE 28
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A.Cross-references: GB.AL139079; GB.AL111168; NID:96968971; PIDN:CAB73566.1; PID:9696 A.Experimental source: serotype O2, strain NCTC 11168 C.Genetics: Genetics: A.Gene: nuoB; Cj1578c C.Superfamily: psbG protein C.Superfamily: psbG protein C.Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-192 <KAW>
A;Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49233.1; PID:9545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49448.1; PID:g545
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: B75144
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Reference number: A75001
A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;anonymous, Genoscope submitted to the Embi Data Library, July 1999 submitted to the Embi Data Library, July 1999 submitted to the Embi Data Library, A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PAB0211 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PAB0359 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                     Length 167;
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                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Pred. No.
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100.0%; Pred. No.
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C;Superfamily: hypothetical protein MJ0882
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                                                                                                                                                                                                                                                                  62.5%;
ilarity 100.0%;
Conservative 0
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
           A; Residues: 1-167 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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| 151 KIRKE 155
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R; anonymous, Genosc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||
15 KIRKE 19
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PS71240

molybdopterin biosynthesis protein E chain [similarity] - Pyrococcus horikoshii

N.Alternate names: maaE protein; molybdopterin-converting factor 16K chain; molybdopteril
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Accession: F71240

R;Kawarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yammanoto, S; Sekir
M; Ohkuu, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yammazaki, J; Kushida, N; Oguchi
DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Glodek, A.; Zhou, L.; Overbeek, B.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Wosse, C.R.; Venter, J.C.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Ritle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
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C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Sep-2000
C; Accession: H81252
R; Parkhili, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A; Reference number: A81250; MUID:20150912
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-144 <KLE>
A;Cross-references: GB:AE001076; GB:AE000782; NID:g2689399; PIDN:AAB90831.1; PID:g265022
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF0414
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain B Cj1578c [imported] - Campylobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP000001; NID:93236128; PIDN:BAA29253.1; PID:93256570
A;Experimental source: strain 0f3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
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A; Status: nucledca caid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-149 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 144;
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C;Superfamily: molybdopterin biosynthesis protein E chain
C;Keywords: molybdopterin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
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100.0%; Pred. No. 34;
iive 0; Mismatches
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100.0%; Pred. No. 35;
iive 0; Mismatches
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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62 KIRKE 66
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66 KIRKE 70
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hypothetical protein AF1487 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: F69435
R;Klerk, H.B.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dod
C;Accession: R-D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Reference number: A69250; MUID:98049343
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A;Molecule type: DNA
Residues: 1-220 - GBUL>
A;Cross-references: GB:U67470; GB:L77117; NID:g2826247; PIDN:AAB98113.1; PID:g1592267
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A;Reference number: A39879; MUID:91302386
A;Contents: erratum
A;Accession: A39879
A;Accession: A39879
A;Molecule type: mRNA
A;Residues: 163-185,'K',187-210 <PA2>
A;Cross-references: GB:S42643; NID:9232953; PIDN:AAB19339.1; PID:9232954
C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: EC 2.7.7.6 [validated; MUID:95129541]
C; Superfamily: DNA-directed RNA polymerase chain RPB5
C; Keywords: nucleotidyltransferase; nucleus; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.5%; Score 5; DB 2; Best Local Similarity 100.0%; Fred. No. 46; Matches 5; Conservative 0; Mismatches
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A, Start codon: TTG
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| 112 KIRKE 116
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                                                                                                                                                                                                                                                                                                                                         RESULT 12
S50709
Probable O-acetyltransferase (EC 2.3.1.-) YJL218w - yeast (Saccharomyces cerevisiae)
Probable O-acetyltransferase (EC 2.3.1.-) YJL218w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein HRA196; hypothetical protein J0224
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: S50709; S57008; S45154
A;Title: Sequence annalysis of a 40.2 kb DNA fragment located near the left telomere of y A;Reference number: S5070; MUID:95242842
A;Reference number: S5070; MUID:95242842
A;Reference number: S5070; MUID:95242842
A;Reference number: S5070; MUID:95242842
A;Reference number: S5070; MUID:95242842
A;Rocession: S50709
A;Status: nucleic acquence not shown; translation not shown
A;Reference number: S56835
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
A;Reference number: S56835
A;Accession: S57008
A;Accession: S57008
A;Accession: S57008
A;Accession: S57008
A;Residues: 1-196 <-VAW>A;Cessidues: EMBL:249493; NID:91015607; PIDN:CAA89515.1; PID:91015608; GSPDB:GNOC
C;GenetLc:
A;Gene: MIPS:YLL218w
A;Acmender Mips:YLL218w
A;Acmen
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A3261B
DNA-directed RNA polymerase (EC 2.7.7.6) II 23K chain [validated] - human
N;Alternate names: RNA polymerase II chain RPB5
C;Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 21-May-1990 & sequence_revision 17-May-1996 #text_change 28-Jul-2000
C; Accession: $52002; A32618; A39879
R;Checon, J. 14, 143-150, 1995
A;Title: Human RPB5, a subunit shared by eukaryotic nuclear RNA polymerases, binds human A; Reference number: $52002; MUID:95129541
A; Reference number: $52002; MUID:95129541
A; Residues: 1-210 ACHE>

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A; Residues: 1-156, Tr. 158-162, 'DKPPREFAAQDPGGGPCGALLWDKAWAGGEDHPAQ'
A; Cross-references: GB: J04965
A; Note: this sequence has been corrected
B; Patt, U.K.; Weissman, S.M.
J. Biol. Chem. 266, 13468, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Search completed: January 31, 2002, 13:20:06 Job time: 107 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:39:12; Search time 46.78 Seconds (without alignments) 6.270 Million cell updates/sec Run on:

US-08-957-709-69 8 Title: Perfect score: Sequence:

1 PDWKIRKE 8

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

0 Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | Q9uxs8 pyrococcus | 90/       | -          |            | ~        | _          | 9 пот      | human     | m          | sacch | . P19388 homo sapien | Q57596 methanococc | P35788 colletotric | . 042767 metarhizium | Q58631 methanococc | _          | 034731 bacillus su | P40961 saccharomyc | P77335 escherichia | escher     | P06669 vicia faba | Q58293 methanococc |            | 4         | P41766 kluyveromyc | 0          |            | 1 pichia   | 3 sacchar  | 7 candida  | 429 | 926      | Q09321 caenorhabdi |
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| SUMMARIES | ΩI            | DCD_PYRAB         | DCD_PYRHO | HLYD_PASHA | HLYD_PASSP | P2X7_RAT | PEPL_HUMAN | CTOG_HUMAN | VPU_HV12H | Y414_ARCFU | - 1   | RPB5_HUMAN           | Y132_METJA         | PYRE_COLGR         | PYRE_METAN           | YC34_METJA         | Y768_METJA | YLBK_BACSU         | PHB_YEAST          | HLYE_ECOLI         | PRRD_ECOLI | CYF_VICFA         | Y883_METJA         | ANXB_XENLA | SYW_CHLPN | LEU3_KLUMA         | LEU3_KLULA | LEU3_PICAN | LEU3_PICJA | LEU3_YEAST | LEU3_CANBO | - 1 | - 1      | YR51_CAEEL         |
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|           | Length        | 154               | 156       | 478        | 478        | 595      | 1756       | . 2032     | 28        | 144        | 196   | 210                  | 220                | 233                | 234                  | 241                | 249        | 260                | 287                | 303                | 313        | 320               | 336                | 339        | 344       | 359                | 362        | 362        | 363        | 364        | 365        | 365 | 368      | 370                |
| æ         | Query         | 100.0             | 100.0     | 75.0       | Τ.         | S.       | 75.0       | S.         | 62.5      | 'n         | ς.    | ς.                   | ď.                 | ö                  | ς.                   | ς.                 | ä          | ς.                 | 'n                 | 'n                 | 62.5       | ς.                | ď                  | ä          | ď         | ď.                 | 'n.        | ς.         | ö          |            | ď.         | 'n  | 62.5     | 62.5               |
|           | Score         | 80                | 80        | 9          | 9          | 9        | 9          | 9          | ស         | S          | S     | വ                    | 2                  | ហ                  | S                    | S                  | S          | S                  | S                  | S                  | 2          | 2                 | S                  | S          | ഗ         | ហ                  | 2          | 2          | Ŋ          | 2          | 2          | S   | ഗ        | 2                  |
|           | Result<br>No. | -                 | 7         | m          | 4          | 'n       | 9          | 7          | œ         | on :       | 10    | 11                   | 12                 | 13                 | 14                   | 15                 | 16         | 17                 | 18                 | 19                 | 20         | 21                | 22                 | 23         | 24        | 25                 | 26         | 27         | 28         | 53         | 30         | 31  | 32       | 33                 |

(Rel. 40, Created) (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)

156 AA.

PRT;

STANDARD;

RESULT 2 DCD\_PYRHO ID DCD\_PYRHO AC 057706; DT 20-AUG-2001 (1 DT 20-AUG-2001 (1 DT 20-AUG-2001 (1

| 34 5 62.5 373 1 LEU3_CANNA 35 62.5 373 1 LEU3_CANNA 36 62.5 473 1 LEU3_CANNA 37 5 62.5 400 1 HENALCLOPE 39 5 62.5 410 1 PRSI_METTH 41 5 62.5 477 1 HATD_ACTPC 42 5 62.5 477 1 HATD_ACTPC 43 5 62.5 477 1 HATD_ACTPC 44 5 62.5 477 1 HATD_ACTPC 45 5 62.5 477 1 HATD_ACTPC 46 5 62.5 477 1 HATD_ACTPC 47 1 HATD_ACTPC 48 5 62.5 478 1 HATD_ECOLI 49 5 62.5 5 478 1 HATD_ECOLI 49 5 62.5 5 478 1 HATD_ECOLI 40 5 62.5 5 478 1 HATD_ECOLI 40 5 62.5 5 52 1 ALG_YEAST 41 5 62.5 5 52 1 ALG_YEAST 42 5 62.5 5 52 1 ALG_YEAST 43 5 62.5 5 52 1 ALG_YEAST 44 5 62.5 52 1 ALG_YEAST 45 5 62.5 52 1 ALG_YEAST 46 5 62.5 52 1 ALG_YEAST 47 1 HATD_ECOLI 48 5 62.5 52 1 ALG_YEAST 48 5 62.5 52 1 ALG_YEAST 490328; 50 7 20-AUG_*2001 (Rel. 40, Last amotation update) 50 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | LEU3_CANAL   P87186 candida alb   LEU3_CANMA   P07139 candida mal   LEU3_LORMA   P07139 candida mal   LEU3_LORMA   P07139 candida mal   LEU3_LORMA   P094114 pichia stip   PRSI_METTH   Q92nd3 clostridium   PRSI_METTH   P66924 methanobact   PRSI_METTH   P66924 pecudomonas   HAYD_ACTPC   P09986 secherichia   HAYD_ECOLI   P09986 secherichia   HAYD_ECOLI   P06739 escherichia   HAYD_ECOLI   P093330 simian sarc   ALO_YEAST   P64783 saccharomyc | ALIGNMENTS  THE  TRAB  DCD_PYRAB  STANDARD; PRT; 154 AA.  00-000XSB;  20-AUG-2001 (Rel. 40, Last sequence update)  20-AUG-2001 (Rel. 40, Last sequence update)  20-AUG-2001 (Rel. 40, Last annotation update)  PEROBALIA DEMINASE  PATOCOCCUS abyssi.  ACACHARIA TO PREMISSION A.  SEQUENCE FROM N.A.  SERRAINANDERSAY;  Heilig R.; abyssi genome sequence: insights into archaeal chromosome structure and evolution.";  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SERRAINANDERSAY;  Heilig R.; apyssi genome sequence: insights into archaeal chromosome structure and evolution.";  20-AUG-2001 (Rel. 40)  EMBL/GenBank/DDBJ databases.  1. CATALYIT: DCTP + H(2)0 = DUTP + NH(3).  1. SAMIANITY: BELONGS TO THE DCTP DEAMINASE FAMILY.  This SWISS-PROT entry is copyright. It is produced through a collaboration between the sysis Institute of Bioinformatics and the EMBL outstation between the sysis Institute of Bioinformatics and the EMBL outstation between the sysis Institute of Bioinformatics and the EMBL outstation between the sysis Institute of Bioinformatics and the EMBL outstation on its one profit institutes requires a license agreement (See http://www.isb-sh.ch/announce/or send an email to license@isb-sib.ch).  EMBL: AJ240288; CAB50689: 1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | UTPase. ; 1. oteomise; 1. 758 MW; C031BEE419094DDB CRC64; 00.0%; Score 8; DB 1; Length 154; 00.0%; Pred. No. 0.0054; ve 0; Mismatches 0; Indels 0; Gaps 0; |                                |
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| 000 Cum                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                          | J, Creat), Last J, Last J, Last INE TRIE INE TRIE Standard TY: DCT TY:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ase; durpase.  TP_deamir  Proteome.  17758 MW;  100.0%;  1100.0%;                                                                                          |                                |
| 000 Cum                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 668255555555555555555555555555555555555                                                                                                                                                                                                                                                                                                                                                                                                                  | STANN  (Rel. 4(Rel. 4(Rel. 4(Rel. 4(Rel. 4) MAN)  SYYCYTID  SYACTABE  SYACTABE  SYACTABE  C. ACTIV  TY. BELC  TY. BE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | R001428,<br>12, dUTP:<br>14900; dC<br>Complete<br>54 AA;<br>Larity<br>Conserv?                                                                             |                                |
| 000 Cum                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                          | PYRAB<br>88;<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>107-2001<br>10 | S31                                                                                                                                                        | PDWKIRK<br>       <br> PDWKIRK |
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Best Local Similarity 100.0%; P:
Matches 6; Conservative 0;
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23 WKIRKE 28
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                                                                                                                                                                                                                                                         Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.",
DNA Res 5:55-76[198].

-I. CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-I. SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                 Pyrococus horikoshii.
Pyrococus Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=53953;
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
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STRAIN-SEROYIPE A1;
MEDIAINS-EROYIPE A1;
LO R.Y.C., Strathdee C.A., Shewen P.E.;
"Nuclectide sequence of the leukotoxin genes of Pasteurella haemolytica A1.";
Infect. Immun. 55:1987-1996(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 8; DB 1; Length 156;
Best Local Similarity 100.0%; Precd. No. 0.0055;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Complete protecome.
SEQUENCE 156 AA; 17871 MW; 96B2C2C50393A985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
LKTD.
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                                                                                                                                                                                                                                         MEDLINE-98344137; PubMed-9679194;
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STRAIN-SEROTYPE A1;
MEDLINE-89123172; PubMed-2914876;
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=75985;
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                     DEAMINASE).
DCD OR PH1997
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P16534;
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TO HLYD_PASHA
DT HLYD_P
DT O1-AUG
DT 30-MAY
DE LEWOT
GN LEWO
GN PASTEU
GN MANNE
GN NGELT
RP SEQUEN
RX STRAIN
RX HABEDLIN
RX HAB
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CC THIS STATEMENT OF THE LEUKOTOXIN.

-1. FUNCTION: INVOLVED IN THE TRANSPORT OF THE LEUKOTOXIN.

-1. SUBCELLULAR LECATION: INNER MEMBRANE=DOUND (POTENTIAL).

-1. SUBCELLULAR LECATION: INNER MEMBRANE=DOUND (POTENTIAL).

-1. SIMILARITY: BELONGS TO THE HLYD FAMILY OF SECRETION PROTEINS.

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Strathdee C.A., Lo R.Y.C.; "Cloning, nucleotide sequence, and characterization of genes encoding the secretion function of the Pasteurella haemolytica leukotoxin determinant."; ".". "J. Bacteriol. 171:916-928(1989).
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MEDLINE-9329310; PubMed-8478098;
MEDLINE-9329320; PubMed-8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin gene from a Pasteurella haemolytica-like organism, encoding a new member of the RIX toxin family";
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SEROTYPE A1 / PHL101;
MEDLINE-89210283; PubMed-2707120;
Highlander S.K., Chidambaram M., Engler M.J., Weinstock G.M.;
"DNA sequence of the Pasteurella haemolytica leukotoxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella haemolytica-like sp. (strain 5943B).
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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Pred. No. 2.6;
Mismatches
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
LEUKOYOXIN SECRETION PROTEIN D.
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Pred. No.
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MEDLINE=99162402; PubMed=10051401; Aho S., Rothenberger K., Tan E.M.L., Ryoo Y.W., Cho B.H., McLean W.H.I., Uitto J.; McLean W.H.I., Uitto J.; "Human periplakin: genomic organization in a clonally unstable region of chromosome 16p with an abundance of repetitive sequence elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aho S., McLean W.H.I., Li K., Uitto J.; "CDNA cloning, mRNA expression, and chromosomal mapping of human and mouse periplakin genes."; Genomics 48:242-247(1998).
                                                                                                     1 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                          . . . ) (POTENTIAL). . . . ) (POTENTIAL). . . . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPL_HUMAN STANDARD; PRT; 1756 AA.

60437; 060434; 060314;
20-A0G-2001 (Rel. 40, Last sequence update)
20-A0G-2001 (Rel. 40, Last sequence update)
20-A0G-2001 (Rel. 40, Last annotation update)
PERIPLAKIN (195 KDA CORNIFIED ENVELOPE PRECURSOR) (190 KDA PARANEOPLASTIC_PEMPHIGUS ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruhrberg C., Hajibagheri M.A.N., Parry D.A.D., Watt F.M.; "Periplakin, a novel component of cornified envelopes and that belongs to the plakin family and forms complexes with envoplakin.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 595,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                      4A6DD6058E598BD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 6; DB 1; 100.0%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                   Pfam; PF00864; P2X_receptor; 1. PRINYS; PR01307; PXRECEPTOR. PRINS; PR01314; P2X_RECEPTOR. PROSITE; PS01212; P2X_RECEPTOR; 1.
  InterPro; IPR001429; P2X_receptor.
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MEDLINE-98075094; PubMed-9412476;
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MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 139:1835-1849(1997)
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MEDLINE=98190524; PubMed=9521878;
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46
334
355
595
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187
202
213
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| 575 WKIRKE 580
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 272:735-738(1996).

- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION CHANNEL. RESPONSTBLE FOR ATP-DEPENDENT LYSIS OF MACROPHAGES THROUGH THE FORMATION OF MEMBRANE PORES PERMEABLE TO LARGE MOLECULES. COULD FUNCTION IN BOTH FAST SYMAPTIC TRANSMISSION AND THE ATP-MEDIATED LYSIS OF ANTIGEN-PRESENTING CELLS.
- SUBUNIT: HOWO- OR HETEROPOLYMERS (BY SIMILARITY).
- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
- SUBLIBARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
               FUNCTION: INVOLVED IN THE TRANSPORT OF THE LEUKOTOXIN. SUBCELLULAR LOCATION: INNER MEMBRANE-BOUND (POTENTIAL). SIMILARITY: BELONGS TO THE HLYD FAMILY OF SECRETION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                      Hemolysis; Cytolysis; Transport; Transmembrane; Inner membrane.
DOMAIN
1 77 CYTOPLASMIC (POTENTIAL).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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221461A69482913A CRC64;
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100.0%; Pred. No. ...
0; Mismatches
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Infect. Immun. 61:2089-2095(1993).
                                                                                                                                                                                                                                                                    EMBL; L12148; AAA16446.1; -.
InterPro. 1PR002215; H1yD.
Pfam; PF0059; H1yD; 1.
PROSITE; PS00543; HLYD_FAMILY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       478 AA;
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SEQUENCE
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Matches

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-953003125; PubMed=7788527; Sazuka T., Seki N., Sato S., Magase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S., Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.; Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.; Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.; Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.; The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of CDNA clones from human cell line KG-I."; DNA Res. 2:37-43(1955).

I-TISSUE SPECIFICITY: OVER-EXPRESSED IN HEPATOMAS AND COLONIC TINGS. ALSO EXPRESSED IN SKELETAL MUSCLE, BRAIN, HEART, PLACENTA, LUNG, LIVER, KIDNEY AND PANCREAS.

I-SIMILARITY: CONTAINS 9 HEAT REPEATS.
                                                                                                                                                                                                           TISSUE-Brain tumor;

MEDLINE-96128167; PubMed-8536682;

Charrasse S., Mazel M., Taviaux S., Berta P., Chow T., Larroque C.;

Charrasse S., Mazel M., Taviaux S., Berta P., Chow T., Larroque C.;

"Characterization of the cDNA and pattern of expression of a new gene over-expressed in human hepatomas and colonic tumors.";

Eur. J. Blochem. 234:406-413(1995).
                                                                      Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                 20-AUG-2001 (Rel. 40, Last annotation update)
CH-TOG PROTEIN (COLONIC AND HEPATIC TUMOR OVER-EXPRESSED PROTEIN)
KIAA0097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2032;
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E -> A (IN REF. 1).
E -> A (IN REF. 1).
W. 0256603047FA45EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.0%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 7.8; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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HEAT 2.
HEAT 4.
HEAT 5.
HEAT 6.
HEAT 7.
HEAT 9.
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EMBL; D43464; BAA07992.2; ALT_INIT.
InterPro; IPR000357; HEAT_REPEAT.
PROSITE; PS50077; HEAT_REPEAT. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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; 225507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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| 874 WKIRKE 879
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VPU_HV1ZH
ID VPU_HV1ZH
AC P08806;
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INDUCTION: DURING DIFFERRITATION OF EPIDERMAL KERATINOCYTES.

INTILARITY: CONTAINS 2 PLECTIN REPEATS.

INTILARITY: CONTAINS 4 SPECTRIN REPEATS.

IN SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.

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Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. IX. Prediction of the coding sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:31-39(1998).
-!- FUNCTION: COMPONENT OF THE CORNIFIED ENVELOPE OF KERATINOCYTES.
MAY LINK THE CORNIFIED ENVELOPE TO DESMOSOMES AND INTERMEDIATE FILAMENTS.
-!- SUBGELLUIT: HOMODIMER OR A HETERODIMER WITH EVPL (POTENTIAL).
-! SUBCELLUIAR LOCATION: ASSOCIATED WITH DESMOSOMES AND INTERMEDIATE FILAMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E (IN REF. 4).
L (IN REF. 1).
557C7D92BE18F107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoskeleton, Structural protein.
125 COLLED COLL (POTENTIAL).
89 COLLED COLL (POTENTIAL).
317 SPECTRIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
PLECTIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF001561; AAC17738 1;
EMBL; AF01317; AAC39668 1;
EMBL; AF041004; AAD17459.1;
EMBL; AF040999; AAD17459.1; JOINED.
EMBL; AF041000; AAD17459.1; JOINED.
EMBL; AF041002; AAD17459.1; JOINED.
EMBL; AF041003; AAD17459.1; JOINED.
EMBL; AB01140; BAAD25494.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001101; Plectin_repeat.
InterPro; IPR002017; Spectrin.
SMART; SM00250; PLEC; 2.
SMART; SM00150; SPEC; 4.
Repeat; Colled Coll; Cytoskeleton; S
DOMAIN
16 1125
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Conservative 0;
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6; Conserv
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Best Local S
Matches 6
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Query Match
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YJV8_YEAST
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                                                                                                                           MEDLINE-89228766; PubMed-2713163;
MEDLINE-89228766; PubMed-2713163;
MIDLINE-89228766; PubMed-2713163;
MCOINTICK J., Tork D., Butler D. Jr., Jannoun-Nasr R., Getchell J., MCOINTICK J., OU C.Y., Myers G., Smith T., Chen E.;
MOlecular characterization of HIV-1 isolated from a serum collected sequence comparison to recent isolates and generation of hybrid HIV-?
AIDS Res. Hum. Retroviruses 5:121-129(1989).
I- FUNCTION: ACTS IN THE DEGRADATION OF CD4 IN THE ENDOPLASMIC RETICULUM AND IN THE ENHANCEMENT OF VIRION RELEASE FROM THE PLASMA MEMBRANE OF INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Moneal L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                 Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 AA; 6789 MW; 40EE98A77BB3DACE CRC64;
(Rel. 09, Created)
(Rel. 09, Last sequence update)
(Rel. 35, Last annotation update)
(U ORF PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
5. 7.6;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 7.6 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5;
Pred. No
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20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last and
HYPOTHETICAL PROTEIN AF0414.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M15896; AAB53947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; M15896; VPU$Z321.
InterPro; IPR002094; Vpu.
Pfam; PF00558; Vpu; 1.
Transmembrane; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.5
Best Local Similarity 100.
Matches 5; Conservative
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9 KIRKE 13
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  01-NOV-1988
01-NOV-1988
01-NOV-1997
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                                            PROTEIN
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029833;
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SEQUENCE
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AC 029833.
AC 029833.
DT 20-AUG.
DT 20-AUG.
DE HYPOTHI
GS Archael
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COX NCBL_T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Yeast 10:1657-1662(1994).
                                                                                                                                        The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                             Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
PUTATIVE ACETYLTRANSFERASE IN HXT11-HXT8 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protéin; Complete proteome.
SEQUENCE 144 AA; 16262 MW; 834C76ECF066EE59 CRC64;
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                                                                                                                                                                         reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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SGD; S0003754; YJL218W.
Interpro: IPR001451; Hexapep_transf.
Pfam: PF00132; hexapep_3; 3.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95242842; PubMed=7725802;
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7JL218W OR J0224 OR HRA196.
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62 KIRKE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KIRKE 8
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                                                                                                      Venter J.C.;
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MISCELLANBOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE POUND IN EUGRAFORT (NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE SILI FOR THE MRNA PRECURSOR, AND POLYMERASE SILI FOR THE ARRA GENES.

SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOH / EUKARYOTIC RPB5 RNA POLYMERASE SILIARM FAMILY.
                                                                                                                                                                                                                        REBULT 11
RPB5_HUMAN STANDARD; PRT; 210 AA.
AC P19388; 043380;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AGG-2001 (Rel. 40, Last annotation update)
DF 20-AGG-2001 (Rel. 40, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE (EC 2.7.7.6) (RPB25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            litted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-95129541; PubMed-7828586;
MEDLINE-95129541; PubMed-7828586;
Greeng J., Yi M., Lin Y., Murakami S.;
"Human RPB5, a subunit shared by eukaryotic nuclear RNA polymerases, binds human hepatitis B virus X protein and may play a role in X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Lamerdin J.E., McCready P.M., Stowners M., Stillwagen S.,
Phan H., Velasco N., Gardon L., Kyle A., Ramirez M., Stillwagen S.,
Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise Trankheim M., Amico-Keller G., Coefield J., Loust S., Lucas S.,
Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
Carrano A.V.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pati U.K., Weissman S.M.;
"Isolation and molecular characterization of a cDNA encoding the
23-Kba subunit of human RNA polymerase II.";
J. Biol. Chem. 264:13114-13121(1989).
                                                                                                        ö
  l protein; Transferase; Acyltransferase; Repeat.
196 AA; 21479 MW; FDE9036757112E84 CRC64;
                                                                   Length 196;
                                                                                                      0; Indels
                                                                 62.5%; Score 5; DB 1;
100.0%; Pred. No. 19;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89327280; PubMed-2753903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS.
MEDLINE-91302386; PUDMed-2071613;
Part U.K., Weissman S.M.;
J. Biol. Chem. 266:13468-13468(1991).
                                                                 Query Match 62.5
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transactivation.";
EMBO J. 14:143-150(1995).
                                                                                                                                                                                                                                                                                                                                                                 (XAP4) (RPB5).
POLR2E.
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                                                                                                                                                           11111
23 KIRKE 27
Hypothetical SEQUENCE 15
                                                                                                                                      4 KIRKE 8
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STRAIN-ALL-I, DSM 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Voerbeek R., Kirkness E.P., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nayven D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- SIMILARITY: TO M.JANNASCHII MJ1220 AND MJECL42.
-!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y132_METJA STANDARD; PRT; 220 AA. 057596 NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL PROTEIN MJ0132.
                                                                                                                                                                                                                                                                                                              EMBL; J04965; AAA62401.1; ALT_SEQ.
EMBL; SA2643; ABB193391; -.
EMBL; D38251; BAA07406.1; -
EMBL; AC004151; AAC03238.1; -.
BIR; A32618; A32618.
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AC 7132_METUA
AC 715596,
AC 057596,
DT 01-NOV
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10) (OMPPPASE) (OPRT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hwang C.-W., Lee D.-K., Kang S.-C.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTILYTY: OROTIDINE-5'-PHOSPHATE + PPHOSPHO-ALPHA-D-RIBOSE 1-DIPHOSPHATE.
-!- PATHWAY: FIFTH STEE IN PYRIMIDINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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0; Mismatches
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Interpro; IPR002375; Pur_pyr_pr_transf.
IERM; PF00156; Pribosyltran; I.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; I.
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ACT_SITE 114 114 BY S
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Matches 5; Conservative
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                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                             Metarhizium anisopliae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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|151 KIRKE 155
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|150 KIRKE 154
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                        4 KIRKE
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YC34_METJA
                                                                                                                                 RESULT 14
PYRE_METAN
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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30-MAY-2000 (Rel. 39, Last annotation update)
OROTATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.10) (OMPPPASE) (OPRT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOI. Gen. Genet. 235:74-80(1992).
-!- CATALYTIC ACTIVITY: OROTIDINE-5'-PHOSPHATE + PYROPHOSPHATE = OROTATA + 5-PHOSPHO-ALPHA-D-RIBOSE 1-DIPHOSPHATE.
-!- PATHWAY: FIFTH STEP IN PYRIMIDINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE PUBLINE/PYRIMIDINE
PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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HSSP; P08970; 1STO.
InterPro; IPR000936; Pribosyltran.
InterPro; IPR000336; Pur_pyr_pr_transf.
Pfam; PF00156; Pribosyltran; 1.
PR0SITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
PYTIMIGINE biosynthesis; Transferase; Glycosyltransferase.
PYTIMIGINE biosynthesis; Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colletotrichum graminicola (Anthracnose fungus) (Glomerella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 233;
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                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                        PION: PEO2384; N6_DNA_Mtase.
Pfam: PF02384; N6_Mtase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 220 Aa; 25766 MW; 710DDAE4C7A47954 CRC64;
                                                                                                                                                                                                                                                            62.5%; Score 5; DB 1;
100.0%; Pred. No. 21;
iive 0; Mismatches
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100.0%; Pred. No. 22;
Live 0; Mismatches
                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93062810; PubMed=1435732;
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(Rel. 39, Last anno
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                                                                                       EMBL; U67470; AAB98113.1; -.
                                                                                                                                                                                                                                                            Query Match 62.5
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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66 KIRKE 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRE_COLGR
P35788;
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Length 234; 0; Indels

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseé!sb-sib.ch).
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

WEDLINE-9637999; Pubmed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.J., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Scribarde A.R., Dougherty B.A., Tomb J.F., Addms M.D., Reich C.I., Gwerbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Cotton M.D., Roberts K.M., Furst M.A., Kaine B.P., Borodovsky M., Cotton M.D., Roberts K.M., Smith H.O., Woese C.R., Venter J.C., Smith H.O., Woese C.R., Venter J.C., Sanis Jannaschili...;

Science 273:1058-1073(1996).
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Pfam; PF01881; DUF57; 1.
Probom; PD008324; DUF57; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 241 AA; 28840 MW; 23AD8F19448CBFC6 CRC64;
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Search completed: January 31, 2002, 13:39:13 Job time: 73 sec

4 KIRKE 8 |||||| 209 KIRKE 213

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Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

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                                                                      Q99rj6 staphylococ
O28785 archaeoglob
Q9nz51 homo sapien
Q9y3e7 homo sapien
                                                                                                                                                Q9gm32 macaca fasc
Q9vn02 drosophila
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JMAR-2001 (TrEMBLrel. 17, Last sequence update)
61-JUN-2001 (TrEMBLrel. 17, Last sequence update)
6LYCOLATE OXIDASE SUBUNIT D-LIKE, D-LACTATE DEHYDROGENASE-LIKE.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Q9bqf7 homo s
Q9bt06 homo s
O76080 homo s
O88878 mus n
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Tabata S.;
Siructural analysis of Arabidopsis thaliana chromosome 5. XI.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002543; BAB11407.1;
PinterPro: IPR001575; Oxid_FRD_bind.
Pfam: PF01565; FAD_binding 4, 1.
SEQUENCE 418 AA; 45807 MW; D8C84FCOCIE60FAZ CRC64;
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Last sequence update)
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O88878
Q99RJ6
O28785
Q9NZ51
Q9Y3E7
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Q9VN02
Q9ER79
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Q12592
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272 WKIRKE 277
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Ogpt63 xenopus lae
Ogdáv8 xenopus lae
O28900 bos taurus
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Q9Kju9 listeria in
Q70888 human immun
Q91sn9 arabidopsis
Q69966 human immun
Q85278 fowlpox vir
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Q99rn6 staphylococ
Q9pm97 campylobact
Q9v1w5 pyrococcus
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Q9f590 agrobacteri
O96038 ciona savig
Q9gzy3 homo sapien
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                                                                                                                         January 31, 2002, 13:37:33 ; Search time 130.99 Seconds (without alignments) 8.933 Million cell updates/sec
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Q9PM97
Q9V1W5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
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sp_phage:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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Match Length DB
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PERFORMANCE FROM N.A.

RA BECKET B.E., Gard D.L.;

RA BECKET B.E., Gard D.L.;

RA BECKET B.E., Gard D.L.;

RA HEDLINE-1050forms of the high molecular weight microtubule associated cell wittiple isoforms of the high molecular weight microtubule associated represent xMAP215 are expressed during development in Xenopus.";

RL Cell Motil. Cytoskeleton 47:282-295(2000).

PROSITE; PS50077; HEAT_repeat.

DR InterPro: IPR000357; HEAT_repeat.

PT VARIANT 821 T -> APT.

FT VARIANT 1103 1105 PPP -> APT.

SEQUENCE 2066 AA; 228516 MW; 4F5CA6E4EA27345F CRC64;
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RA Shima D.T., Saunders K.B., Gougos A., D'Amore P.A.;

RA Shima D.T., Saunders K.B., Gougos A., D'Amore P.A.;

RA Shima D.T., Saunders K.B., Gougos A., D'Amore P.A.;

RA Cardiothelial differentiation;

R. Differentiation;

R. Differentiation;

R. Differentiation;

R. Differentiation;

R. Differentiation;

BR S1217-226(1995).

DR InterPro;

IPR000058;

ZE-ANI;

DR SAART;

SMO0154;

ZE-ANI;

NON_TER

SOURCE & ANI;

SQ SEQUENCE & ANI;

SQ SEQUENCE & ANI;

C DR 6: Length 46;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2004 (TrEMBLrel. 17, Last annotation update)
01-UNV-2004 (TrEMBLrel. 17, Last annotation update)
01-UNV-2004 (TREMBLR)
01-UNV-2004 (TREMBLR)
Bos taurus (Bovine)
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Novidee; Bos taurus (Bovinea; Bos taurus Last Despis);
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MICROTUBULE ASSOCIATED PROVERN XMAP215 ISOFORM M.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphblais, Batrachla; Anura; Mesobatrachia; Pipoldea; Pipldae;
Xenopodinae; Xenopus.
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Post Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 45;
iive 0; Mismatches
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01-NOV-1996 (TrEMBLEEL: 01,
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Best Local Similarity 100.
Matches 5; Conservative
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871 WKIRKE 876
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SEQUENCE FROM N.A.

MEDLINE-20089046; Pubmed-10620801;

MEDLINE-20089046; Pubmed-10620801;

Tournebize R., Popov A., Kinoshita K., Ashford A.J., Rybina S.,

Pozniakovsky A., Mayer T.U., Walczak C.E., Karsenti E., Hyman A.A.;

"Control of microtubule dynamics by the antagonistic activities of XMP215 and XKM1 in Xenopus egg extracts.";

NAT. Cell Biol. 2:13-19(2000).

RENEL, AJ251130; CAB61894.1;

INTERPOS ITROWORD ST. HEAT_repeat.

PROSITE; PSSO077; HEAT_REPEAT; 2.

PROFITE; PSSO077; HEAT_FREEAT; 2.
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OPPT63: OPPT63: OPPT63: DELIMINARY; PRT; 2065 AA.
O1-MAY-2000 (TEMBLE-1. 13, Last sequence update)
O1-MAY-2000 (TEMBLE-1. 17, Last annotation update)
MICROTUBULE ASSOCIATED PROFEIN 215 KDA (XMAP215).
XMAPA215.
Xenopus laevis (African clawed frog).
BUKATYOTA: Metazoa. Chordata. Craniata; Vertebrata; Euteleostomi; Amplibia. Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
MICROTUBULE ASSOCIATED PROTEIN XMAP215 ISOFORM Z.
Stropus Laevis (African clawed frog).
Eukaryota; Metazoa; Chorodata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Pred. No. 65;
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... 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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                                                                             Xenopodinae; Xenopus.
NCBL_TaxID-8355;
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871 WKIRKE 876
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Q9DDV8;
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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC clones.";
DNA Res. 7:131-135(2000).
EMBL; AB026636; BAA94986.1; -.
SEQUENCE 134 AA; 15641 MW; F6E8BCE61B5D588E CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
SIMILARITY TO PAPAVER NIDUCAULE SELF-INCOMPATIBILITY PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota; Viridiplantae; Streptophyta; Eukaryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                    STRAIN=003;
Cornelissen M., Goudsmit J.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases. EMBL; U13479; AAA73671.1; -. InterPro; IPR000777; GP120. Pfam; PF00516; GP120; 1.
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                                                                                    01-NOV-1996 (TIEMBLEEL. 01, Created)
01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-JUN-2001 (TIEMBLEEL. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN V1V2 REGION (FRAGMENT).
                                                                                                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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100.0%; Pred. No. 73;
Live 0; Mismatches
                                            87 AA.
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STRAIN-COLUMBIA;
MEDLINE-20277480; PubMed=10819329;
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Best Local Similarity 100.
Matches 5; Conservative
                                              PRELIMINARY;
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54 KIRKE 58
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SEQUENCE
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                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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C STRAIN-LEMIS; TISSUB-LIVER;

MEDLINE-97236424; PubMed-9116048;

A ROThermel E., Rolf O., Goetze O., Zwirner J.;

T ecombinant rat annaphylatoxin C5a.";

I Nucleotide and corrected amino acid sequence of the functional recombinant rat annaphylatoxin C5a.";

E Biochim. Biophys. Acta 1331:9-12(1997).

R HSSP: PO1031; IKJS.

R InterPro: IPR001840; Anaphylatoxin.

P fam: PF01821; ANATO: 1.

R PRINTS: PR00004; ANRPHYLATOXN.

R PRINTS: SMO0104; ANRPHYLATOXN.
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"Region homologous to teichoic acid glycosylation gene gtcA in Listeria innocua strain F8596.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF160251; AFF80387.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) C5A COMPLEMENT COMPONENT PROTEIN (FRAGMENT).
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Last annotation update)
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Bacillus/Staphylococcus group; Listeria.
NCBL_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.5%; Score 5; DB 2;
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                               NCBI_TaxID=10116;
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63 KIRKE 67
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40 WKIRK 44
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SEQUENCE
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62.5%; Score 5; DB 10; 100.0%; Pred. No. 1e+02;
Query Match
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SEQUENCE FROM N.A.
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71 KIRKE 75
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MEDLINE-561750;
MEDLINE-561750;
Packer M.L., De Jager G., Becker W.B.;
Backer M.L., De Jager G., Becker W.B.;
From southern Africa.
AIDS Res. Hum. Retroviruses 11:1265-1267(1995).
EMBL, 070701; ABABID36.1; -.
INTERPETO; IPRO00777; GP120.
Pfam: PF00516; GP120; 1.
NON_TER 13 137
NON_TER 137
NON_TER 137
SEQUENCE 137 AA; 14933 MW; 7B95641B8FCF096D CRC64;
   Gaps
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MEDIATR=-39709881: PubMed=1333124;
MEDIATR=-93709881: PubMed=1333124;
Calvert J.G., Ogawa R., Fanagida N., Nazerian K.;
"Identification and functional analysis of the fowlpox virus homolog of the vaccinia virus p37k major envelope antigen gene.";
virology 191:783-782(1929).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
FOUNDAY SINGEN ENVELOPE ANTIGEN (P43K) (FRAGMENT).
FOUNDAY VITUS.
VITUSES; GADNA VITUSES, no RNA stage; Poxviridae; Chordopoxvirinae;
NCBI_TAXID=10261;
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MEDILINE-91021027; PubMed-2219722;
Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
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Pred. No. 1e+02;
0; Mismatches 0; Indels
Indels
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Mismatches
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SEQUENCE FROM N.A.
MEDLINE-93139784; PubMed-8380837;
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Best Local Similarity 100.0%; Pr
Matches 5; Conservative 0;
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5; Conservative
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                                                                                           110 WKIRK 114
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62 KIRKE 66
                                                        3 WKIRK 7
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AC 085278
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Ogawa R., Yanagida N., Nazerian K., Calvert J.G.;
"Insertional inactivation of a fowlpox virus homologue of the vaccinia virus F12L gene inhibits the release of enveloped virions.";
J. Gen. Virol. 74:55-64(1993).
BOBL. M88587: AAA43818 1;
NOW TER 146
SEQUENCE 146 AA: 17065 MW; IBF8FE96F824A32C CRC64;
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Rawarabbayasi Y. Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Rawarabbayasi Y. Sawada M., Horikawa H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Runahashi T., Tanaka T., Rudoh Y., Yasubida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
EMBL: AP000001; BAA29253.1;
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
149AA LONG HYPOTHETICAL MOLYBDOPPERINCONVERTING FACTOR, SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                               Length 146;
                                                                                                                                                                                                                                                                                                           Query Match 62.5%; Score 5; DB 12; Length 146 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001348; MoeA.
InterPro; IPR000513; TonB_boxC.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 149 AA. 17105 MW; BCEAC6734DE299D5 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 149 AA.
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15 KIRKE 19
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                                                                      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawanon T., Inoue R.I., Kaito C., Sekimizu K.,
HIrakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Whole genome sequencing of meticillin-resistant Staphylococcus
aureus."
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MEDIATOR-120912; PubMed-10688204;
MEDIATOR-20150912; PubMed-10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.W., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandraam M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.5%; Score 5; DB 2; Length 150;
100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Lancet 357:1225-1240(2001).

EMBL; AP003137; BAB43483.1; -
Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.

Hypothetical AA; 17150 WW; 006D965569DFCCDD CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
NADH DEHYDROGENASE I CHAIN B (EC 1.6.5.3).
NUOB OR CJ1578.
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Q9VIW5;
01-MAY-2000 (TrEMBLrel. 13, Created)
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InterPro; IPR002096; Complex1_20kD.
Pfam; PF01058; oxidored_q6; 1.
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Nature 403:665-668(2000).
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Best Local Similarity 100.05
تمام 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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NCBI_TaxID=158879;
                                                            SEQUENCE FROM N.A.
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SEQUENCE 167 AA
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|151 KIRKE 155
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18 KIRKE 22
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09PM97
AC 09PM97
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DT 01-JUN
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DT 01-MAY-2000 (TrEMBLRel. 13, Last sequence update)

DF 01-JUN-2001 (TrEMBLRel. 17, Last annotation update)

DE HPOTHETICAL 21.6 KDA PROTEIN.

ON Archaea; Buryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.

OX Archaea; Buryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.

OX Archaea; Buryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.

NBL TAXID-2929;

RA FAILUR.

RE SEQUENCE FROW N.A.

RA PARIOL R.:

RA PLASIAN-ORBAY;

RA PLASIAN-ORBAY;

RA PLASIAN-ORBAY;

RA PLASIAN-ORBAY;

RA PROJUCTURE and evolution.

R. Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

DR REMBL; ANA14884; CABA9233.1; -.

DR HSEP: P013045; CARO.

DR InterPro; IPRO01387; HTH.3.

DR SMART; SW00116; CBS. 2.

DR SWART; SW00116; CBS. 3.

DR SWART; SW00116; CBS. 3.

OUMETY MATCH B.:

DR SWART; SW00116; CBS. 2.

SEQUENCE 192 AA; 21645 MM; EDELIE4F88F7A7AA CRC64;

OUMETY MATCH B.

DR SWARTS SW00116; CBS. 2.

A KIRKE 8

ON 4 KIRKE 8

ON 4 KIRKE 8

ON 4 KIRKE 8

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DD 15 KIRKE 19

SEGATCH COMPLETED: 13:37:35

JOD time: 160 Sec
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AIL protein-maltos

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Sequence:

protein

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Scoring table:

Human secreted pro Arabidopsis thalia Arabidopsis thalia

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enhancing factor; PEF; dUTPase; DNA polymerase; PCR;
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2..15
/note= "N-terminal peptide used to generate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymerase enhancing factor; PEF; dUTPe
amplification; sequencing; replication
                                                                                                                                                                                                                                                                                                     AAB27581
AAY60464
AAY40052
AAG13285
AAG08097
AAG11055
AAG11055
AAY37542
AAY37542
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AAY37542
AAY37542
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AAB93202
AAB93202
AAX23996
AAX399795
AAX65947
AAX66872
AAB60913
AAB73485
AAX54453
AAX60922
AAB134642
AAB3734642
AAM37947
AAG17889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furiosus strain DSM 3638
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97US-0822774
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WO9842860-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1997;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1999
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Peptide
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  RESULT
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Polymerase enhanci
Pyrococcus furisos
Polymerase enhanci
Polymerase enhanci
Bordetella pertuss
Attachment-invasio
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S. epidermidis ope
Arabidopsis thalia
Arabidopsis thalia
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82.521 Million cell updates/sec
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1 Milpowkirkeiliepfsee......pyrgnyqgstrlafskrkl 156
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              4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    Potal number of hits satisfying chosen parameters:
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              GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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AAW72849
AAW72846
AAW72870
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AAR96207
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Match Length
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162
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164
171
198

    protein search,

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Score

Result Š 

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This peptide comprises an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEP) of pyrococcus furiosus DSM 3638. It has been obtained from isolated P45; a full-length sequence is provided in AAW2847. BEF, the predominant components of which are P45 and P90 (see AAW2844) proteins, enhances the replication products of greater length and purity. P45 is a ctivity of P. furiosus DNA polymerase, thereby providing a ctivity of P. furiosus DNA polymerase, thereby providing provides novel extracts, proceins and complexes that improve the polymerisation activity of nucleic acid polymerases. These complexes may include proteins including the P45 N-terminal polymerase enhancing activity, for purifying and using these compositions, and specific extracts, proteins and complexes that included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that included are methods for identifying and using these compositions, and specific activity, for purifying and using these reactions can be enhanced (claimed) by mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase inhancing activity. Kits are provided for replicating nucleic acid sequencing or amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                    Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; sequencing; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%; Score 14; DB 19; Length 15; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furisosus P45 dUTPase uridine-binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                   Claim 17; Page 33; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW72849 standard; Peptide; 14 AA.
97US-0957709.
97US-0822774.
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Best Local Similarity 100.
Matches 14; Conservative
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                                                              (STRA-) STRATAGENE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
24-OCT-1997;
21-MAR-1997;
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21-MAR-1997;
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                                                                                                       Hansen CJ,
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                                                                                                                                                    This is the amino acid sequence of the P45 component of the polymerase enhancing factor (PEF) of Pyrococus furiosus DSM 368.

The sequence is predicted from a DNA sequence (see AAV63860) obtained from genomic DNA by PCR. P45 and P50 (see AAW2844) are the redeminant components of PEF, which acts to enhance the activity of PF furiosus DNA polymerase. P45 functions as a durpase, and can be used to enhance nucleic acid replication, polymerisation or PCR complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies. Also included are methods for identifying compositions with PEF activity. For printifying and using these compositions, and specific extracts, or proteins and complexes that function to enhance polymerase activity. Wucleic acid polymerase reactions can be enhanced (claimed) by mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase enhancing activity. Mixs are provided for replicating nucleic acid sequencing or site-directed mutagenesis, for nucleic acid sequencing or amplification (preferably PCR or PPCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LILERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; sequencing; replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 156; DB 19; Length 156; Best Local Similarity 100.0%; Pred. No. 1.4e-149; Matches 156; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymerase enhancing factor P45 component N-terminal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furiosus strain DSM 3638.
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                                                                                                                     Claim 17; Page 43; 161pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA;
N-PSDB; AAV63860
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                                                                                                                             This is the uridine-binding motif of the P45 component (see
AAW72847) of the polymerase enhancing factor (PEF) of Pyrococcus
C furiosus DSM 368. P45 has been identified as a durpase that
that polymerase enhancing activity. Sequences are provided (see
AAW72849-57) of the uridine-binding motifs of dUTPasses and dCTP
C deaminases of P. furiosus, Methanococcus jannaschii, Desulfurolobus
ambivalens, Escherichia coli, yeast, human and herpesvirus; a
consensus (see AAW72848) is also provided. A claimed method of
the reaction in the presence of one or more of the following: a
the reaction in the presence of one or more of the following: a
C PEF, a dUTPasse, a protein that turns over dUTP and a protein
having one or more of the sequences provided in AAW72848-57. A
C claimed protein having PEF activity comprises one or more of
sequences given in AAW72848-57. A
C claimed protein having PEF activity surprises one or more of
ucclaimed protein having PEF activity surprises one or more of
sequencing or for site-directed mutagenesis, for nucleic acid
sequencing or for amplification (preferably PCR or RT-PCR).
                                                         Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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                                                                                                                                                                                                                                                                                                                                                                                   Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 11; DB 19; I
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus furiosus strain DSM 3638.
                                                                                                           Claim 71; Page 47; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW72846 standard; Peptide; 8 AA.
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          Hansen CJ, Hogrefe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-542284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                 91 FAWVDPGWDGN 101
                                   WPI; 1998-542284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 fawvdpgwdgn 11
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                                                                                                                                                                                                                                                                                                                                              14 AA;
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                                                                                                                                                                                                                                                                                                                                                Sequence
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This peptide comprises an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEP) of Pyrococcus furiosus DSM 3638. It has been obtained from isolated P45. PCR primers can AAV63861-64) based on the peptide were used to amplify P45 DNA (see AAV63860). A full-length P45 sequence is provided in AAW72847. PEP, a predominant component of which is P45 protein, enhances the activity of P. furiosus DNA polymerase, thereby providing activity of P. furiosus DNA polymerase, thereby providing replication products of greater length and purity. P45 is a durpase and possesses polymerase enhancing activity. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These complexes may include proteins including the P45 N-terminal peptide. Also included are methods for identifying compositions (with polymerase enhancing activity, for purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase compositions can be enhanced (claimed) by mixing a nucleic acid polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acids. The kits can be used in site-directed mutagenesis, nucleic acids sequencing or amplification (preferably PCR or RT-PCR).
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Claim 17; Page 33; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW72870 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Arg, Pro
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Best Local Similarity
Matches 8; Conserv
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21-MAR-1997;
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WPI; 1996-251447/25.
N-PSDB; AAT27536.
                                                          153 AA;
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86 yalilt| 92
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   virulence
pertussis
caused by
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                                                            Sequence
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Peptide
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AAR96207
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                         Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                             This is an N-terminal peptide of the P45 component of the polymerase enhancing factor (PEF) of Pyrococous furiosus DSM 3638. PEF, the predominant components of which are P50 (see AMV72844) and P45 (see AMV72847), enhances the activity of P. furiosus DNA polymerase. P45 functions as a durphase. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases. These can be used to improve nucleic acid replication, polymerisation and amplification (especially in PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orf9; bacterial infection; anti-bacterial; vaccine; whooping cough; type III secretion system; virulence factor; pathogenicity island.
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                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                Score 7; E
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 138-139; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bollen A, Fauconnier A, Godfroid E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB14140 standard; Protein; 153 AA
                                                                                   Example 5; Page 33; 161pp; English
                                                                                                                                                                                                                                                                                                             Query Match 4.5%; Sco
Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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N-PSDB; AAA64878, AAA64890.
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WPI; 1998-542284/46
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                                                                                                                                                                                                                                                                     Sequence
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to treat or diagnose cough is a disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a bacterial attachment-invasion-locus (AIL) protein, which may be complexed with a therapeutic agent to transport the agent across the gastrointestinal membrane barrier by transcytosis to increase bioavailability 5- to 100-fold. The agent and bacterial protein may be linked via a degradable peptide as equence as a fusion protein. The receptor binding region of the AIL protein involves all or some of the regions from the 4 extracellular loops. This region retains the binding affinity of the protein, and may be used alone or as part of a fusion protein for drug delivery. The protein may be fused with maltose binding
                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
19..34
/note= "Peptide from extracellular loop-1"
58.76
/note= "peptide from extracellular loop-2"
102..19
/note= "Peptide from extracellular loop-3"
145..152
/note= "Peptide from extracellular loop-3"
                                                                                                                    Query Match 4.5%; Score 7; DB 21; Length 153; Best Local Similarity 100.0%; Prect. No. 34; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Attachment-invasion-locus protein; drug delivery; gastrointestinal membrane; transcytosis; bloavallability; fusion protein; enterocyte; Peyers patch M-cell.
genes. The present protein may be used infection, e.g. as a vaccine. Whooping infection by B. pertussis.
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                                                                                                                                                                                                                                                                                                               AAR96207 standard; Protein; 162 AA.
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                                                                                                               Gaps
protein (AAR96208) to form a fusion protein (AAR96209) which may be purified easily by amylose affinity chromatography. The delivery system allows improved transport across enterocytes and Peyers patch M-cells. The system is not prone to degradation in the gut or early release of biologically active material, and eliminates the need for parenteral administration.
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                                                                                           DB 17; Length 162; 5. 36;
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                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 58037.
                                                                                           Score 7; DB 1; Pred. No. 36; 0; Mismatches
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                                                                                     4.5%; Scc...
100.0%; Pre
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990S-0123548.
990S-0125788.
990S-012654.
990S-0126785.
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99US-0134256
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                                                                                          Query Match 4.5
Best Local Similarity 100.
Matches 7; Conservative
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49 gvigsfa 55
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09-MAR-1999

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99US-0160767
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II) and (II) and have antibacterial activity and therefore can be used (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors (II) appertides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides may also be used to assay for other inhibitors of their used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH5509 represent specifically claimed S. epidermidis genomic DNA AH5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH5509 to AAH5509 represent oligonucleotide sequences and primers which are used in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                             S. epidermidis open reading frame protein sequence SEQ ID NO:2478.
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                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                   DB 21; Length 164;
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                                                                                     0; Indels
                                                                                     Mismatches
                                             Query Match 4.5%; Score 7; I
Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
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                                                                                                                                                                                                                                         AAG82692 standard; Protein; 164 AA.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                           03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis
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N-PSDB; AAH53542.
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Best Local Similarity
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28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Gaps
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                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 58036.
0; Mismatches
                                                                              AAG46154 standard; Protein; 171 AA
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99US-0136782.
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                                                                                                                18-OCT-2000 (first entry)
7; Conservative
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                           EKEGKVV 51
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24 MAY - 1999;
25 MAY - 1999;
27 MAY - 1999;
01 - JUN - 1999;
03 - JUN - 1999;
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                                                                                               AAG46154;
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Matches
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 58035.
                                     AAG46153 standard; Protein; 198 AA.
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  RESULT 1
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9905 - 014856 5 9905 - 014856 5 9905 - 014856 8 9905 - 014936 8 9905 - 014936 8 9905 - 014936 8 9905 - 014936 9 905 - 014936 9 905 - 014932 9 905 - 014932 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 015936 9 905 - 016098 9 905 - 016098 9 905 - 016098 9 905 - 016098 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9 905 - 016136 9
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reafvkg 126
13. AUG 1999

13. AUG 1999

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18. AUG 1999

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25. SEP 1999

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27. AUG 1999

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26-0CT-1999;
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28-0CT-1999;
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99US-0145951.
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99US-0147038.
99US-0147204.
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99US-0148565.
99US-0148684.
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990S-0139463.
990S-0139750.
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990S-0139819.
990S-0140353.
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99US-0145087.
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99US-0140823.
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99US-0143542
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99US-0144005
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99US-0145088
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PR 22-ANC-1999; 9918-0110666
PR 27-ANC-1999; 9918-0110666
PR 27-ANC-1999; 9918-0110666
PR 31-ANC-1999; 9918-0110666
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PR 31-ANC-1999; 9918-01101676
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PR 31-ANC-1999; 9918-011016769
PR 31-ANC-1999; 9918-01101676
PR 32-ANC-1999; 9918-01101676
PR 32-AN
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AAB44561 standard; Protein; 250 AA.

AAB44561

33 REAFVKG 39 ||||||| 147 reafvkg 153

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08-FEB-2001 (first entry)

AAB44561;

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The present sequence is that of human protease and associated protein-18 (PBPG-18), which is expressed in hemantopoletic, immune, nervous and reproductive tissues. It is encoded by cDNA identified in Incyte clone 2820384 derived from BRSTNOT14 cDNA library. Anti-PPRG antibodies can be used as therapeulic antagonists, reagents for diagnosis and monitoring diseases and for isolating PPRG. PPRG nucleotide sequence can be used as probe or primer for diagnosis and monitoring proliferative disorders like cancer, arteriosclerosis, atherosclerosis, proliferative disorders like cancer, arteriosclerosis, atherosclerosis, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis and amyloidosis syndrome, allergies,
                                                                                             108
e= "Signature sequence of ubiquitin carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human proteases, useful for diagnosis, treatment and prevention cell proliferative disorders such as atherosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;
, Yue H, Tang YT, Reddy R, Patterson C, Au-Young
Lu DAM;
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               /note= "Potential Phosphorylation site"
                                            /note= "Potential Phosphorylation site"
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166
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348
                                                                              /note= "Potential Phosphorylation
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Pred. No. 74;
0; Mismatches
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ID AAR96210 standard; Protein; 568 AA.
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100.0%; Pre
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                                                                                                                                hydrolase"
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                               /note=
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N-PSDB; AAZ50935.
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273 eafvkgk 279
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11-FEB-1999;
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Corley NC,
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Shih LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and wound infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease and associated protein-18; PPRG-18; anti-PPRG antibody; dagnosis; treatment; cell proliferative disorder; cancer; cirrhosis; arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder; AIDS; Addison's disease; adult respiratory distress syndrome; allergy; ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic; hepatototropic; antiarialmamatory; virucide; antipsoriatic; anti-HIV; antiallergic; immunosuppressive; antidiabetic; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                  Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                            Virulence gene; antibacterial; vaccine; bacterial infection; septicemla; bronchopneumonia; rhinitis; wound infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%; Scor.
100.0%; Pred. No. 20,
'~ 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Pages 232-233; 322pp; English.
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                                                                                                                                                                                                                                                                                                                  Kennedy MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY70024 standard; Protein; 362 AA
                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN INC
                                                                                                                                                                                                 06-APR-2000; 2000WO-US09218.
                                                                                                                                                                                                                                99US-0128689.
             Virulence gene protein #41
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Best Local Similarity 100.0
These 7; Conservative
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                                                                                               Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-647422/62.
N-PSDB; AAC79622.
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38 slaregv 44
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10-SEP-1999;
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                                                                                                                                                               19-OCT-2000
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AAB48087 standard; Protein; 607 AA.

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RESULT 1

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bacterial ALL protein may be complexed with a therapeutic agent to transport the agent across the gastrointestinal membrane barrier by transcytosis to increase bicavailability 5- to 100-fold. The delivery system allows improved transport across enterocytes and peyers patch M-cells. The system is not prone to degradation in the quit or early release of blologically active material, and eliminates the need for parenteral administration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Therapeutic delivery system utilising bacterial invasin protein - is not readily degraded in the gut, enhances systemic bio-availability of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a fusion protein of a Yersinia enterocolitica attachment-invasion-locus (AIL) protein (AAR86207) with maltose binding protein (MBP, AAR96208). The MBP N-terminal portion of the fusion protein acts as an affinity tail, allowing efficient recombinant protein purification by amylose affinity chromatography. The receptor binding region of the AIL protein involves all or some of the regions from the 4 extracellular loops. This region retains the binding affinity of the protein, and may be
                                           Attachment-invasion-locus protein; maltose binding protein; fusion protein; affinity tail; amplose; affinity chromatography; purification; drug delivery; gastrointestinal membrane; transcytosis; bioavailability; enterocyte; Peyers patch M-cell.
                                                                                                                                                                                                                                                                                          /note= "Peptide from extracellular loop-3"
/note= "Peptide from extracellular loop-3"
                                                                                                                                                                                                                                                                 "Peptide from extracellular loop-1"
                                                                                                                                                                                                                                                                             ..482
hte= "Peptide from extracellular loop-2"
                                                                                                                                                                                                                                                                                                                                                            /note= "Peptide from extracellular loop-4"
                                                                                                                                                                                                                                   "Attachment-invasion-locus protein"
              protein-maltose binding protein fusion protein.
                                                                                                                                                                                                  /note= "Maltose binding protein"
                                                                                                                                                                       Location/Qualifiers
                                                                                                                         Synthetic;.
Yersinia enterocolitica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-0CT-1995;
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                                                                                                                      Chimeric:
Chimeric:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to acquired resistance genes Nphl from rice, and Nph2-1 and Nph2-2 from wheat. The Nph1 and Nph2 polypeptides can be expressed by standard recombinant methodology. The Nph1 and Nph2 polynucleotides or polypeptides can be used to enhance acquired resistance in plants (e.g. wheat or rice) to control plant pathogens e.g. the genes can be introduced to make transgenic plants with increased disease resistance. The polynucleotides are also useful to produce probes and primers useful to detect the polynucleotides (to identify transgenic plants containing an acquired resistance gene) and to isolate similar sequences e.g. from other species. The polypeptides can be used to make antibodies useful to monitor protein production e.g. in transgenic plants. The present sequence represents the amino acid sequence of the wheat Nph2-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New acquired resistance genes Nphl from rice, Oryza sativa, and Nph2-1 and Nph2-2 from wheat, Triticum aestivum, useful for producing transgenic plants with increased disease resistance
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                                                                                                   Acquired resistance gene; Nph1; Nph2; rice; Nph2-1; Nph2-2; wheat;
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                                                                                                                     plant pathogen; transgenic; disease resistance.
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100.0%; Pred. No. 1.2
iive 0; Mismatches
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                                                                 Wheat Nph2-1 protein sequence.
                                                                                                                                                                                                                                                           .2-MAY-2000; 2000WO-US13307.
                                                                                                                                                                                                                                                                                           99US-0133965.
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                                 (first entry)
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Best Local Similarity 100.
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                                                                                                                                                   Triticum aestivum.
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                                                                                                                                                                                    WO200070069-A1.
                                                                                                                                                                                                                                                                                           13-MAY-1999;
                                 19-MAR-2001
                                                                                                                                                                                                                         23-NOV-2000
 AAB48087;
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Gaps

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Length 568; 02; 0; Indels

4.5%; Score 7; DB 17; Le 100.0%; Pred. No. 1.1e+02; ative 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 7; Conservative

86 GVIGSFA 92 |||||||| 455 gvigsfa 461

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us-08-957-709-71.rai

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Sequence 41, Appl Sequence 51, Appl Sequence 13, Appl Sequence 13, Appl Sequence 6, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appli Sequence 6, Appli Sequence 8, Appli Sequence 9, Appli
                                                                                          January 31, 2002, 13:15:08 ; Search time 65.13 Seconds (without alignments) 53.900 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, App]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                               156
1 MLEPDWKIRKEILIEPFSEE......PYRGNYQGSTRLAFSKRKKL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10
Sequence 2,
Sequence 2,
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-822-774-44
US-08-822-774-41
US-08-822-774-11
US-08-822-774-54
US-08-822-774-38
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US-08-747-137-16
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                                                                                                                                                                                                                                                                            212252 segs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                                                             OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                              US-08-957-709-71
                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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114
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27
2482
3248
3248
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                                                                                                                                                                               Perfect score:
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                                                              OM protein
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                                                                                                                                                                                              Sequence:
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| Sedneuce Sed |            | (PEF) d Identifying Same Gwards &                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | gth 246;<br>Indels 0; Gaps                                       | GERFVQIAFIRLE 131<br>                                            |
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| US-08-479-802A-46 US-08-477-446 US-08-199-802A-58 US-08-105-454-2 US-08-477-928A-3 US-08-477-928A-3 US-08-477-928A-6 US-08-477-928A-6 US-08-924-183-1 US-08-924-183-7 US-09-488-364-1 US-09-488-364-1 US-09-488-364-1 US-09-488-364-1 US-09-488-364-1 US-08-477-928A-34 US-08-477-928A-34 US-08-477-928A-34 US-08-477-928A-34 US-08-477-928A-34 US-08-477-928A-34 US-08-476-088-49 US-08-833-485-49 US-08-833-485-49                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ALIGNMENTS | 4 Enhancing Factor (P EF Protein Complexe for Purifying and venson, McKeown, Ed uite 700 0, Version #1.25 774 7714                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Score 85; DB 4; Length; Pred. No. 1.1e-74; 0; Mismatches 0; Inde | VMGDWKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLE<br> |
| 110<br>120<br>120<br>120<br>120<br>120<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            | NN:  NEEE, Holly  REFE, Holly  CON: Polymerase  CON: Extracts, P  FON: and Methods  CON: And Methods  NUESS: 61  NUBRES: 61  STREET, N.W. S  STREET, N.W. S  STREET, N.W. S  TON PATA:  TON BATA:  NHENRATION:  A: 436  NN: 436  NN: 436  NN: 436  NN: 436  NN: 436  NN: 528-8800  SOL) 628-8800  SOL) 628-8 | 54.5%;<br>100.0%;<br>ive                                         | IGSFAW<br>       <br> GSFAW                                      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            | pplicatio 3997 MATION: HOGREFE, VENTION: VENTION: CE ADDRE CE CE ADDRE CE C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | milarity<br>Conservat                                            | KIRSSLAREGV<br>                                                  |
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| 20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            | RESULT Sequence Sequence Sequence TITL TITL TITL TITL NUMB ST                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Query Match<br>Best Local<br>Matches 8                           | Qy 7<br>Db 2                                                     |

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100.0%; Pred. No. 5e-07;
tive 0; Mismatches 0; Indels
STREET: 1200 G Street, N.W. Sullericolory:
CITY: Washington
STAPE: D.C.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: A36
ATOREX/AGENT INFORMATION:
NAME: KULLK, DAVIG J.
REGISTRATION NUMBER: 1486/43163
FELECOMMUNICATION NUMBER: 1486/43163
TELECOMMUNICATION NUMBER: 1486/43163
TELEFRANCE/DOCKET NUMBER: 1486/43163
TELEFRANCE CASO ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENDETAL: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-822-774-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.0
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                     Patent No. 619397

Patent No. 619397

Patent No. 619397

Patent No. 619397

Patent No. 619397

TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)

TITLE OF INVENTION: and Methods for Purifying and Identifying Same

NUMBER OF SEQUENCES: 61

CORRESPONDENCE David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Leanhan, P.L.L.C.

STREET: 1200 G Street, N.W. Suite 700

STATE: Doc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08822774
Fatent No. 618397
Releaf InfoRmATION:
APPLICANT: HOGREFE HOlly
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &
ADDRESSEE: Lenahan, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 4; Length 42;
Pred. No. 1.7e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRINT APPLICATION NOTAR:
APPLICATION NOTAR: 21-MAR-1997
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTONNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 1486/43163
TELEPHONE: (202) 628-8840
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TVEE: amino acid
                             132 GPARNPYRGNYQGSTRLAFSKRKKL 156
                                                    80 GPARNPYRGNYQGSTRLAFSKRKKL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLLPDWKIRKEILIEPFSEE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
Z
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; FRAGMENT TYPE:
US-08-822-774-41
                                                                                                                        RESULT 2
US-08-822-774-41
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US-08-822-774-11
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NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERNEC/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION:
TELEPHONE: (202) 628-8800
                                                                                           Sequence 38, Application US/08822774 Patent No. 6183997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 amino acids
                                                                                                                                                APPLICANT: HOGREFE, HOLL
TITLE OF INVENTION: POLY
TITLE OF INVENTION: EXET
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.5
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                    STREET: 1200 G St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
 12 RKEILIE 18
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                                                                                                                                                                                                                                                                                                                                                            20002
                                                                         US-08-822-774-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-13749-5
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q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08822774
Patent No. 6183997
CENERAL INFORMATION:
PAPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                           7.1%; Score 11; DB 4; Length 14;
100.0%; Pred. No. 0.00034;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
RILING DATE: 21-MARR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.5%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 3.1
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David J. Kulik, Evenson, ADDRESSEE: Lenahan, P.L.L.C. STREET: 1200 G Street, N.W. Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
(202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminal
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                             Query Match 7.1
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                        91 FAWVDPGWDGN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                            1 FAWVDPGWDGN 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                  ; ANTI-SENSE: NO
; FRAGMENT TYPE:
US-08-822-774-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FRAGMENT TYPE:
US-08-822-774-13
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-822-774-13
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Holly Polymerase Enhancing Factor (PEF) Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
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GENERAL INFORMATION:
APPLICANT: Angen Inc.
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                            ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C. STREET: 1200 G Street, N.W. Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1:0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 91320-1789
COMPUTER READABLE FORM:
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Gaps

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RESULT 10
PCT-US95-16216-1
Sequence 1, Application PC/TUS9516216
GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YEN, TIMOTHY J.
APPLICANT: YEN, TIMOTHY J.
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
STREET: 1601 MARKET STREET, SUITE 720
COMPUTER: PA
COMPUTER: PA
COMPUTER: ELOPPY disk
COMPUTER: ISN PC COMPATIBLE
COMPUTER: DALCHIIN Release #1.0, Version #1.25
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
CORPERATING SYSTEM: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION NUMBER: 35,252
TELECOMMUNICATION INFORMATION:
NAME: REED, JANET E. 36,252
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION PROPERED TO NO:
TELECOMMUNICATION PROPERED TO NO:
TELECOMMUNICATION TO NO:
TELECOMMU
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                      Indels
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                 Mismatches
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; Sequence 1, Application US/08353700
; Patent No. 5599919
; GENERAL INFORMATION:
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                 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: prote HYPOTHETICAL: NO ANTI-SPNCT
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US-08-353-700-1
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                             2054 VEKEGKV 2060
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ORIGINAL SOURCE:
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                 Matches
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Patent No. 5710022
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
STRATE: California
COUNTRY: USA
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MEDIUW TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
FILING DATE: 24-OCT-1994
FILING DATE: 12-OCT-1993
FILING DATE: 12-OCT-1993
FILING DATE: 12-OCT-1993
FILING DATE: 13-OCT-1993
FILING DATE: 13-OCT-1994
FILIN
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
CORPTANE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFILING DATE:
CLASSIFICATION:
INFORMATION FOR END IN O: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TYPE: unknown
MOUBCOUSE TYPE:
PCT-USS9-13749-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.5%; Score 7; DB 5; Best Local Similarity 100.0%; Pred. No. 53; Matches 7; Conservative 0; Mismatches
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US-08-328-254-6
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-70M-1991
ATTONNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION OF 15-576-0200
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                         US 08/069,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Photorhabdus luminescens US-09-251-645-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-07-781-355-2
; Sequence 2, Application US/07781355
Patent No. 524684
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/09251645; Patent No. 6281413
                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: not relevant US-08-747-137-16
                                            01-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Anderson, Arne R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.8
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                         APPLICATION NUMBER: FILING DATE: 01-JUN
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
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; Patent No. 5945033
; GENERAL INFORMATION:
APPLICANT: PRIN. Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3248;
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ZIP: 94111
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PROCOMPASSION #1.30

"""TON DATA:
"""TON DATA:
""""TON DATA:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 5;
; Pred. No. 2.26
0; Mismatches
                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0; 7
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LENGTH: 3248 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.5
Best Local Similarity 100.
Matches 7; Conservative
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CITY: San Francisco
STATE: CA
                                                                                                             ZIP: 19103-2307
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PCT-US95-16216-1
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                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
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US-08-747-137-16
                                                                   STATE: P
COUNTRY:
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APPLICANT: Hart, Hope
APPLICANT: Hart, Hope
APPLICANT: Hart, Hope
APPLICANT: Warren, Gregory W.
APPLICANT: Ounn, Martha
APPLICANT: Chen, Jeng S.
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: CCG1963/A
CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 253
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                                                   Indels
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3.8%; Score 6; DB 2; Length 8; 100.0%; Pred. No. 1.6e+05; tive 0; Mismatches 0; Indels
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APPLICANT: Weber, J. Mark
APPLICANT: Weber, Paul E.
APPLICANT: Hessler, Paul E.
APPLICANT: Hessler, Paul E.
APPLICANT: Larsen, Peter E.
APPLICANT: Larsen, Methods and Compositions for Enhancing TITLE OF INVENTION: Methods and Compositions for Enhancing TITLE OF INVENTION: Erythromycin Production
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite STREET: 2 Prudential Plaza, 180 N. Stetson, Suite STREET: 4 Tolicago
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite STREET: 4 Tolicago
STATE: 111inois
COMPUTER READABLE FORM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATA: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/852,401
FILING DATE: CLASSIFICATION: APPLICATION NUMBER: S8,978
REPRENCE/DOCKET NUMBER: 38,978
TELEPOMENT/ACTION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPOMENT/ACTION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 283;
0. 2.8e+02;
cches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.6
Best Asches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                      Sequence 4, Application US/08852401; Patent No. 5976336; GENERAL INFORMATION:
APPLICANT: Weber. J. Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 283 amino acids
TYPE: amino acids
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-852-401-4
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206 LYNASN 211
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                                                                                      RESULT 15
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| Sequence | 11, Application US/09058489 |
| Sequence | 11, Application US/09058489 |
| Patent No. 6103886 |
| GENERAL INFORMATION: | APPLICANT: Wittehead Institute for Biomedical Research |
| APPLICANT: Page, David |
| APPLICANT: Page, David |
| TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of |
| TITLE OF INVENTION: Canes in the No. 6103886-Recombining Region of |
| TITLE OF INVENTION: Canes in the No. 6103886-Recombining Region of |
| TITLE OF INVENTION: UNHUBER: 'US/09/058,489 |
| CURRENT FILING DATE: 1998-04-10 |
| SARLIER PILING DATE: 1998-04-10 |
| NUMBER OF SEO ID NOS: 91 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LENGTH: 261
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No. 2.5e+02;
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APPLICANT: No. 5246844ris, Steven J.
APPLICANT: BATDOUY, Alan G.
TITLE OF INVENTION: BORRELIA BURGDORFERI (BD)
TITLE OF INVENTION: BORRELIA BURGDORFERI (BD)
TOWBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 4433
CITY: HOUSEN OF STREET: TEXAS
COUNTRY: USA
STATE: TEXAS
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/781,355
FILING DATE: US/07/781,355
CLASSITICATION NUMBER: US/07/781,355
CLASSITICATION NUMBER: US/07/781,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATORNEY AGENT INFORMATION:
NAME: Kitchell, Berbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET UNMER: UTSH
TELECOMMULCATION INFORMATION:
TELEFAX: 512.474-757
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
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US-09-058-489-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-781-355-2
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Mycobacterium tube

Perfect score:

Sequence:

OM protein

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Scoring table:

Searched:

Jatabase

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Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; sequencing; replication.
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AAY17899
AAY52017
AAY51646
AAY41140
AAY41139
AAW28034.
                                                      AAG30341
AAG30340
AAX29166
AAAX29062
AAW53668
AAG81199
AAG81199
AAG826421
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AAW71498
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AAW20648
AAR89265
AAR60812
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AAY67287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STRA-) STRATAGENE.
                                                                                                                                                                            WO9842860-A1.
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21-MAR-1997;
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Peptide
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Corynebacterium gl
Protein encoded by
Antigen 3 from clu
Protein involved i
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Amino acid sequenc
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                                                                                         January 31, 2002, 13:07:05; Search time 33.61 Seconds (without alignments) 343.809 Million cell updates/sec
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Polypeptide encode
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                                                                                                                                                                             1 MLLPDWKIRKEILIEPFSEE.......PYRGNYQGSTRLAFSKRKKL 156
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                           Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAWB9B18
AAW37187
AAY34994
AAX29169
AAB35755
AAY29165

    protein search, using sw model

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AAG92886
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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116.7
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242 218 196 196 181 149.5 134.5 119.5

4 5 7 11 11

Score

Result Š

Protein encoded by Helicobacter polyp Pyrococcus furisos H. pylori cytoplas Heparinase-III. F Agarase UlO7 from H. pylori ORF 07ap Methanococcus jann M. jannaschii MJ07 Mouse mammary tumo Mouse mammary tumo Amino acid sequenc Polymerase enhanci Arabidopsis thalia 
Human zona pelluci

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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 LILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A sequence encoding a thermostable DNA ligase was cloned into the plasmid ppam-13. The DNA ligase is APP dependent and is useful for detecting nucleic acids by hybridising two oligonuclectides with adjacent sequences of the target nucleic acid, ligating the two oligonuclectides (using the ligase) and detecting the ligation product. Analysis of the fragment revealed three other open reading frames (ORF's). This is a polypeptide encoded by ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 ILIEPFSEESLQPAGYDLRVG-----REAFVKGK----LIDVEKEGKVVIPPREYA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                             Thermostable ligase from archaebacteria - and DNA coding for it, useful for nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
30.0%; Score 242; DB 14; Length 173;
Best Local Similarity 35.9%; Pred. No. 3.6e-21;
Matches 56; Conservative 30; Mismatches 56; Indels 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C glutamicum protein fragment SEQ ID NO: 6640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 GERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRK 154
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                                                                                                                                      Example 3; Figure 1; 26pp; German.
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2000JP-0159162.
2000JP-0280988.
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Tateishi N, Senoh A, Ik
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N-PSDB; AAH68105.
                    WPI; 1993-378402/48.
N-PSDB; AAQ62300.
                                                                                                                                                                                                                                                                                                                                  173 AA;
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07-APR-2000; 2
03-AUG-2000; 2
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                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                               This is the amino acid sequence of the P45 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638.

The sequence is predicted from a DNA sequence (see AAV63860) obtained from genomic DNA by PCR. P45 and P50 (see AAW72844) are the predominant components of PEF, which acts to enhance the activity of P. Furiosus DNA polymerase. P45 functions as a dUTPase, and can be used to enhance nucleic acid replication, polymerisation or PCR reactions. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies. Also included are methods for identifying compositions with PEF activity, for purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Whicher acid polymerase reactions can be enhanced (claimed) by mixing a nucleic acid template, at least 1 polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acid sequencing or amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligase, thermostable; thermostability; Desulfurolobus ambivalens; archaebacteria; detection; ligation; ATP; adenosine triphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
100.0%; Score 806; DB 19; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e.89;
Matches 156; Conservative 0; Mismatches 0; Indels 0.
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide encoded by pDam-L3 plasmid fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR51078 standard; Protein; 173 AA
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                                                                                                                   Claim 17; Page 43; 161pp; English
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N-PSDB; AAV63860
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Sequence
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                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::|| |: ||: ||: ||: ||: ||: ||: ||| ||: ||: ||| ||: ||: ||| ||: ||: ||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                     Claim 17; SEQ ID NO: 6640; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.0%; Score 218; DB 22; Length 189; 33.7%; Pred. No. 3.3e-18;
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99DE-1030476.
99DE-1031415.
99DE-1031418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 AA;
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08-JUL-1999;
08-JUL-1999;
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, putine and pyrimidine bases, nucleosides, nucleotides, incleding status acids, acids, diols, carbohydrates, ilpids, compounds, vitamins, cofactors, polyketides and enzymes.
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99DE-1032125.
99DE-1032126.
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99DE-1032186.
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99DE-1032922.
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99DE-1031634.
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160 AA

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                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                41 --LIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVI--GSFAWVDP
                                24;
   Length 160;
24.3%; Score 196; DB 22; Length 1 32.9%; Pred. No. 1.2e-15; Live 29; Mismatches 53; Indels
                                                            1 MLLPDWKIRK-----EILIEPFSEESLQPAGYDLRVGR--EAFVKGK----
                                                                                                                                                                                  GWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPA 134
                                                                                                                                                                                                  Claim 15; Page 104-105; 402pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by clone B17 ORF4.
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97US-0045107
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                Similarity 32.99 52; Conservative
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N-PSDB; AAV90555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9849314-A2.
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25-APR-1997;
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 Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                       AAW89818;
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The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with in pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. In pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                        48 GKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLY 107
New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LIEPFSEE------SLQPAGYDLRVGRE-----AFVKGK------LIDVEKE 47
                                                                                                                                                                                                                                                                                                                                           Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.5%; Score 181; DB 20; Length 190; liarity 28.0%; Pred. No. 9.90-14; Conservative 29; Mismatches 64; Indels 26
                                                                                                                          NASNEPVELRYGERFVQIAFIRLEGPARNPYR---GNYQGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 236-237; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chow TP, Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                AAW89897 standard; Protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US08487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061958.
97US-0045107.
                                                                                                                                                                                                                                                                                                             Antigen 3 from cluster 28c.
                                                                                                                                                                                                                                                                             18-FEB-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori.
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 AA;
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25-APR-1997;
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Gaps

64; Indels 28;

22.5%; Score 181; DB 20; Length 188; 28.0%; Pred. No. 9.8e-14; ive 29; Mismatches 64; Indels 29

Query Match 22.5 Best Local Similarity 28.0 Matches 47; Conservative

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(GEST ) GENSET
                                                                                                                                                                                                                                         WO9927105-A2
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21-NOV-1997;
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                                                                                                                      13-SEP-1999
                                                                                                                                                                                                                                                                 03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                             Griffais R;
                                                                                               AAY34994;
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                                                            AAY34994
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye
                                                                                                                                                                                                                Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
| : || : : : || :| :| :| :| :| || odpkcftedalisi-vddvciippnsfalarsveyfriprnvltvcigkstyarcglivn 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 ----AFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 nw-irkmaieegmiepfadsgvklhpetgeklisyglssygydlrisrefkvftnvynsl 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------SLQPAGYDLRVGRE------ 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 FAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY---RGNYQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.5%; Score 149.5; DB 20; Length 190; 26.1%; Pred. No. 6.5e-10; Live 31; Mismatches 60; Indels 39;
                                                                                                                                                                                           Protein involved in intermediate metabolism of nucleic acids.
                                   108 NASNEPVELRYGERFVQIAFIRLEGPARNPYR---GNYQGSTRLAFSK 152
                                                Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 961; 1755pp; English.
                                                                                                                    AAY37187 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 DWKIRK----EILIÉPFSEE----
                                                                                                                                                                                                                                                                                                                                                                            98US-0107077.
                                                                                                                                                                                                                                                                                                                                                                                    97FR-0015041.
                                                                                                                                                                                                                                                                                                                                                    98WO-IB01939
                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 26.1 es 46; Conservative
                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                   W09928475-A2
                                                                                                                                                                                                                                                                                                                                                   27-NOV-1998;
                                                                                                                                                                   07-0CT-1999
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                                                                                                                                                                                                                                                                                                                           10-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyagitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae mucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   si-tddvcivppnsfalarsveyfriprnvltmciqkstyarcqiivnvtpfepeweghv 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 DVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purulent otitis media; erythema nodosum; pharyngitis;
Length 190;
                                                                                                                                                                                                                                                                                                                                                                                        Protein involved in intermediate metabolism of nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY --- RGNYQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.1%; Score 138; DB 20; 24.4%; Pred. No. 1.6e-08; iive 31; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 LIEPF-----SEES-----LQPAGYDLRVGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 901; Disclosure; 1912pp; English.
                                                                                                                                                                                               AA.
                                                                                                                                                                                               190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; neutralising epitope.
                                                                                                                                                                                            AAY34994 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-IB01890
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97FR-0014673
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Best Local Similarity 24.4
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae.
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This invention relates to a full length provirus genomic DNA sequence AAC66881 of equine infectious anemia virus (EIAV) from the donkey leukocyte strain. Included in the invention are the gag, pol, env, rev, tat, and S2 gene sequences AAC66314 - AAC66319 and their encoded proteins AAB35754 - AAB35759. The invention also relates to PCR primers AAC66282 - AAC66389 which are used to isolate the EIAV DNA sequences other primers represented in AAC66289 - AAC66313 are also used in the sequences identified in the invention. The genes and proteins can be used for preparing gene mutation and deletion vaccines, DNA vaccines and flagnostics and in producing an equine infectious anemia virus gene transfer system for gene therapy. The proteins and polynucleotides may also be used in the study of HIV.
                                                                                                   Equine infectious anemia virus; EIAV; donkey leukocyte strain; vaccine; gene therapy; human immunodeficiency virus; pol; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Full-length DNA sequence of provirus genomes, sequences of various functional genes and protein of dondey leukocyte strain of equine infectious anemia virus, used for preparing vaccines and studying HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|::| | : :||:||::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::
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                                   EIAV pol gene product amino acid sequence SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 119.5; DB 21;
ilarity 24.4%; Pred. No. 3.7e-05;
Conservative 33; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jia B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NAAI-) NAT CENT AIDS PREVENTION & CONTROL.
(HARB-) HARBIN VETERINARY RES INST CHINESE ACAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY29165
ID AAY29165 standard; Protein; 181 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu K,
Zhao L;
                                                                                                                                                                                                       Equine infectious anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99CN-0105852.
                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000; 2000WO-CN00096.
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Fan X, Lue X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672738/65.
N-PSDB; AAC66315.
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Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                          26-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shao Y, Xiang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY29165;
       οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a Pseudomonas aeruginosa polypeptide sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.

In some listances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given is not entirely correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 VVIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| ||: : | : |:|||: : |
12 vrdgklikhlahrelttpegvgfdlrlaglsrltvgggslrestrrtpasevvladpddc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----REAFVK---GKLIDVEKEGK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodman HM, Mahajan-Miklos S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                   Amino acid sequence of a virulence factor encoded by ORF19027c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.7%; Score 134.5; DB 20; Length 26.5%; Pred. No. 3.8e-08; Live 31; Mismatches, 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                      Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| |:: | || : | : | |:| :|| 132 hseafeiqigarfahvifqavsgdi-grykgqwqg 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 SNEPVELRYGERFVQIAFIRLEGPARNPYRGNYQG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRKEILIEPFSEESL -- - QPAGYDLRVG ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 228pp; English.
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standard; Protein; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ausubel F, Cao H, Drenkard E,
Rahme LG, Tan M, Tsongalis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0066517
                                                                                                                                       (first entry)
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Best Local Similarity 26.58
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-357851/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1998;
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DB 21; Length 1143;

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21 SLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human dUTPase (given in AAQ83219) was cloned into pUC19 and recombinants used to transform E. coli BW 286. A transformant selected for growth at 39 deg was cultured overnight. Recombinant human dUTPase was purified and shown to be identical in sequence to the natural protomeric peptide (AAR70144).
                                                                                                                                                                                                                                                                                                                              Pure native human deoxyuridine tri:phosphate nucleotido:hydrolase used to identify inhibitors, potentially useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dUTPase; DUT-N; human; cell proliferation; inhibitor; cytostatic;
antiviral; antibacterial; antifungal; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLAREGVIGSFAWV-DPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%; Score 111; DB 16; Length 141; 30.7%; Pred. No. 1.9e-05; Live 17; Mismatches 46; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-terminal peptide unique to DUT-N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "O-phosphorylated"
                                                                                                                                                                                               (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                                                                                                                                                                     antimicrobial and anticancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig.1; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW30280 standard; Protein; 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human dUTPase (nuclear form):
                                                                                                                          94CA-2126001
                                                                                                                                                               93US-0097220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.8% Best Local Similarity 30.7% Matches 35; Conservative
                                                                                                                                                                                                                                    Climie S, Vandenberg
                                                                                                                                                                                                                                                                        WPI; 1995-115928/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA;
                                                                                                                                                                                                                                                                                            N-PSDB; AAQ83219
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Modified-site
                 Homo sapiens.
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                                                                                                                        16-JUN-1994;
                                                                                                                                                               27-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9736916-A1
                                                   CA2126001-A
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                                                                                      28-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Pseudomonas aeruginosa polypeptide sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.

Is a P. aeruginosa infection.

In some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAR--EGVIGSFAWVDPGWDGNLTL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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               Amino acid sequence of a virulence factor encoded by ORF17793c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 MLYNASNEPVELRYGERFVQIAFIRLEGPARNPYRGNY-----QGSTRLAFSK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahajan-Miklos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 112; DB 20; Length 181; 24.9%; Pred. No. 2.1e-05; Live 28; Mismatches 76; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                      Virulence factors useful in developing disease treatments
                                               Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deoxyuridine-triphosphate-nucleotidohydrolase; dUTPase; antimicrobial; anticancer; cytostatic; screening.
                                                                                                                                                                                                                                                                                                                                Goodman HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 228pp; English.
                                                                                                                                                                                                                                                                                                                          Ausubel F, Cao H, Drenkard E, Rahme LG, Tan M, Tsongalis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR70144 standard; Protein; 141
                                                                                                                                                                                                                 98WO-US25247.
                                                                                                                                                                                                                                                   97US-0066517
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                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human dUTPase protomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not entirely correct
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-357851/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AA;
                                                                                                                                        W09927129-A1
                                                                                                                                                                                                                 25-NOV-1998;
                                                                                                                                                                                                                                                   25-NOV-1997;
                                                                                                                                                                              03-JUN-1999,
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Best Local Simi
Matches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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16; Gaps

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WO9736916-A1.
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                                                                                                                                                                                       This polypeptide comprises the nuclear form, designated DUT-N, of muman devayuridine triphosphate nucleotidohydrolase (dyrbase). Its amino acid sequence was deduced from a T-cell cDNA clone (see AAT90987). A single gene codes for 2 isoforms of human durpase, the nuclear form (DUT-N) and a cytoplasmic form (DUT-N, see AAT80381) which is targeted to the mitochondria. The isoforms arise by the use of alternative 5 exons which then join in a common sequence. The DUT-N isoform is produced at low or undetectable levels during non-proliferative periods of the cell cycle, and can be used as a marker for cellular proliferation. It is phosphorylated by plactoc2 at a Ser residue within the consensus sequence for cyclin-dependent can be used to determine its proliferative status (or changes in this status), particularly in nutrient-deprived or neoplastic cells can be used to determine on be used for determining the effect of calmed). This method can be used for determining the effect of claimed). Agents that inhibit durpase are potential

(claimed). Agents that inhibit durpase are potential

can inneoplastic, antiviral, antibacterial and antifungal agents.

(The durpase can also be used to raise antibodies for assaying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; Score 111; DB 18; Length 164;
30.7%; Pred: No. 2.4e-05;
Live 17; Mismatches 46; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 SLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dUTPase; DUT-M; human; cell proliferation; inhibitor; cytostatic;
antlviral; antibacterial; antifungal; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
70..93
/note- "DUT-M unique sequence 5' to common Glu
residue of DUT-M and DUT-N"
                                                                                                                      Nucleic acid encoding two isoform(s) of human dUTPase - used assays for assessing status of cell proliferation, effect of anticancer agents and progress of treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human dUTPase (mitochondrial form).
                                                            Lynch F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW30281 standard; Protein; 252 AA
                                                                                                                                                                      Claim 6; Fig 1A-B; 89pp; English.
 97US-0824405.
96US-0014748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 30.78,
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                            Caradonna SJ, Ladner RD,
                                    (UYNE-) UNIV NEW JERSEY.
                                                                                 WPI; 1997-503040/46.
N-PSDB; AAT90987.
                                                                                                                                                                                                                                                                                                                                                                                                                                             164 AA;
26-MAR-1997;
29-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW30281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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This polypeptide comprises the mitochrondrial form, designated DUTA, of human decoyuridine triphosphate nucleotidohydrolase to DUTA, of human decoyuridine triphosphate nucleotidohydrolase (dUTPASS). Its amino acid sequence was deduced from a fibroblast CDNA clone (see AAT90989). A single gene codes for 2 isoforms of human dUTPASS, the nuclear form (DUTA, N. see AAN90280) and the cytoplasmic form (DUTA) which is targeted to the mitochondria. The isoforms arise by the use of alternative S exons which then join in a common sequence. The DUTA isoform is detectable in proliferating and non-proliferating cells, but is produced in tumours. Unlike DUTA, it is not phosphorylated in vivo. Measuring the amount of dUTPASS of non-proliferation in certain tumours. Unlike DUTA, it is not phosphorylated in vivo. Weasuring the amount of dUTPASS in this status), particularly in nutrient-deprived or neoplastic cells (claimed). This method calls, or monitoring the effect of (A) (claimed). Agents that including tumpasse are potential antineoplastic, antiviant, antibacterial and antifungal agents. The dUTPASS can also be used to raise antibodies for assaying the enzyme and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding two isofcrm(s) of human dUTPase - used in assays for assessing status of cell proliferation, effect of anticancer agents and progress of treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 SLAREGVIGSFAWV-DPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGP 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.8%; Score 111; DB 18; Length 252; Best Local Similarity 30.7%; Pred. No. 4.5e-05; Matches 35; Conservative 17; Mismatches 46; Indels 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 2A-B; 89pp; English.
                                                                        97US-0824405.
96US-0014748.
97WO-US04886
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N-PSDB; AAT90989.
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29-MAR-1996;
26-MAR-1997;
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FR2586427-A. 27-FEB-1987.

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                                                                                                                                                                                                                                                                                                                                     19 EESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKI 78
                                                                                                                                                                                    New envelope protein of Visna virus, its fragments - and DNA coding sequences, useful in diagnosis and for making vaccines
                                                                                                                                                                                                                                                                                     13.8%; Score 111; DB 8; Length 1105; 24.8%; Pred. No. 0.00038; tive 24; Mismatches 53; Indels 20
                                                                                                                                                                                                                      Example; Fig 1-6; 27pp; French.
                                               85FR-0512543.
                                                                     85FR-0012543.
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Best Local Similarity 24.8%
Matches 32; Conservative
                                                                                                                      Sonigo P, Wain-Hobson S;
                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                               WPI; 1987-095919/14.
N-PSDB; AAN70608.
                                                                                                                                                                                                                                                 1105 AA;
                                                                       20-AUG-1985;
                                              20-AUG-1985;
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Search completed: January 31, 2002, 13:07:06 Job time: 58 sec

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Sequence:

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Scoring table:

Searched:

Database

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Sequence 44, Application US/08822774

Patent No. 6183997

GENERAL INFORMATION:
APPLICANT: HORMATION:
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 PPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNE 112
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Sequence 25, Al
Sequence 25, Al
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Sequence 25, Al
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                                                                                                Sequence 8, P
Sequence 8, P
Sequence 8, P
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Sequence 8, P
Sequence 8, P
                                                                             Sequence 61,
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                                                    Sequence 7,
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STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 246;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULK, David J.
REGISTRATION NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%; Score 533; DB 4; L
ilarity 98.1%; Pred. No. 9.5e-59;
Conservative 2; Mismatches 0;
                   US-08-453-952-7
US-08-682-903-7
US-08-484-158B-61
US-08-484-158B-8
US-08-484-156A-8
US-08-489-150A-8
US-08-489-731-8
US-08-489-731-8
US-08-374-483-5
US-08-374-17144-25
US-09-069-226-22
US-09-089-272-2
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEO ID NO: 44
SEQUENCE CHARACTERISTICS:
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Matches 102; Conserv
MOLECULE TYPE:
HYPOTHETICAL:
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Sequence 9,
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Sequence 4
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-822-774-41
US-08-822-774-41
US-08-822-774-41
US-08-824-405-11
US-08-824-405-2
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US-08-453-472-7
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length

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US-08-024-105-11

Sequence 11. Application US/08024405

Patent No. 596224

Patent No. 596224

Sequence 11. Application US/08024405

Patent No. 596224

APPLICANT: Ladner, Robert D.

APPLICANT: Caradonna, Salvatore J.

TITLE OF INVENTION: Diagnostic and Other Uses

TORRESPONDERS: Dechert, Price & Rhoads

STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre

CITY: Philadelphia Alantic Tower, 1717 Arch Stre

COUNTRY: USA

COUNTRY: USA

COUNTRY: Diskette

COMPUTER: Lad Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastERO for Windows Version 2.0

CHASSIFICATION NUMBER: US/08/824,405

FILING DATE: 26-MAR.1997

FILING DATE: TOWERT ON DATA:

APPLICATION NUMBER: COUNTRY OF TOWERT ON 
                                                                                                                           ZIP: 20005
COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MODIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION HARR-1997
ATCASSIFICATION NUMBER: 36.576
ATTORNEX/AGENT INPORMATION:
NAME: KULIK, David J.
REGISTRATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8800
TELEFAX: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SED ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: MAINOWN
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TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: T
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Pred. No. 2.8e-08;
1; Mismatches 2;
STREET: 1200 G Street, N.W. Suite 700 CITY: Washington STATE: D.C. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.8%;
Best Local Similarity 88.9%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NC
; FRAGMENT TYPE:
US-08-822-774-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ōλ
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APPLICANT: HOGREE, Holly
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
CORRESPONDENCES:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &
ADDRESSEE: Leahan, P.L.L.C.
CITY: Washington
STATE: D.C.
STREET: 1200 G Street, N.W. Suite 700
STATE: D.C.
STATE: D.C.
STREET: D.C.
COMPUTER: IBEM PC Compatible
COMPUTER: IBEM PC COMPATION
NAME: WILK, David J.
REGISTRATION NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
NAME: CAD2) 628-884
INFORMATION FOR READ SECTION COMPATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TVPE: amino acids
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Patent No. 618397
GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: BYLEACES, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &
ADDRESSEE: Lenahan, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                   113 PVELRYGERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRKKL 156
                                                                                                 61 PVELRYGERFVQIAFIRLEGPARNPYRGNYQGSTRLAFSKRKKL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.9%; Score 160; DE Best Local Similarity 96.9%; Pred. No. 3.9e Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLLPDWKIRKEILIEPFSEESLQPAGYDLRVG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 MLLPDWKIRKEILIEPFSEEWLQPAGYDLRVG 42
                                                                                                                                                                                                                                                                                                                                                   Sequence 41, Application US/08822774; Patent No. 6183997; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE:
US-08-822-774-41
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US-08-822-774-38
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US-08-822-774-41
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 RSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                    Length 138
                                                                                                                                                                                                                                                                 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS-08-824-405-2
| Sequence 2, Application US/08824405
| Patent No. 5962246
| Patent No. 5962246
| GENERAL INFORMATION:
| APPLICANT: Ladner, Robert D.
| APPLICANT: Lynch, Frank
| APPLICANT: Lynch, Frank
| APPLICANT: Garadonna, Salvatore J.
| TITLE OF INVENTION: duTPease, Its Isoforms, and
| TITLE OF INVENTION: Diagnostic and Other Uses
                                                                                                                                                                                                 13.8%; Score 111; DB 2; 24.8%; Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: FASTERS DOS SUFTWARE: FASTERO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no/FILING DATE:
                                                                                                                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/ACENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFRENCE/DOCKET NUMBER: 3501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 164 amino acids amino acid
                                                                                                                                                                                             Query Match
Best Local Similarity 24.89
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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US-08-824-405-2
          TYPE: amino acid
                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 RGNYQGSTR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                        STRANDEDNESS:
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                                                                       ; TOPOLOGY:
US-08-824-405-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 RSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGPARNPY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----IMIPVSDTKIIPTDVKIQVPPNSFGWVTG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 EESLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08824405
Patent No. 5962246
GENERAL INFORMATION:
APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TILLE OF INVENTION: Diagnostic and Other Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.2%; Score 114.5; Best Local Similarity 22.8%; Pred. No. 1.1 Matches 28; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 350163-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
                                     350163-101
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
TELEFAX: 609/520-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRX:
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 138 amino acids
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14 EKRDEDAGFDLCVPYD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 609/520-3259
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 DEN 121
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US-08-824-405-11
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US-08-824-405-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
21 SLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 SLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRS 80
                                         42 SARAAGYDLYSAYD------YTIPPMEKAVVKTDIQIALPSGCYGRVAPRS
                                                                                                                       81 SLAREGVIGSFAWV-DPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SLAREGVIGSFAWV-DPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GLAAKHFIDVGAGVIDEDYRGNVGVVLFNFGKEKFEVKKGDRIAQLICERIFYP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
13.8%; Score 111; DB 2; Length 252;
Best Local Similarity 30.7%; Pred. No. 7.6e-06;
Matches 35; Conservative 17; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
OPTWARE: FASTESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
FILING DATE: 26-MAR-1997
CLASSIFICATION A 35
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPase, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50163-101
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US-09-238-303-9
: Sequence 9, Application US/09238303B
                                                                                                                                                                                                       RESULT 7
US-08-0844-405-4
US-08-0844-05-6
Sequence 4, Application US/08824405
Patent No. 5962246
Patent INFORMATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 3501/
TELECHONE: 609/520-3214
TELEFAX: 609/520-3259
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SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-824-405-4
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ZIP: 19103-2793
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GRERAL INCORNATION:
APPLICANT: Barr, Margaret C.
APPLICANT: Barr, Margaret C.
APPLICANT: Barr, Margaret C.
TILE REFERENCE: 18617.0059
CURRENT APPLICATION NUMBER: US/09/238,303B
CURRENT APPLICATION NUMBER: US/09/238,303B
CURRENT APPLICATION NUMBER: US/09/238,303B
CURRENT FILING DATE: 1999-01.28
EARLIER APPLICATION NUMBER: US 60/072,927
EARLIER PILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 17
LENGTH: 1150
TYPE: PRT
ORGANISM: Unknown
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 QPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 AREG--VIGSFAWYDPGWDGNLTLMLYNASNEPVELRYGERFYQIAFI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08824405; Patent No. 5962246; Batent No. 5962246; GENERAL INFORMATION: Robert D. APPLICANT: Ladner, Robert D. APPLICANT: Caradonna, Salvatore J. TITLE OF INVENTION: Diagnostic and Other Uses NUMBER OF ENUMENTION: Diagnostic and Other Uses STREET: 4000 Bell Atlantic Tower, 1717 Arch Street COUNTRY: USA STATE: Philadelphia STATE: Philadelphia STATE: Diskette NUMBER READABLE FORM: MEDIUM TYPE: DISKETE: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER IS IS COMPUTED: DISKETE: DISKETE: DISKETE: COMPUTER: DISKETE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DAYS

CURRENT APPLICATION DAYS:

APPLICATION NUMBER: US/08/824,405

FLING DATE: 26-MAR.1997

CLASSIFICATION: 435

PLOR ADDITOR: 435
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
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TELEFAX: 609/520-3259
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-238-303-9
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65 PRSGLSLKGIDIGGGVIDEDYRGNIGVILINNGKCTFNVNTGDRIAQLIYQRIYYP 120
                                                          78 IRSSLAREGVIGSFAWVDPGWDGNLTLMLYNASNEPVELRYGERFVQIAFIRLEGP 133
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                       Its Isoforms, and
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ladder, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPASE, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
                                                                                                                                                                                                  Sequence 6, Application US/08824405
Patent No. 5962246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
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LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: 609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-824-405-6
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COUNTRY:
                                                                                                                                                            RESULT 11
US-08-824-405-6
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                                                                                                                                                                                                                                          51 VIPPREYALILTLERIKLPDDVMGDMKIRSSLAREGVIGSFAWVDPGWDGNLTLMLYNAS 110
                                                                                                                                                                                                                                                                   40 VIPSHCSRVVFTDLLIKPPSGCYGRIAPRSGAVKHFIDVGAGVIDEDYRGNVGVVLFNFG 99
                                                                                                                                                              Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Dechert, Price & Rhoads
: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPase, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                            Score 87; DB 2;
Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DARFO: US/08/824 405
FILING DARFO:
                                                                                                                                                                                                    16; Mismatches
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CLASSIFFCATION: 435
                                                                                                                                                                                                                                                                                                                                              100 NSDFEVKKGDRIAQLICERISCPA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08824405 Patent No. 5962246
                                                                                                                                                                                                                                                                                                                       111 NEPVELRYGERFVQIAFIRLEGPA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                          10.8%;
illarity 27.4%;
Conservative 10
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ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
              LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Dieter
  SEQUENCE CHARACTERISTICS
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TELEFAX: 609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                            Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 40
                                                                             ; TOPOLOGY:
US-08-824-405-12
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US-08-824-405-13
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10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 || 10 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 SLQPAGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SATAAGYDIYASQD-----ITIPAMGQGMVSTDISFTVPVGTYGRIAPRS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 147;
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9.9%; Score 79.5; DE
Best Local Similarity 23.0%; Pred. No. 0.03;
Matches 32; Conservative 22; Mismatches
TOKNEI, ASSOCIATION ALLEN REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 -- LEGPARNPYRGNYQGST 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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Query Match 10.1%; Score 81.5; D Best Local Similarity 24.1%; Pred. No. 0.01 Matches 28; Conservative 19; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 NXNIDIGGGVI-----DSDYRGEIGIVFINNGCSDFNIKVGDRIAQIIFERVEYPIMEE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AGYDLRVGREAFVKGKLIDVEKEGKVVIPPREYALILTLERIKLPDDVMGDMKIRSSLAR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AGYDLYSAYSYTVK-------PYNRILVRTDICLMIPDKCYGRISPRSGLSL 69
                                                                      APPLICANT: Woyer, Richard W. APPLICANT: Woyer, Richard W. APPLICANT: V1 uela, Eladio APPLICANT: V1 uela, Eladio APPLICANT: V1 uela, Eladio APPLICANT: Glabs, E. P. J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a TITLE OF INVENTION: Live Vaccine Vector NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSE: David R. Saliwanchik STREET: David R. Saliwanchik STREET: Lorida CUNTRY: U.S.A. CONTRY: U.S.A. ZIP. STATE: Florida COUNTRY: U.S.A. ZIP. 32606.

CONTRY: JOSA. COMPUTER READABLE FORM: MEDIUM TYPE: Florida COMPUTER PREADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 9.7%; Score 78.5; DB 1; Length 142; Cocal Similarity 25.2%; Pred. No. 0.038; Losservative 14; Mismatches 49; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 13,794
REGISTRATION NUMBER: 13,794
REGISTRATION NUMBER: US 07/342,212
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-299-268-22
; §equence 22, Application US/09299268
Sequence 22, Application US/08307499 Patent No. 5651972 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 142 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-307-499-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 ---ARNPYRGN 141
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Best Local S
Matches 33
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PERREAL NO. 6217982.

PERREAL NO. 6217982.

PAPLICANT: WORKER, IT. WORKE, RECEARTED WITH CONTRIBUTION: WORKER, IT. WORKE, Eladio

APPLICANT: WILL WORKER, ELADIO

APPLICANT: WILL WORKER, IT. WORKER,
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4 PDWK-----IRKEILIEPFSEESLQP----AGYDLRVGREAFVKGKLIDVEKEGK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 VVIPPREYA-----LILTLERIKLPD---DVMGDMKIRSSLAREGVIGSFAWVDP----- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- GWDGNLTLMLYNAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 KYFATDGKQGKAPNFLSKALSNAGFYTFRSGWDKNATVMVLKAS 418
                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,639A
FILING DATE: 10 JUNE 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%; Score 76.5; DB 23.2%; Pred. No. 0.66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.5%; Score 76.5; Di
Best Local Similarity 23.2%; Pred. No. 0.66
Matches 38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 31, 2002, 13:07:52
Job time: 44 sec
                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Healey, William J.
REGISTRATION UNDRER: 36,104
REFERENCE/DOCKET UNDRER: 10438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)942-8484
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 659 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
TITLE OF INVENTION: Flavobacterium heparinum
                                                                                 TITLE OF INVENTION: POLYMENT P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76.5; DB 4; Length 14;
Pred. No. 0.0023;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION BELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULLX, David J.
REGISTRENCE/DOCKET NUMBER: 1486/43163
TELEPANTON NUMBER: 36,576
TELEPANTON ON SEQ. 1D NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08258639A Patent No. 5681733 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Su, Hongsheng
APPLICANT: Blain, Francoise
APPLICANT: Bennett, Clark
APPLICANT: Gu, Kangfu
APPLICANT: Zimmermann, Joseph
APPLICANT: Musll, ROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hale and Dorr
               GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1455 Pennsylva
CITY: Washington, D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FAWVDPGWDGN-TLM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20004
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US-08-258-639A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-822-774-54
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Indels

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:39:15; Search time 46.78 Seconds (without alignments) 10.189 Million cell updates/sec Run on:

US-08-957-709-72 13 Title: Perfect score:

1 XGXXDXXXGXXXX 13 Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

0 Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | dР             |        |    | SUMMARIES  |                    |
|---------------|-------|----------------|--------|----|------------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB | ID         | Description        |
|               | 2     |                | 34     | Н  | m,         | Ē                  |
| 7             | 7     | 15.4           | 40     | Н  | RIP1_SAPOF | P98185 saponaria o |
| m             | 7     | 15.4           | 466    | Н  | RBL_CORKO  | Q33369 cornus kous |
| 4             | 1     | 7.7            | m      | Н  | GRWM_HUMAN | P01157 homo sapien |
| S             | 7     | 7.7            | m      | Н  | LUXE_VIBFI | vibr               |
| 9             | 1     | 7.7            | 4      | Н  | ACH1_ACHFU | P35904 achatina fu |
| 7             | 1     | 7.7            | 4      | Н  | DCML_PSECH | P19916 pseudomonas |
| ۵             | -     | 7.7            | 4      | -  | EOSI_HUMAN | P02731 homo sapien |
| σ             | 1     | 7.7            | 5      |    | AL14_CARMA |                    |
| 10            | 1     | 7.7            | 5      | -  | BIOA_CITFR | P13071 citrobacter |
| 11            | ٦     | 7.7            | 5      | -  | BIOA_SALTY | P12677 salmonella  |
| 12            | -     | 7.7            |        | ٦  | PAP2_PARMA | parda              |
| 13            | н     | 7.7            |        | Н  | TPIS_CANFA |                    |
| 14            | 1     | 7.7            |        | ~  | TRM3_ECOLI | P13973 escherichia |
| 15            |       | 7.7            | S      | -  | UF01_MOUSE |                    |
| 16            | н     | •              | S      | ٦  | UXA4_CHLTR | P38005 chlamydia t |
| 17            | -     | 7.7            |        | -  | ASP2_LACSN | P82655 lactobacill |
| 18            | 7     | 7.7            |        |    | CIP1_MYTED |                    |
| 19            | 7     | 7.7            |        |    | CIP2_MYTED | P13737 mytilus edu |
| 20            | 1     | •              | 9      | -  | FARP_MONEX | _                  |
| 21            | 1     | 7.7            | •      | Н  | LOK1_LOCMI | P41491 locusta mig |
| 22            | 1     | 7.7            |        | -  | TRPI_PSEPU |                    |
| 23            | т     | 7.7            |        | -  | ALL2_CARMA | P81805 carcinus ma |
| 24            | 7     | 7.7            |        | Н  | ALL3_CARMA | P81806 carcinus ma |
| 25            | -     | 7.7            |        | -  | ALL4_CARMA | P81807 carcinus ma |
| 56            | 7     | 7.7            | 7      | -  | ALL5_CARMA |                    |
| 27            | 1     | 7.7            | 7      | Н  | ALL7_CYDPO |                    |
| 28            | 1     | 7.7            | 7      | m  | CHOX_ALCSP |                    |
| 29            | H     |                | 7      | ٦  | FAR1_HELTI |                    |
| 30            | 1     | 7.7            | 7      | -  | FAR2_PROCL | -                  |
| 31            | 1     | 7.7            | 7      | Н  | FAR5_HIRME |                    |
| 32            | -     | 7.7            | 7      | -  | FARB_CALVO | 998                |
| 33            |       | 7.7            | 7      | П  | IGAO_DACDE | P06294 dactylium d |
|               |       |                |        |    |            | •                  |

Saponaria officinalis (Common soapwort).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.

20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RICOSOME-INACTIVATING PROTEIN SAPORIN-1 (SAP-1) (SO-4) (RRNA N-GLYCOSIDASE) (EC 3.2.2.22) (FRAGMENT).

40 AA.

PRT;

STANDARD;

RIP1\_SAPOF P98185;

RESULT 2 RIP1\_SAPOF

| cer<br>llu<br>llu<br>llu<br>ilu<br>ma<br>ma<br>ma<br>ma<br>ma<br>ma<br>ma                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 6                                                  |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------|
| carnobacter<br>leptinotars<br>mus musculu<br>mus musculu<br>ratus norv<br>pinus pinas<br>thunnus alb<br>carcinus ma<br>gryllus bim<br>melolontha<br>tabanus atr<br>carcinus ma | inaceae;<br>nce alignments<br>ogenic archaeon<br>EDOXIN =<br>E DELTA AND<br>2-OXOBUTYRATE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Gaps                                               |
|                                                                                                                                                                                | aceae)<br>e aliç<br>enic e<br>OXIN •<br>DELTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 6                                                  |
| P36960<br>P4298641<br>P38641<br>P38642<br>P56576<br>P81691<br>P8091<br>P14086<br>P14086<br>P14086<br>P14086<br>P14086                                                          | ENT).  nosarcinac sequence nethanogen neth one DE NA, ONE DE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Length 34;<br>0; Indels                            |
| C_CARUI<br>C_LEPDE<br>3_MOUSE<br>4_MOUSE<br>1_RAT<br>C_RAN<br>C_CARMA<br>G_GRYBI<br>G_GRYBI<br>TABAT<br>2_CARMA                                                                | Created) Last sequence update) Last sequence update) Last annotation update) Last annotation update) Last annotation and sequence in managemether of also and sequence in oxidoreductase from the mell oxidoreductase from                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | DB 1;<br>0;<br>hes                                 |
| LANC_CARUI<br>MNPL_LEPDE<br>UF03_MOUSE<br>UF04_MOUSE<br>UH11_RAT<br>UN06_PINS<br>ACI_THUAL<br>ACI_CARMA<br>AKH_MELML<br>AKH_MELML<br>AKH_TABAT<br>AL12_CARMA                   | PBA<br>PERMETER STANDARD; PRT; 34 AA.<br>1522; SEB-1996 (Rel. 33, Created)<br>FEB-1996 (Rel. 33, Last sequence update)<br>FEB-1996 (Rel. 33, Last sequence update)<br>FEB-1996 (Rel. 40, Last annotation update<br>RUVATE SYNTHAES BETA CHAIN (EC 1.2.7.1) (F<br>Lhanosarcina barkeri.<br>Phanosarcina.<br>PLA TAXID-2208;<br>ALTAXID-2208;<br>ALN=FUSARO / DSM 804;<br>ALN=FUSARO / DSM 804;<br>ALNE-96203906; Pubmed=8620891;<br>JUENCE<br>ALNE-96203906; Pubmed=8620891;<br>JUENCE STAINT (Allogonia parkeri (Strain Fusaro).";<br>ALN SICCINA DARKETI (Strain Fusaro).";<br>CATALYTIC ACTIVITY: PYRUVATE + COA + OXI<br>ACETYL-COA + CO(2) + REDUCED FERREDOXIN.<br>CATALYTIC ACTIVITY: PYRUVATE + COA + OXI<br>ACETYL-COA + CO(2) + REDUCED FERREDOXIN.<br>CATALYTIC ACTIVITY: PYRUVATE + COA + OXI<br>ACETYL-COA + CO(2) + REDUCED FERREDOXIN.<br>CONE GAMMA CHAIN.<br>MISCELLANEOUS: IT ALSO CATALYZES THE OXI<br>ALTER 34 AA; 3372 MW; C913DA5DDEID75F                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Sco<br>Pr                                          |
| аннаннанна                                                                                                                                                                     | Created) Last sequest                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 15.4%;<br>100.0%;<br>cive (                        |
| ~~~~~~                                                                                                                                                                         | BA STANDARD; PRT 996 (Rel. 33, Created) 996.(Rel. 33, Last sequen 996.(Rel. 33, Last sequen 996.(Rel. 34, Last annota 10. SYNYHASE BETA CHAIN (EC arcina barkeri. EUTYATCHAECT: Methanosa arcina barkeri. 1D=2208; 1. 95203906; PubMed=8620891; 6. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | vat                                                |
|                                                                                                                                                                                | STI<br>(Rel.<br>(Rel.<br>(Rel.<br>(Rel.<br>(Rel.<br>O / D<br>3906;<br>Nunchor<br>(Runchor<br>ferr<br>ferr<br>ferr<br>ferr<br>(C ACT<br>(C | arit                                               |
|                                                                                                                                                                                | METE<br>22,<br>22,<br>22,<br>31,<br>32,<br>33,<br>34,<br>34,<br>34,<br>34,<br>34,<br>34,<br>34                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Simi<br>4;<br>D 5<br>D 21                          |
| 00000000000000000000000000000000000000                                                                                                                                         | PYSB_METBA PYSB_METBA AC PYSB_METBA AC O1-FEB-19 DT 01-FEB-19 DT 01-FE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Query Match<br>Best Local<br>Matches<br>2 GXX<br>1 |
|                                                                                                                                                                                | PYS<br>PYS<br>PYS<br>PYS<br>PYS<br>PYS<br>PYS<br>PYS<br>PYS<br>PYS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Oy Au                                              |

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186 GXXD 189
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P01157;
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P24272;
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LUXE_VIBET
LUXE_VIBET
TD LUXE_V
AC 0.74.77
DT 0.1-07
DT 0
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GRWM_HUMAN
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                                                                                                                                  TABLE TO STATE THE STATE TO STATE THE STATE TO STATE ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE STATE STAT
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO REC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                  TISSUE-Leaf.

WEDLINE-89326691; PubMed-2753596;

Montecucchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cornus kousa.
Chloroplast.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; Cornales; Cornaceae; Cornoideae; Cornus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Leaf;
Olmstead R.G., Bremer B., Scott K.M., Palmer J.D.;
A parsimony analysis of the Asteridae sensu lato based on rbcL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2.9-PHOSPHO-D-GLYCERATE.
CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: CHLOROPLAST.
SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 40;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.4%; Sco
ilarity 100.0%; Pr
Conservative 0;
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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35 GXXD 38
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SEQUENCE.
SCALESINGE TO H., Pickart L., Thaler M.M.;
Schlesinger D.H., Pickart L., Thaler M.M.;
I-TARGELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio fischeri.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
LONG-CHAIN-FATTY-ACID--LUGIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
(ACYL-PROTEIN SYNTHETASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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0
                                                                                                                                                                                            BINDING OF CO(2) ACTIVATES THE 3E27F2E9D798EC69 CRC64;
                                                                                                              Photorespiration;
                                                                                                                                                                                                                                                                                                       Length 466;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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EMBL; L14395; AAA19755.1; -.
InterPro: IPR000685; Ruaisco_large.
PROSITE; PF00016; Ruaisco_large; 1.
PROSITE; PS00157; RUBISCO_LARGE: PARTIAL.
PROSITE; PS00157; RUBISCO_LARGE: PARTIAL.
PROSITE; PS00157; RUBISCO_LARGE: PARTIAL.
PROSITE; PS00157; RUBISCO_LARGE: PARTIAL.
NONCOUNTER 10.

MON TER 10.

MON TER 192 192 BINDING OF CO(2) ACTI.
SEQUENCE 466 AA: 51909 WW; 3E27F2E9D798EC69 CR
                                                                                                                                                                                                                                                                                                       DB 1;
. 0;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
GOWTH-MODULATING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AA.
                                                                                                                                                                                                                                                                                                          15.4%; Score 2; DB 1
100.0%; Pred. No. 0;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.7
Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Goetzl E.J., Austen K.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCML_PSECH
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     161
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DCML_PSECH
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                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libe.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                       FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID. IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCLEBRASE-CATALYZED REACTION.
                                                                                                                     CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN = AMP + PYROPHOSPHATE + AN ACYL-PROTEIN THIOLESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Achatina fulica (Giant African snail).
Bukaryota: Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FERUSSAC; TISSUE-Heart atrium;
MEDLINE-91264856; PubMed-1675568;
Fujimoto K., Kubota I., Yasuda Kamatani Y., Minakata H., Nomoto K.,
Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
"Purification of achatin-I from the atria of the African giant snail,
Achatina fulica, and its possible function.";
Biochem. Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Funateni Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P., Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.; "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina Filica Ferussac containing a D-amino acid residue."; Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                      PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M62812; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-FERUSSAC; TISSUE-Ganglion;
MEDLINE-89273551; PubMed-2597281;
Bacteriol. 172:6797-6802(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inescence; Ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH1_ACHFU
P35904;
                                                                                                                                                                                               COMPLEX
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ACH1_ACHFU
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-!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- COFACTOR: MOLYBDENUM.
-i- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-FEB-1991 (Rel. 17, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
Pseudomonas carboxydohydrogena.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes
carboxydotrophic bactain.";
Arch. Microbiol. 152.335.34[1989].
-!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
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                                                                                                                            D-PHENYLALANINE.
6AADD9C810000000 CRC64;
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100.0%; Pred. No. 0;
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l, Last annotation update)
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SEQUENCE.
MEDLINE=76078412; PubMed=1060093;
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21-JUL-1986 (Rel. 01, Last seq
21-JUL-1986 (Rel. 01, Last and
EOSINOPHILOTACTIC PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Molybdenum.
                                                                                                                            MOD_RES 2 2
SEQUENCE 4 AA; 408 MW;
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria.
NCBI_TaxID=290;
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                                                                                                    Hormone; D-amino acid. MOD_RES 2 2
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Best Local Similarity
Local 1; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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BIOA_SALTY
P12677;
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"Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.";

Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

-I. MISCELLANDOUS: THEER PEPPIDES ARE RELEASED FROM MAST CELLS IN LUNG (AND OTHER ISSUES) DURING HYPERSENSITYUTY REACTIONS (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-JAN-1990 (Rel. 13, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
(EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA BXDA.
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                                                                                                                                                                                                                                                                                                                                                                                        Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 1; DB 1; Length 5; 100.0%; Pred. No. 0; tive 0; Mismatches 0; Indels
                                                                                                                                                      Length 4;
                                                                                                    1 1 V -> A (IN OTHER PEPTIDE).
/FTIG=VAR_005201.
4 AA; 390 MW; 6B055862A0000000 CRC64;
                                                                                                                                                    Query Match 7.7%; Score 1; DB 1; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                              30-MAY 2000 (Rel. 39, Created)
30-MAY 2000 (Rel. 39, Last sequence update)
30-MAY 2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 14.
                                                                                                                                                                                                                                                                5 AA.
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Best Local Similarity 100.
Matches 1; Conservative
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P13071;
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P81817;
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                                                                                                                  SEQUENCE FROM N.A.

MEDLINEE 89065280; Dubwed-2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-! CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
OXONONANOADE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
7.8-DIAMINONOANOADE PROSENTE PROSENTE.
-! COPACTOR: PYRIDOXAL PHOSPHATE.
-! COPACTOR: PORTHOSIS.
-! SIMINITY: BIOTIN BIOSYNTHESIS.
-! SIMINITY: BLOINER.
-! SIMINITY: BLOINES.
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MEDLINE=89006280; Pubmed-2971595;
Shiuan D., Campbell A.;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli, citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-! CATALYTIC SADENOSYL-L.METHIONINE + 8 AMINO-7-
OXONONANOATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
7.8 DIAMINONANOATE.
-!- COPACTOR: PYRIDOXAL POSCHATE.
-!- PATHWAY: BIOTIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; · Gaps
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1-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
(EC 2.6.1162) (7.8 DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
AMINOTRANSFERASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
Citrobacter freundii.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M21922; -; NOT_ANNOTATED_CDS.
InterPro; IPR000954; Aminotran, 3.
PROSITE; PS00600; Am_TRANSFER_CLASS_3; PARTIAL.
Biotin blosynthesis; Transferase; Aminotransferase;
Pyridoxal phosphate.
Show_TER
SS2 WW; 6AAABIBIA6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 1; DB 1;
100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                   Citrobacter.
NCBI_TaxID=546;
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Dunn M.J., Corbett J.M., Wheeler C.H.; HSC-2DPROES and the two-dimensional gel electrophoresis database of and heart profess.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and tray genes of plasmid R100.";
J. Bacteriol. 170:2749-2757(1988).
-!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
HSC-ZDPAGE; P54714; DOG.
InterPro; IPR000652; Trioseph_isomrse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88227859; PubMed-2836369; Inamoto S., Yoshioka Y., Ohtsubo E.; "Identification and characterization of the products from the traJ
                                                                                                                                                                                                                                                                                                                                                                        dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00171; TIM; PARTIAL.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Plasmid IncFII R100.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
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01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRAM PROTEIN (FRAGMENT).
                                                        5 AA.
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                                                                                                                                                                                                                                                                                                                    MEDLINE=98163340; PubMed=9504812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 MW;
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                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                  Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETONE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                        NCBI_TaxID=9615;
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P13973;
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                                                      TPIS_CANFA
P54714;
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                                    TPIS_CANFA
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-87057369; PubMed-3782138;
Lazarovici P., Primor N., Loew L.M.;
Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardachirus marmoratus).";
SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIO1. Chem. 261:16704-16713(1986).
FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES. FORMS VOLTAGE-DEPRENBENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
SUBGNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
SUBGELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pardachirus marmoratus (Red sea moses sole).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Soleoidei; Soleidae; Pardachirus.
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                        InterPro; IPR000954; Aminotran_3.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
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                                                                                                                                                                                                                                                                                                                                                     5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-NUG-2001 (Rel. 40, Last annotation update)
PARDAXIN II (PXII) (FRAGMENT).
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100.0%; Pre
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Best Local Similarity
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Matches 1; Conserv
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P81864;
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

FIRIS, A2014; A32014.

Conjugation; Plasmid; DNA-binding.

NON_TER

SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;
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UFOL_MOUSE
ID UTOL_MOUSE
ID 0.FOL_MOUSE
ID 0.CCT-1994 (Rel. 30, Last sequence update)
DT 0.1-CCT-1994 (Rel. 30, Last sequence update)
DT 0.1-CCT-1994 (Rel. 31, Last annotation update)
DT 0.1-REB-1995 (Rel. 31, Last annotation update)
REPARTION REPARTIVE TWO-dimensional gel electrophoresis.";
RESURANTE SECTION THE DESTRAINED PI OF THIS UNKNOWN PROTEIN IRS 6.6, ITS MM IS: 19 KDA.
FT NON_TER 5 AS: 717 MM; 7364087043100000 CRC64;
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MEDLINE-95009907; PubMed=7523108;
MEDLINE-95009907; PubMed=7523108;
MESTICK B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).

"MISCELLANDOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
SEQUENCE S AA; 717 MW; 7364087043100000 CRC64;
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7.7%; Score 1; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indel:
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Search completed: January 31, 2002, 13:39:16 Job time: 76 sec

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Run on:

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Q9nnj2 leishmania
096082 stephanoste
094205 agrobacteri
099wy1 leishmania
P82070 litoria rub
007354 synechococc
047029 enterobacte
047029 enterobacte
048420 coryctolagus
049223 glycine max
049223 glycine max
09553 arabidopsis
055184 rattus norv
05540 tereptococc
05542 thermus agu
09258 synechococc
05542 thermus agu
 Q9zzz5 steatomys s
Q9axk8 solanum tub
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavlidae.
NCBL_TaxID=10140;
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MEDLINE-95355312; PubMed=7629028;
Motojima K., Goto S.,
M. Biochem. 117:597-602(1995).
SROUENCE 19 AA; 2184 MW; A53237547BE09F0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090v94;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ORGAN OF CORTI PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
C-REACTIVE PROTEIN (FRAGMENT).
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100.0%; Pred. No. 0;
Live 0; Mismatches
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Q9ZZZS
Q9AXK8
Q9XNZ4
                                              Q9NNJ2
Q96082
P94205
Q9GWY1
P82070
P82073
Q47505
Q47505
Q4923
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Matches 4; Conserv
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Oggv94 cavia (quin
Oggv30 leishmania
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Q98y82 human immun
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Q98z23 human immun
                                                                                                           January 31, 2002, 13:37:37 ; Search time 130.99 Seconds (without alignments) 14.517 Million cell updates/sec
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032870 pyramimonas
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Q9GX46
Q9GX39
Q9GXR7
Q9N7N4
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sp_human:*
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sp_mammal:*
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Result Š us-08-957-709-72.rspt

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PRELIMINARY;
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Hypothetical protein.
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MurDhy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
Oliver K.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL390114; CAC02703.1;
Hypothetical protein.
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01-MAR.2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
14-MAR-2001 (TrEMBLrel. 16, Last annotation update)
15-MAR-2001 (TrEMBLrel. 16, Last annotation update)
15-MAR-2001 (TrEMBLrel. 16, Last annotation update)
15-MAR-2001 (TrEMBLrel. 16, Last BROTEIN (FRAGMENT).
16-ISHmania major.
16-MAR-2001 (TremBLrel. 16, Last Broten)
16-MAR-2001 (TremBLrel. 16, Last Broten)
16-MAR-2001 (TremBLrel. 16, Last Broten)
17-MAR-2001 (TremBLrel. 16, Last Broten)
18-MAR-2001 (TreMBLRel. 16, Last Broten)

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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MON-2001 (TrEMBLrel. 17, Last annotation update)
101-MON-2001 (TREMBLR)
LM12.231 MARIAN (FRAGMENT).
Leishmania major.
Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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STRAIN-FRIEDLIN;
Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B., Oliver K.; Gudail M., Harris D., Rajandream M., Ivens A., Barrell B., Oliver K.; Gudain D., Coliver K.; Gudain C., Coliver K.; Gudain C., Coliver K.; Submitted (Aug-2009 to the EMBL/GenBank/DDBJ databases. EmBL; AL390114; CAC02096.1; -..
InterPro; IPR001208; MCM.
PROSITE; PSS0051; MCM.2; 1.
                                                   Thalmann I., Suzuki H., McCourt D.W., Comegys T.H., Thalmann R.;
"Partial amino acid sequences of organ of Corti proteins OCP1 and OCP2: a progress report.";
Hear. Res. 64:191-198(1993).
SEQUENCE 49 AA; 5327 MW; A90E7FE21BB986CA CRC64;
                                                                                                                                                                                                                                                                                                                             ;
0
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55 AA; 6092 MW; A325DA28305F9331 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 AA.
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SEQUENCE.
MEDLINE-93163013; PubMed-8432690;
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32 GXXD 35
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SEQUENCE
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MurDhy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
Oliver K.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL390114; CACC02694.1;
NON TER 1
NON TER 75
SEQUENCE 75 AA; 7754 MW; 507158F8252B1A42 CRC64;
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STRAIN-FRIEDLIN;
MULPHY L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B., Oliver K.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL390114; CAC02097.1;
InterPro; IFF001208; MCM.
PROSITE; PS50051; MCM.2; 1.
Hypothetical protein.
NON_TER 92 92
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Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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64 64
64 AA; 7016 MW; 515441B7AFD6EBBA CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 7.8 KDA PROTEIN (FRAGMENT).
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 10.0 KDA PROTEIN (FRAGMINT).
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Oliver K.;
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NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 139 AA; 15117 MW; 084D966737E6BFBB CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHEFICAL 15.1 KDA PROTEIN (FRAGMENT).
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U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 15.2 KDA PROTEIN (FRAGMENT).
                DB 5;
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                                               0; Mismatches
                15.4%; Score 2; I
100.0%; Pred. No.
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                Query Match 15.4
Best Local Similarity 100.
Matches 4; Conservative
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58 GXXD 61
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Q9GXR7
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NCBI_TaxID=5664;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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TISSUB-ETICLATED HYPOCOTYLS;
Subenfuehr A., Lomax T.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022020; AAC13260.1; -.
Mendel, 28774; Lyces;1524;28774.
InterPro; IRRO3311; AUX_IAA.
PF02309; AUX_IAA; 1.
                                               Length 92;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL390114; CAC02345.1; -.
Hypothetical protein.
NON_TER 134 134
SEQUENCE 134 AA; 14304 MW; F39B00EC2A8D22A4 CRC64;
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99 AA; 10767 MW; 9F9F01A3EBCAF243 CRC64;
9991 MW; BE1E32EA37C402B9 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 14.3 KDA PROTEIN (FRAGMENT).
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                                           Query Match 15.4%; Score 2; DB 5; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches
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100.0%; Pre
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Best Local Similarity 100.
Matches 4; Conservative
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92 AA;
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Leishmania major.
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32 GXXD 35
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75 GXXD 78
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SEQUENCE A.S.; Normark B.B.; Farrell B.D.;

Trom recent associations in bark beetles.";

L Proc. R. Soc. Lond., B. Biol. Sci. 0:0-0(2001).

- 1- SIMILARITY: TO GTP-BINING ELONGATION FACTOR FAMILY.

R FIRE, AF308408; AAG45067.1;

R PRIMTS; PRO03095; GTP_EFTU.

R PRIMTS; PRO0309; GTP_EFTU.

R PRIMTS; PRO0301; EFACTOR_GTP: 1.

R GTP-binding; Protein biosynthesis.

T NON_TER

200

SEQUENCE 290 AA; 31705 MW; 32CD038BA32IA628 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B., Oliver K.;
Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AL390114; CAC02208.1; -..
Hypothetical protein.
NON_TER 1 1
NON_TER 261 261
SEQUENCE 261 AA; 27941 MW; E1C505B36BEA9832 CRC64;
                                                                                                                                                                                                                                                                                                       LM12.383.
Leisbhmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hylurgops rugipennis.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Scolytidae; Hylurgops.
NCBI_TaxID=141166;
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  Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ELONGATION FACTOR 1 ALPHA (FRAGMENT).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 27.9 KDA PROTEIN (FRAGMENT).
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  0; Mismatches
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  4; Conservative
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                                        2 GXXD 5
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Q9GXI5
ID Q9GXI5
AC Q9GXI5;
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WEDLINE-9824614; PubMed-9582120;

Frenkel L.M., Mullins J.I., Learn G.H., Manns-Arcuino L.,

Frenkel L.M., Mullins J.I., Steketee R.W., Thea D.M., Nichols J.E.,

Herring B.L., Karlache M. L., Steketee R.W., Thea D.M., Nichols J.E.,

Harae A.T., Lustmache A., He X., Muthui D., Madan A., Hood L.,

Haase A.T., Zupanic M., Steskus K., Wolinsky S.M., Krogstad P.,

Zhao J.-Q., Chen I., Koup R., Ho D.D., Korber B.T., Apple R.J.,

Coombs R.W., Pahwa S., Roberts N.J. Jr.,

"Genetic evaluation of suspected cases of transient HIV-1 infection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MUTDHY L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
Mutphy L., Quail W., Harris D., Rajandream M., Ivens A., Barrell B.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL390935; CAC00903.1; -.
NON_TER 1 1
NON_TER 166
SEQUENCE 166 AA: 17573 MW; 111FFE2C415FB6C4 CRC64;
                                                                                                                                                         01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
10-05SIBLE NUCLEOLAR TRANSCRIPTION FACTOR 2 (FRAGMENT).
14:Shmania major.
14:Shmania major.
15:Lastyota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID-5664;
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15.4%; Score 2; DB 5; Length 166; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches 0; Indels
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17573 MW; 111FFE2C415FB6C4 CRC64;
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21540 MW; 95E23174393B1028 CRC64;
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01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01.01V-2001 (TrEMBLrel. 17, Last annotation update)
01.01V-2001 (TREMBLREL. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                           166 AA.
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EMBL; AF065590; AAC21548.; Interpro; IPR000777; GP120.
Envelope Promise Research 1. 1
NON_TER 192 192
SEQUENCE 192 AA; 21540 MW; 9!
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"Recovery of HIV-1 pol gene sequences by direct sequencing of amplification products derived from plasma samples.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF347587; AAK32663.1; -.
NON_TER 320 320
SEQUENCE 320 AA; 36480 MW; 89F1BA75FE57B37A CRC64;
Query Match 15.4%; Score 2; DB 5; Length 290; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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40 GXXD 43
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Q98Y82;
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DT 01-JUN-
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Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels

Search completed: January 31, 2002, 13:37:38 Job time: 163 sec

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Thu-Jan, 31 13:32:36 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:20:08 ; Search time 78.64 Seconds (without alignments) 12.592 Million cell updates/sec Run on:

US-08-957-709-72 13 1 XGXXDXXXGXXXX 13 Title: Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 segs, 76174552 residues Searched:

0

Word size :

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|   | ρt             | trichocyst protein |        | rRNA N-glycosidase | auxin-induced prot |      | Ig heavy chain V r | growth-modulating |        | spinal cord peptid | spinal cord peptid | T-cell receptor be | T-cell receptor be | antho-RFamide neur | tyrosine-melanocyt | carbon-monoxide de | biotin A - Citroba | protein D - Escher | ~      | globulin IV alpha | hypothetical prote | COI intron 16 prot | autho-RF amide neu | u      | achatin-I - giant | metallothionein-A |        | heavy  | heavy cha | Ig mu chain V regi |
|---|----------------|--------------------|--------|--------------------|--------------------|------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|--------------------|--------------------|--------|-------------------|-------------------|--------|--------|-----------|--------------------|
|   | ID             | A60698             | S65417 | S16331             | T05708             | GCPG | B31790             | GKHU              | A60898 | A23751             | B23751             | PT0636             | PT0571             | ECXAA              | A32039             | PL0140             | 140697             | A41890             | D41654 | S09478            | T30569             | I38888             | A25844             | A34626 | A32480            | 151049            | 839390 | PT0240 | 0         | S43959             |
|   | DB             | 7                  | ~      | ~                  | ~                  | Н    | 7                  | ~                 | 7      | ~                  | 7                  | ~                  | 7                  | Н                  | 7                  | 7                  | ď                  | N                  | ~      | ~                 | ~                  | N                  | 7                  | ~      | 7                 | ~                 | ~      | ~      | 7         | 7                  |
|   | Length         | 28                 | 34     | 40                 | 66                 | 158  | 254                | m                 | m      | m                  | m                  | e                  | m                  | 4                  | 4                  | 4                  | 4                  | 4                  | 4      | 4                 | 4                  | 4                  | 4                  | 4      | 4                 | 4                 | 4      | 4      | 4         | 4                  |
| æ | Query<br>Match | 15.4               | 15.4   | 15.4               | 15.4               | 15.4 | 15.4               | 7.7               | 7.7    | 7.7                | 7.7                | 7.7                | 7.7                | 7.7                | 7.7                | 7.7                | 7.7                | 7.7                | 7.7    | 7.7               | 7.7                | 7.7                | 7.7                | 7.7    | 7.7               | 7.7               | 7.7    | 7.7    | 7.7       | 7.7                |
|   | Score          | 2                  | 7      | 7                  | 2                  | 7    | 7                  | г                 | 7      | <b>.</b>           | -                  | 1                  | -                  | -                  | -                  | Н                  |                    |                    | -      | н                 | П                  | . <del>-</del>     | П                  | -      | H                 | -                 | Н      | Н      | Н         | Н                  |
|   | Result<br>No.  | П                  | 7      | ო                  | 4                  | S    | 9                  | 7                 | 89     | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18     | 19                | 20                 | 21                 | 22                 | 23     | 24                | 25                | 56     | 27     | 28        | 59                 |

| T-cell receptor be<br>T-cell receptor be<br>T-cell receptor be |                                              | receptor receptor receptor receptor tin - rat            | protein-glutamine<br>cholecystokinin-5<br>spinal cord peptid<br>mitosis inhibiting |
|----------------------------------------------------------------|----------------------------------------------|----------------------------------------------------------|------------------------------------------------------------------------------------|
| 2 A53284<br>2 B53284<br>2 PT0696                               | 2 PT0633<br>2 PT0711<br>2 PT0698<br>2 PT0677 | 2 PT0675<br>2 PT0675<br>2 PT0721<br>2 PT0566<br>2 S47552 | 2 A26209<br>2 A32516<br>2 C23751<br>2 A26830                                       |
| 444                                                            | ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '      | T T T T T                                                | 4 N N N                                                                            |
| 7.7                                                            | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,       |                                                          | r.r<br>r.r<br>r.r                                                                  |
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# ALIGNMENTS

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| SULT | 808 |

RESULT 1
A60698
Lilchooyst protein 12 - Paramecium tetraurelia (fragment)
C.Species: Paramecium tetraurelia
C.Species: Paramecium tetraurelia
C.Species: Paramecium tetraurelia
C.Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 07-Dec-1999
C.Accession: A60698
R.Tindall, S.H.; Devito, L.D.; Nelson, D.L.
J. Cell Sci. 92, 441-47, 1989
A.Title: Biochemical characterization of the proteins of Paramecium secretory granule
A.Reference number: A60698; MUID: 90078398
A.Accession: A60698
A.Molecule type: protein
A.Residues: 1-28 <a href="https://www.nified">https://www.nified</a> from the extruded matrix (contents) of trichocys
C.Comment: This protein was purified from the extruded matrix (contents) of trichocys
C.Genetics:
A.Genetic code: SGC5
C.Keywords: extracellular protein

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||||| |GXXD 25 GXXD 5 ~ οy q

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### 7 RESULT

Pyruvate synthase (EC'1.2.7.1) beta chain - Methanosarcina barkeri (fragment)
N.Alternate names: pyruvate:ferredoxin 2-oxidoreductase (CoA-acetylating) beta chain
C.Species: Methanosarcina barkeri
C.Date: 28-oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-May-2000
C.Accession: S6547
R.Bock, A.K.; Kunow, J.; Glasemächer, J.; Schoenheit, P.
Eur. J. Biochem. 237, 35-44, 1996
A.Title: Catalytic properties, molecular composition and sequence alignments of pyruv
A.Reference number: S65416; MUID:96203906
A.Accession: S65417
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1-34 ABCC
C.Keywords: coenzyme A; oxidoreductase

Gaps ö Indels Length 34; ; Query Match 15.4%; Score 2; DB 2; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches

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A: Residues: 1-69 cPH1>
R: Thin, L: Moody, A. J.
Regul. Pept. Suppl. 2, S33, 1983
A: Title: Primary structure of a possible porcine proglucagon fragment.
A: Title: Primary structure of a possible porcine proglucagon fragment.
A: Reference number: A60312
A: Moodelle type: protein
A: Moodelle type: protein
A: Moodelle type: protein
A: Residues: 1-30 c*H2>
A: Moodelle type: protein
A: Residues: 1-30 c*H2>
A: A: Sinn. Li. G; Behrens, O.K.
J. Am. Chem. Soc. 79, 2807-2810, 1957
A: Title: The amino acid sequence of glucagon. V. Location of amide-groups, acid degrae A: A: Accession: Ab1781
A: Moodelle type: protein
A: Reference number: A91781
A: Moodelle type: protein
A: Residues: 3-6 c*Ro>
A: Title: Complete sequences of glucagon. V. Location of amide-groups, acid degrae A: Reference number: A92732; MUID: 89327238
A: Title: Complete sequences of glucagon-like peptide-1 from human and pig small intes A: Residues: 78-107 complete sequences of glucagon-like peptide-1 from human and pig small intes A: Residues: 78-107 complete sequences of glucagon-like peptide-1 from human and pig small intes A: Moodelle type: protein
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GCPG

GLOGGON

N.Alternate names: glicentin; oxyntomodulin

N.Alternate names: glicentin; oxyntomodulin

N.Alternate names: glicentin; oxyntomodulin

N.Alternate names: glicentin; oxyntomodulin

N.Alternate names: glicentin: related beptide; glucagon; glucagon-37 (oxyntomodulin); glucagon-6

C; Species: Sus scrofa domestica (domestic pig)

C; Date: 17-Dec-1982 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998

C; Accession: A01540; A60312; A91781; B32614; A28064

R; Thin, L.; Moody, A.J.

C; Accession: A01540; A60312; MUID: 81248172

A; Title: The primary structure of porcine glicentin (proglucagon).

A; Reference number: A94233; MUID: 81248172

A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď.
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T05708
auxin-induced protein IAA9 - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Accession: 109708
R:Nebeniuehr. A.; Lomax, T. L.
Submitted to the EMBL Data Library, September 1997
A:Description: Auxin-regulated LelAA genes of tomato.
A:Reference number: 215303
A:Accession: T05708
A:Reference number: 215303
A:Accession: T05708
A:Reference number: 21590
A:Reference number: 21590
A:Reference number: 215303
A:Accession: T05708
A:Reference number: 21590
A:Re
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35 GXXD 38
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spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Accession: B23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fetal T cell receptor beta chains have few N regions
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
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PT0571
C. Cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C. Species: Mus musculus (house mouse)
C. Species: Als musculus (house mouse)
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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                        Length 3;
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A:Accession: PT0636
A:Status: translation not shown
A:Molecule type: MRNA
A:Residues: 1-3 <FEE>
A:EEE>
C:Keywords: T-cell receptor
                     DB 2;
. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 1; DB 2;
100.0%; Pred. No. 0;
ative 0; Mismatches
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                                                                   0; Mismatches
                     7.7%; Score 1;
.00.0%; Pred. No.
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Astaclause type: protein
Astaclause: 1-3 <4SL>
Csuperfamily: unassigned animal peptides
                                           100.08;
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                                                                     Conservative
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Matches 1; Conserv
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                                        Best Local Similarity
Matches 1; Conserv
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R; Feeney, A.J.
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PT0636
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                                                                                                                                                                                                                                                                                                                                    A; Accession: A01421
A; Molecule type: protein
A; Residues: 1-3 SCKH-
A; Note: this serum tripeptide is found to stimulate growth of some cell types and to inh
C; Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60898
bursin - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Date: 31-Pec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Accession: A60898
R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A;Title: Trippelide structure of bursin, a selective B-cell-differentiating hormone of A;Reference number: A60898; MUID:86122916
A;Accession: A60898
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Spinal cord peptide SCP-4 - pig

Spinal cord peptide SCP-4 - pig

Spinal cord peptide SCP-4 - pig

C; Species: Sus scrofa domestica (domestic pig)

C; Species: Sus scrofa domestica (domestic pig)

C; Species: Sus scrofa domestica (domestic pig)

C; State: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000

C; Accession: A23751

R; HSi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, Arch. Biochem. Biophys. 240, 178-188, 1985

A; Reference number: A23751; MUID: 85250425
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                                                                                                                                                    growth-modulating peptide - human
C;Species: Homo sapiens (man)
C;Daces: 23-0ct-1981 #sequence_revision 26-May-1995 #text_change 20-Jun-2000
C;Accession: A01421
R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Bxperientia 33, 324-325, 1977
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369
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A;Residues: 1-3 <AUD>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; hormone
F;3/Modified site: amidated carboxyl end (Gly) #status experimental
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A; Molecule type: protein
A; Residues: 1-3 <HSI>
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Carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrog claston-monoxide dehydrogenae (Specifes: Pseudomonas carboxydohydrogenae (Specifes: Pseudomonas carboxydohydrogenae (Spacession: PLO140 (Spa
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Cipate: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
CiAccession: A2666
R;Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-981, 1986
A;Grimmelikhuijzen, C.J.P.; Graff, D.
A;Reference number: A26666; MUID:87092339
A;Accession: A26666
A;Accession: A
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Yayosine—melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C;Species: Bos primigenius teurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accesation: A303
Biol. Chem. 264, 2175-2179, 1989
J. Biol. Chem. 264, 2175-2179, 1989
A;Accession of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
A;Reference number: A32039
A;Accession: A32039
A;Accession: A32039
A;Molecule type: protein
A;Respeimental source: brain
A;Respeimental source: brain
A;Experimental source: brain
A;Experimental source: brain
A;Experimental source: brain
A;Experimental source: brain
B;C;Cymords: amidated carboxyl end
E;4/Modified site: amidated carboxyl end (Gly) #status experimental
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A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
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Copyright (c) 1993 - 2000 Compugen Ltd.
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# ALIGNMENTS

Holly Polymerase Enhancing Factor (PEF) Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same ö Gaps ó ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
STREET: D.C.
ZITY: Washington
ZITY: D.C. Indels COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/008/822,774 Ouery Match 100.0%; Score 14; DB 4; L Best Local Similarity 100.0%; Pred. No. 9.1e-10; Matches 14; Conservative 0; Mismatches 0; ATTING DATE: 13. MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/POCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION: Sequence 54, Application US/08822774 Patent No. 6183997 GENERAL INFORMATION: TELEPHONE: (202) 628-8800 TELEFAX: (202) 628-8844 INFORMATION FOR SEQ ID NO: 54: SEQUENCE CHARACTERISTICS: 14 amino acids APPLICANT: HOGREFE, HOLL
TITLE OF INVENTION: BCLY
TITLE OF INVENTION: BCKT
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: internal MOLECULE TYPE: peptide HYPOTHETICAL: NO unknown amino acid ; FRAGMENT TYPE: US-08-822-774-54

1 FAWVDPGWDGNTLM 14

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Squence 98, Application US/08934222
Squence 98, Application US/08934222
Patent No. 5928866
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interacti
TITLE OF INVENTION: Site
TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 561;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PILOR APPLICATION DATA:
APPLICATION NUMBER: 03-MAY-1996
PILING DATE: 23-CT-1993
PRIOR APPLICATION NUMBER: 0.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY-AGENT INFORMATION:
NAME: ISACOSO, JOHN P.
NAME: ISACOSO, JOHN P.
NAME: ISACOSON, JOHN P.
                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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REFERENCE/DOCKET NUMBER: 040433/0148
                                                                                                                                                                                                 CURRENT ACCULATION DATA:
CURRENT APPLICATION NUMBER: US/08/559,492
FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REPERENCE/DOCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: ACCULATION OF TELECOMMUNICATION OF TELECOMMUNICATION: ACCULATION OF TELECOMMUNICATION: ACCULATION OF TELECOMMUNICATION OF TELECOMMUNICA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 561 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-559-492-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 WDGNTL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-08-934-222-98
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                                                                                                                                                                                                                                                                                        Sequence 44, Application US/08822774

Patent No. 6183997

CENERAL INFORMER:
PAPLICANT: HOGREE, Holly

TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes of INVENTION: ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C.

STRRET: 1200 G Street, N.W. Suite 700

CITT. Washington
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5-08-559-492-12
Sequence 12, Application US/08559492
Sequence 12, Application US/08559492
Sequence 12, Application US/08559492
Sequence 12, Application US/08559492
SEREAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: Street
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION NUMBER: 136,576
ATTORNEY/AGENT INPORMATION:
NAME: KULIK, DAVId J.
REGISTRATION NUMBER: 36,576
REPERBANCE/DOCKET NUMBER: 1486/43163
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFRAX: (202) 628-8800
TELEFRAX: (202) 628-8804
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: AMINO acids
TERMIN MAIN ACIDE TO THE TERMIN ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.6%; Score 11; DB 4;
100.0%; Pred. No. 2e-05;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.6
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
1 FAWYDPGWDGNTLM 14
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STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FAWVDPGWDGN 11
                                                                                                                                                                                                                            RESULT 2
US-08-822-774-44
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NS-09-207-621-98
Sequence 98, Application US/09207621
Sequence 98, Application US/09207621
Sequence 98, Application US/09207621
Sequence 98, Application US/09207621
Sequence 98, Application:
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE 153
CORRESPONDENCE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Sulte 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
APPLICATION NUMBER: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
FILING DATE: 29-OCT-1993
APPLICATION DATA:
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Isacson, John P.
• REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 98:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 5; I
Pred. No.
                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 98, Application US/08532818; Patent No. 5965698; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.7%; Scc.
100.0%; Pre
0; /
                                                                                                                                                                                                                                                                                                                COMPTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC COMPACION
OPERATING SYSTEM: PC CDOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 DGNTL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 DGNTL 11
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APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                      Length 13;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: US. 08/143,364
FILING DATE: 23-APR-1993
PRIOR APPLICATION NUMBER: US. 08/103,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%; Score 5; DB 2;
100.0%; Pred. No. 7.3;
tive 0; Mismatches
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    35.7%; Score 5; E
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 98, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
                                        ; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 amino acids
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                                                                                                                                                                    Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                      SEQUENCE CHARACTERISTICS
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserva
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7 DGNTL 11
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COUNTRY: USA
ZIP: 20007
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version MILES
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE: 21.APR.1994
FILING DATE: 21.APR.1994
FILING DATE: 21.APR.1994
FILING DATE: 29-OCT.1993
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-OCT.1993
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 23-APR.1994
APPLICATION NUMBER: US. 08/13,364
FILING DATE: 23-APR.1993
ATTORNEY/AGENT INFORMATION:
NUMBER: US. 08/051,741
FILING DATE: 23-APR.1993
ATTORNEY/AGENT INFORMATION:
NAME: LIGACOD. 100hn DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Innear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Isacson, John P.
REGISTRATION NUMBER: 3, 751
REFERENCE/DOCKET NUMBER: 040433/0148
REFERENCE/DOCKET NUMBER: 040433/0148
REFERENCE/DOCKET NUMBER: 040433/0148
REPERENCE/DOCKET NUMBER: 040433/0148
REPERENCE/DOCKET NUMBER: 040433/0148
TENGTH: 13 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 DGNTL 13
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7 DGNTL 11
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US-09-231-797-98
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US-08-934-224-98
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; TOPOLOGY:
US-08-934-224-98
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US-09-231-797-98
Sequence 98, Application US/09231797
Sequence 98, Application US/09231797
Sequence 98, Application US/09231797
Sequence 98, Application US/09231797
Sequence 98, Application Sequence 98, Application Sequence No. 6084066
GENERAL INFORMATION: Constraining Groups Which Flank A Proten-Protein Interaction STREET SULE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction STREET: Sulte 500, 3000 K Street NW
CITY: Washington STREET: Sulte 500, 3000 K Street NW
CITY: Washington STATE: DC
COUNTRY: USA
IPP C COMPUTER: DC
COMPUTER: DC
COMPUTER: PLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: PAPPL CATION DATA:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PELING DATE:
PERING DATE:
PELING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: US/08/532,818
FILING DATE: 21-APR-1994
PROR APPLICATION NUMBER: US.08/143,364
FILING DATE: 21-APR-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: US.08/13,364
FILING DATE: 23-CCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/13,364
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
ANALICATION NUMBER: US.08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.7%; Score 5; DB 3 Best Local Similarity 100.0%; Pred. No. 7; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
FILING DATE: 29-OCT-1993
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Sequence 98, Application US/09413492
Patent No. 6258550
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE SITE
NUMBER OF SEQUENCES: 153
CORRESPONDENCE SITE
STREET: Suite 500, 3000 K Street NW
Constraining Groups Which Flank A Protein-Protein Interacti
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                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
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APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
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33,751
เคล: 040433/0148
                                                                           ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U.S. 08/051,741 FILING DATE: 23-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ISacson, John P.
REGISTRATION NUMBER: 33,75
REFERENCE/DOCKET NUMBER: 0
INFORMATION FOR SEQ ID NO: 98:
                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
TITLE OF INVENTION: CO
TITLE OF INVENTION: SI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                             Sequence 98, Application US/08933843

Patent No. 611069
GENERAL INFORMATION:
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
TITLE OF INVENTION: Site
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Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
Length 13;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  DB 3;
                                         Mismatches
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APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: 0.S. 08/143,364
FILING DATE: 29-0CT-1993
FILING DATE: 29-0CT-1993
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
ATTONNEY,FAGENT INFORMATION:
NAME: 1sacson, John P.
REGISTRATION NUMBER: 33,751
                                                                                                                                                                                                                                                                                                                                                                                                                   E: Foley & Lardner
Suite 500, 3000 K Street NW
    Score 5;
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FILING DATE: 19-SEPT-1997
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100.0%; Pit
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      35.75
100.0%; Fr.
0;
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INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 5; Conservative
                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: PC
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                Best Local Similarity
Matches 5; Conserv
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7 DGNTL 11
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US-08-933-843-98
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US-08-934-223-98
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  Query Match
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Gaps

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RESULT 14
US-09-103-44-7
US-09-103-44-7
Sequence 7, Application US/09103434
Fatent No. 6133421
GENERAL INFORMATION:
APPLICANT: MARK S. PAYNE
FAPLICANT: MARK J. NELSON
TITLE OF INVENTION:
TITLE OF INVENTION: STEREOSPECIFIC NITRILE HYDRATASE AND AMIDASE ENZYMES AND
TITLE OF INVENTION: THE PRODUCTION OF CHIRAL AMIDES OF SEQUENCES:
TITLE OF INVENTION: THE PRODUCTION OF CHIRAL AMIDES AND ACIDS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE NOT DE NEMOURS AND COMPANY
CORRESPONDENCE NEMOURS NEMOURS AND COMPANY
CORRESPONDENCE NEMOURS NEMOURS AND COMPANY
CORRESPONDENCE NEMOURS NEMOU
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ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 1989BALE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER READABLE FORM:
MEDIUM TYPE: ELOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: MCROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
FLING DATE: US/09/103,434
FLING DATE: US/09/103,434
FLING DATE: OCTOBER 6, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FLOYEY, LINDA A.
REGISTRATION NUMBER: GV/04914
FILING DATE: OCTOBER 6, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FLOYEY, LINDA A.
REGISTRATION NUMBER: CR-9677
TELECOMMUNICATION INFORMATION:
NAME: FLOYEY, LINDA A.
TELECOMMUNICATION INFORMATION:
TELEFONEN: 302-892-173-4144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 5; DB 3
Pred. No. 8.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.7%;
nilarity 100.0%;
Conservative 6
                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: No
US-08-726-136-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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unknown
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                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: un
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Best Local Similarity
Matches 5; Conserv
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| AWVDP 13
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US-08-726-136-7
US-08-726-7
US-0
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COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,136
                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ISAGEON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/004914
FILING DATE: CCTOBER 6, 1995
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET WUMBER:
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pi
Matches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 DGNTL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 DGNTL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
US-09-413-492-98
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NUCLEIC ACID FRAGMENTS ENCODING
STEREOSPECIFIC NITRILE HYDRATASE AND AMIDASE ENZYMES AND
RECOMBINANT ORGANISMS EXPRESSING THOSE ENZYMES USEFUL FOR
THE PRODUCTION OF CHIRAL AMIDES AND ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                ö
35.7%; Score 5; DB 4; Length 16; 100.0%; Pred. No. 8.7; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 16;
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS ENCODIN TITLE OF INVENTION: STEREOSPECIFIC NITRILE HYDRATATION: STEREOSPECIFIC NITRILE HYDRATATION: RECOMBINANT ORGANISMS EXPRESSS TITLE OF INVENTION: THE PRODUCTION OF CHIRAL AMIDE NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
CITI: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19898

ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: ELOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/687,594
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9677
TELEPHONE: 302-8912
TELEPHONE: 302-892-8112
TELEPHONE: 302-973-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELAWARE : UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/726,136
                                                                                                                                                                                                                                                ; Sequence 7, Application US/09687594
; Patent No. 6251650
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               APPLICANT: ROBERT D. FALLON
APPLICANT: MARK S. PAYNE
APPLICANT: MARK J. NELSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 16 amino acids
Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid

STRANDEDNESS: unknow

TOPOLCGY: unknown

MOLECULE TYPE: peptid

HYPOTHETICAL: NO

US-09-687-594-7
                                                                                                               11111
9 AWVDP 13
                                                                                        2 AWVDP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DI
COUNTRY:
                                                                                                                                                                                                      RESULT 15
US-09-687-594-7
                                                                                                                                    g
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Search completed: January 31, 2002, 13:15:11 Job time: 92 sec

|||||| | AWVDP 13

δγ Dp

2 AWVDP 6

This Page Blank (uspto)

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein

January 31, 2002, 13:20:09; Run on:

Search time 78.64 Seconds (without alignments)
13.561 Million cell updates/sec

US-08-957-709-73

1 FAWVDPGWDGNTLM 14 score: Sequence: Perfect

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

0

Word size :

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 1   |       |       | •               |    | SUMMAKIES |                    | 20    |
|-----|-------|-------|-----------------|----|-----------|--------------------|-------|
| NO. | Score | Match | Match Length DB | DB | ID        | Description        |       |
| н   | 11    | 78.6  | 154             | 7  | G75030    | dCTP deaminase (EC |       |
| 7   | 11    | 78.6  |                 | 7  | E71216    | dCTP deaminase (EC |       |
| m   | 9     | 42.9  |                 | ď  | T31661    | hypothetical prote |       |
| 4   | 9     | 42.9  |                 | N  | T48164    | hypothetical prote | α     |
| 2   | 9     | 42.9  |                 | 7  | S77654    | isocitrate lyase ( |       |
| 9   | 9     | 42.9  |                 | 7  | H72485    | probable hydantoin | Ω     |
| 7   | 9     | 42.9  |                 | 7  | B72608    | probable hyuA APE1 |       |
| 80  | 9     | 42.9  | 803             | ~  | B82099    | surface antigen VC |       |
| 6   | 2     | 35.7  |                 | 7  | C44918    | lactococcin G pept | 24    |
| 10  | S     | 35.7  | 115             | 7  | E85592    | hypothetical prote | Œ     |
| 11  | S     | 35.7  |                 | 7  | B85883    | probable transcrip | ъ     |
| 12  | 5     | 35.7  |                 | 7  | A82306    | conserved hypothet | υ     |
| 13  | Ŋ     | 35.7  |                 | 7  | C72247    | ribosomal protein  | υ     |
| 14  | Ŋ     | 35.7  |                 | Н  | R5HQ25    | ribosomal protein  | υ     |
| 15  | ŝ     | 35.7  |                 | 7  | 830000    | ribosomal protein  | 24    |
| 16  | S     | 35.7  |                 | 7  | 829999    | ribosomal protein  |       |
| 17  | ς.    | 35.7  |                 | ~  | G81236    | smg protein, proba | Ω     |
| 18  | S     | 35.7  |                 | ď  | E70540    | hypothetical prote | 4     |
| 19  | ťΩ    | 35.7  |                 | 7  | A46618    | platelet aggregati | æ     |
| 20  | S     | 35.7  |                 | 7  | H83695    | deoxycytidine trip | ď     |
| 21  | 2     | 35.7  | 178             | 7  | S77760    | probable ABC-type  | Æ     |
| 22  | Ŋ     | 35.7  |                 | 7  | A33104    | tenebrosin C - sea | Ø     |
| 23  | S     | 35.7  |                 | 7  | B24479    | calcium-binding pr | A     |
| 24  | S     | 35.7  |                 | ~  | S13183    | calcium-binding pr | æ     |
| 25  | S     | 35.7  | 185             | 7  | S13184    | calcium-binding pr | ď     |
| 56  | 5     | 35.7  |                 | 0  | S13185    | calcium-binding pr | Ø     |
| 27  | 5     | 35.7  |                 | 0  | S54177    | PSR protein - Ente | υ     |
| 28  | Ŋ     | 35.7  | 200             | П  | A42725    | nitrile hydratase  | Ø     |
| 29  | 5     | 35.7  |                 | 7  | S19716    | nitrile hydratase  | ບ<br> |
|     |       |       |                 |    |           |                    |       |
|     |       |       |                 |    |           |                    |       |

| beta-crystallin Adequinatoxin II preconserved hypothetical protehypothetical protehypothetical protehypothetical protehypothetical protehypothetical protehorophyll a/b-bichlorophyll a/b-bichlorophyll a/b-bichlorophyll a/b-bichlorophyll a/b-bichlorophyll a/b-bichlorophyll a/b-bidhorophyll a/b-bi | • |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---|
| JH0603<br>JC4682<br>G59047<br>G59047<br>H70866<br>G75196<br>G75196<br>G704049<br>T702251<br>T702251<br>T702251<br>T702251<br>T702251<br>T702251<br>G8682<br>T702251<br>G8682<br>T702251<br>T702251<br>T702251<br>T702251<br>T702251                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |   |
| понапапапапапапа                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |   |
| 2210<br>2210<br>2210<br>2210<br>2210<br>2210<br>2210<br>2210                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |   |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |   |
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| 010000000000444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |   |

## ALIGNMENTS

| П |     |
|---|-----|
|   | 503 |

deaminase (EC 3.5.4.13) PAB1164 [similarity] - Pyrococcus abyssi (strain Orsay)

C.Species: Pyrococcus abyssi C.bate: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

C; Accession: G75030

R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A;Reference number: A75001 A;Accession: G75030

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-154 <KAW>

A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAB50685.1; PID:9545

A.Experimental source: strain Orsay C.Genetics: A.Gene: dcd; PAB1164 C.Superfamily: dCTP deaminase C.Keywords: hydrolase

ő Gaps ó Length 154; 0; Indels 78.6%; Score 11; DB 2; Le 100.0%; Pred. No. 1.1e-05; Live 0; Mismatches 0; Best Local Similarity 100. Matches 11; Conservative Query Match

1 FAWVDPGWDGN 11 à

91 FAWVDPGWDGN 101 οp

dCTP deaminase (EC 3.5.4.13) PH1997 [similarity] - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000 C;Accession: E71216

R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: E71216

A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A:Note: this accession replaces an interim accession for a sequence replaced by GenBa C;Genetics: A;Residues: 1-156 <KAW> A;Cross-references: GB:AP000007; NID:93236134; PIDN:BAA31124.1; PID:93258441 A; Experimental source: strain OT3

A;Gene: PH1997 C;Superfamily: dCTP deaminase

ő

Gaps

.; 0

C; Keywords: hydrolase

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C; Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 22-Jun-1999
C; Accession: 877654; 849515
F8 Faih; H: Colle, S.T.
Mol. Microbiol 16, 909-919, 1995
A; Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key
A; Reference number: 877652; MUID:96059637
A; Reference number: 877654
A; Status: nucleic acid sequence not shown; translation not shown
A; Rocious: Lofo ersis
A; Rocious: Lofo ersis
A; Rocious: EMBL:246257; NID:9559905; PIDN:CAA86357.1; PID:9559906
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Accession: H72485
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takanhya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. G. 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A. Accession: H72485
A. Accession: H72485
A. Accession: H72485
A. Accession: H72485
A. Accession: H72485
A. Accession: H72485
A. Residues: Treliminary
A. Accession: H72485
A. Residues: Telerance DDBJ. APPO00064; NID:95105945; PIDN:BAA81544.1; PID:95106233
A. Esperimental source: strain Kl
C:Genetics:
A. Genetics:
A. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BESULT 7
BIOLOBOLE HOUR APEL328 - Aeropyrum pernix (strain Kl)
C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 16-Feb-2001
C;Accession: B72608
B,Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, T. Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A;Reference number: A72450; MUD:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable hydantoinase APE2528 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%, Pred. No. 16; Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: aceA
C;Superfamily: isocitrate lyase
C;Keywords: carbon-carbon lyase; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: preliminary
A:Molecule type: DNA
A;Residues: 1-785 <KAW>
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348 AWVDPG 353
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148164

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15 Species: Arabidopsis thaliana (mouse-ear cress)

C; Species: Arabidopsis thaliana (mouse-ear cress)

C; Date: 20.4pt-2000

C; Accession: T48164

S: Bevan, M; Pohl, T; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.; Reference number: 22486

A; Reference number: 22486

A; Accession: T48164

A; Accession: T48164

A; Residues: preliminary

A; Molecule type: DNA

A; Residues: 1-401 < GEV>

A; Residues: 1-401 < GEV>

A; Residues: cultivar Columbia; BAC clone T1008

C; Genetics:

A; Map position: 5

A; Note: T1008.130
                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Fred. No. 6.3; Matches 6; Conservative 0; Mismatches
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Pred. No. 12;
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               91 FAWVDPGWDGN 101
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71 WVDPGW 76
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probable transcription regulator LYSR-type yfeR_2 [imported] - Escherichia coli (stra C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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Loginary Loginary (C; Burland, V; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Accession: B85883
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Chardson, D.; Ermolaevan, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                            C;Accession: E85592
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May Liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-115 <STO>
A;Cross-references: SSTOA
A;Cross-references: Strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-115 <STO>
A;Cross-references: STO>
A;Experimental source: strain O157:H7, substrain EDL933
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                                                                                                                             hypothetical protein 21051 [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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5, Conservative
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Best Local Similarity
`~hes 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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        7 AWVDP 11
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C;Species: Lactococcus lactis
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Dates: 01-Apr-1993
R;Nissen-Meyer, J; Holo, H.; Havarstein, L.S.; Sletten, K.; Nes, I.F.
J; Bacteriol. 174, 5686-5692, 1992
A;Title: A novel lactococcal bacteriocin whose activity depends on the complementary act
A;Reference number: A44918; MUID:92380946
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-803 <HEL>
A;Cross-references: GB:AE004297; GB:AE003852; NID:g9656810; PIDN:AAF95396.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80320.1; PID:g5105006
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1328
C;Superfamily: Pseudomonas D-amino acid hydantoin hydrolase (ATP-hydrolyzing) hyuA
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A;Note: sequence extracted from NCBI backbone (NCBIP:112782)
                                                                                                                                                                                   DB 2;
o. 20;
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100.0%; Pred. No. 22;
tive 0; Mismatches
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Live 0; Mismatches
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100.0%; Pred. No. 20;
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C;Superfamily: protective surface antigen D-15
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                          6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                      Query Match
Best Local Similarity
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448 AWVDPG 453
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Length 142;

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A;Introns: 5/1
C;Superfamily: rat ribosomal protein L23a
C;Reywords: protein biosynthesis; ribosome; RNA binding
                                                                                                                                                                                                                        Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 68; Matches 5; Conservative 0; Mismatches
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78 DGNTL 82
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Indexonal protein S11 - Thermotoga maritima (strain MSB8)

C.Species: Thermotoga maritima
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A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833
A;Accession: A82106
A;Status: preliminary
A;Melecule type: DNA
A;Residues: 1-122 cHEI>
A;Cross-references: GB.AE004143; GB.AE003852; NID:g9555003; PIDN:AAF93748.1; GSPDB:GN001
A;Cross-references: Serogroup 01; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCOS80
A;Gene: VCOS80
A;App position: 1
C;Superfamily: hypothetical protein H11656
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C; Superfamily: Escherichia coli ribosomal protein S11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.7%; Score 5; DB 2; Best Local Similarity 100.0%; Pred. No. 63; Matches 5; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 DGNTL 13
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Length 142; 0; Indels .

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Thu Jan 31 13:32:38 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:18:06; Search time 140.03 Seconds (without alignments) 7.406 Million cell updates/sec Run on:

US-08-957-709-73 14 1 FAWVDPGWDGNTLM 14 Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

/SIDSZ/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

SUMMARIES

|   | Description                 | Pyrococcus furisos | Polymerase enhanci | Peptide sequence d | Human novel protei | Rabbit complement | Porphorymonas ging | Porphorymonas ging | Schizophrenia-asso | Antiplatelet pepti | Porphyromonas ging | Nitrile hydratase |
|---|-----------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
|   | ID                          | AAW72849           | AAW72847           | AAY40052           | AAU14180           | AAW18311          | AAY34495           | AAY34369           | AAU15304           | AAR67105           | AAB14944           | AAW17823          |
|   | DB                          | 19                 | 19                 | 20                 | 22                 | 18                | 20                 | 20                 | 22                 | 15                 | 21                 | 18                |
|   | Query<br>Match Length DB ID | 14                 | 156                | 55                 | 106                | 561               | 891                | 899                | σ                  | 13                 | 13                 | 16                |
| æ | Query<br>Match              | 100.0              | 78.6               | 42.9               | 42.9               | 42.9              | 42.9               | 42.9               | 35.7               | 35.7               | 35.7               | 35.7              |
|   | Score                       | 14                 | 11                 | 9                  | 9                  | 9                 | 9                  | 9                  | S                  | 2                  | S                  | Ω.                |
|   | Result<br>No.               | -                  | 7                  | e                  | 4                  | S                 | 9                  | 7                  | æ                  | 6                  | 10                 | 11                |

| Random biotinylati | Biotinylation pept | Biotinylation pept | ø        | Human colon cancer | Human secreted pro | Human secreted pro | Arabidopsis thalia | #53      | #5552    | . Pro seguence of be | Bacteriocin deriva | Peptide #4822 enco | Peptide #4903 enco | Peptide #4666 enco | Human colon cancer | Murine OR-like pol | P.judaica pollen a | C glutamicum prote | C albicans apoptos | Alternatively spli | Human ORFX ORF2612 | Porphyromonas ging | Arabidopsis thalia | Arabidopsis thalla | Human colon cancer | B. burgdorferi ant | Moubatin platelet | Alternatively spli | Amino acid sequenc |          | Alpha subunit of p | e        | Mittell of Property |
|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|----------|--------------------|----------|---------------------|
| AAR65038           | AAW46641           | AAY 24499          | AAG73565 | AAG75841           | AAY00340           | AAY 00273          | AAG33744           | AAM18941 | AAM31515 | AAR49133             | AAR95262           | AAM18388           | AAM30866           | AAM05984           | AAG74048           | AAG72675           | AAW78444           | AAG92317           | AAG70915           | AAW59862           | AAB42848           | AAB14942           | AAG26215           | AAG42746           | AAG76100           | AAY19895           | AAR41488          | AAW59860           | AAW59857           | AAW01616 | AAR13831           | AAR13902 | AAW17816            |
| 16                 | 19                 | 20                 | 22       | 22                 | 20                 | 20                 | 21                 | 22       | 22       | 15                   | 17                 | 22                 | 22                 | 22                 | 22                 | 22                 | 20                 | 22                 | 22                 | 19                 | 21                 | 21                 | 21                 | 21                 | 22                 | 20                 | 14                | 19                 | 19                 | 17       | 12                 | 12       | α                   |
| 2.7                | 27                 | 27                 | 41       | 43                 | 54                 | 54                 | 55                 | 28       | 28       | 09                   | 74                 | 94                 | 94                 | 94                 | 121                | 123                | 131                | 135                | 142                | 143                | 148                | 148                | 159                | 159                | 159                | 164                | 171               | 172                | 175                | 193      | 200                | 207      | 210                 |
| 35.7               | 35.7               | 35.7               | 35.7     | 35.7               | 35.7               | 35.7               | 35.7               | 5        | 35.7     | 35.7                 | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 'n                 | 35.7               | 35.7               | 35.7               | ٠.<br>کا           | Š.                 | ς.                 | 35.7               | 35.7               | 35.7               | 35.7               | 5                 | 35.7               | 35.7               | 'n       | 35.7               | 35.7     | 75 7                |
| 2                  | Ŋ                  | Ŋ                  | S        | 2                  | Ŋ                  | Ŋ                  | 2                  | 2        | Ŋ        | 5                    | S                  | 5                  | 5                  | Ŋ                  | 2                  | 5                  | S                  | S                  | S                  | 2                  | Ŋ                  | 2                  | Ŋ                  | Ŋ                  | Ŋ                  | 2                  | Ŋ                 | 2                  | S                  | Ŋ        | 2                  | 2        | Ľ                   |
| 12                 | 13                 | 14                 | 15       | 16                 | . 17               | 18                 | 19                 | 20       | 21       | 22                   | 23                 | 24                 | 25                 | 26                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                | 40                 | 41                 | 42       | 43                 | 44       | 4.5                 |

# ALIGNMENTS

AAW72849 RESULT

AAW72849 standard; Peptide; 14 AA

AAW72849;

(first entry) 01-MAR-1999

Pyrococcus furisosus P45 dUTPase uridine-binding motif.

Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; sequencing; replication.

Pyrococcus furiosus strain DSM 3638.

WO9842860-A1.

01-OCT-1998

98WO-US05497 20-MAR-1998;

97US-0957709. 24-OCT-1997; 21-MAR-1997;

(STRA-) STRATAGENE.

Hansen CJ, Hogrefe H;

WPI; 1998-542284/46.

Polymerase enhancing factor proteins, extracts and complexes -improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

οy Q

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This is the amino acid sequence of the P45 component of the polymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638.

The sequence is predicted from a DNA sequence (see AAW67860) obtained from genomic DNA by PCR. P45 and P50 (see AAW72844) are the predominant components of PEF, which acts to enhance the activity of the furiosus DNA polymerase. P45 functions as a durpase, and can be tactions. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid replication, provided snowel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid for included are methods for identifying compositions with PEF activity, for purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Nucleic acid polymerase reactions can be enhanced (claimed) by mixing a nucleic acid template, at least I polymerase and a composition having polymerase enhancing activity. Kits are provided for replicating nucleic acids enhancing activity. Kits are provided for replicating nucleic acids sequencing or amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; gene therapy; cancer; tumor; fetal deficiency; neurodegenerative disorder; developmental abnormality; blood disorder; immune system disease; autoimmune disease; leukemia; inflammation; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; obesity; osteoporosis; arthritis; infection, AIDS; diabetes; asthma; connective tissue disorder; transplant rejection; sepsis; acne; psoriasis; cardiovascular disorder; reproductive disorder; food additive; food preservative; storage capability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.6%; Score 11; DB 19; Length 156; 100.0%; Pred. No. 6.8e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide sequence derived from a human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY40052 standard; Peptide; 55 AA.
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98US-0076052.
98US-0076053.
98US-0076054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US03939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.6
Best Local Similarity 100.
Matches 11; Conservative
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26-FEB-1998;
26-FEB-1998;
26-FEB-1998;
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                                                      This is the uridine-binding motif of the P45 component (see
AWA7281) of the polymerase enhancing factor (PEF) of Pyrococcus
furiosus DSM 3638. P45 has been identified as a duTpase that
the polymerase enhancing activity.
Sequences are provided (see
AWA72849-57) of the uridine-binding motifs of duTpases and dCTP
deaminases of P. furiosus, Methanococcus jannaschii, Desulfurolobus
ambivalans, Escherichia coli, yasat, human and herpesvirus; a
consensus (see AAW7284) is also provided. A claimed method of
the reaction in the presence of one or more of the following:
the reaction in the presence of one or more of the following:
a dUTPase, a protein that turns-over dUTP and a protein
having one or more of the sequences provided for replicating
claimed protein having DEF activity comprises one or more of
sequences given in AMY2848-57. A
claimed protein having DEF activity Comprises one or more of
claimed protein for Site-directed mutagenesis, for neglicating
cucled acids, for site-directed mutagenesis, for neglicating
sequencing or for amplification (preferably PCR or RT-PCR).
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improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100 0%; Score 14; DB 19; Length 14; Best Local Similarity 100.0%; Pred. No. 6e-09; Matches 14; Conservative 0; Mismatches 0; Indels
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2..15
/note= "N-terminal peptide used to generate
primers"
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      Claim 71; Page 47; 161pp; English
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97US-0822774
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N-PSDB; AAV63860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9842860-A1
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21-MAR-1997;
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AMY72847
XX AMY7847
XX AMY7847
XX X AMY78
XX Y POLY
XX AMY78
XX AMY7
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New human genes and the secreted polypeptides they encode, useful for

Rosen CA;

Ruben SM,

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                                                                                                                                      AAY40001-92 are derived from human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the polynucleotide. Specific uses include developing products for the diagnosis or treatment of cancer, tumors, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, sepsis, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, obesity, osteoporosis, arthritis, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, and reproductive disorders. The polypeptides or polynucleotides can also be used as food additives or preservatives, such as to increase or decrease storage capabilities, fat content, libid, protein, caraconders.
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diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 6.9
Live 0; Mismatches
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                                                                                           Disclosure; Page 44; 246pp; English
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Best Local Similarity 100.
Matches 6; Conservative
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of reatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides Polynucleotides of the invention are used as probes and production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumnour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and and many and survival of stem cells, as a contraceptive treating osteopoxosis and osteoarthritis, anaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
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100.0%; Pred. No. 12;
tive 0; Mismatches
Example 4; Page 556; 894pp; English
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Disulfide-bond 389..418
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N-PSDB; T688887.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 106 AA;
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91 awvdpg 96
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Gaps

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Porphorymonas gingivals (PG) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX9199 polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
                                                                           AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                        Length 891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DM, Margetts MB, Patterson
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                          Score 6; DB 2
Pred. No. 64;
0; Mismatches
                                     Claim 1; Page 476-477; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 332-333; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphorymonas gingivalis protein PG36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY34369 standard; Protein; 899 AA.
                                                                                                                                                                                                                                                                                                                                        42.9%; Sconsarity 100.0%; P. Conservative 0;
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Webb EA;
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97AU-0000139.
97AU-0001182.
98AU-0002264.
98AU-0002211.
98AU-0003128.
98AU-0003138.
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Ross BC, Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-385613/32.
N-PSDB; AAX91587.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; antigenic
                                                                                                                                                                                                                                                                               891. AA;
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359 fawydp 364
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31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
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23-APR-1998;
05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
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qinqivitis
                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                  A polypeptide (AAM18311) comprises rabbit complement C9. Chimeric proteins were constructed in which the segment of C9 corresponding to the putative CD59 binding site were interchanged between rabbit and human C9 (see also AAW18310). These were tested for haemolytic substn. of human C9 residues 334-415 into rabbit C9 resulted in a protein that was indistinguishable from human C9 is its sensitivity to inhibition by membrane CD59 in a protein that was indistinguishable from human C9 in its sensitivity to inhibition by CD59. When this same segment of human C9 was replaced by the corresponding rabbit sequence (a339-424), the unaffected by the presence of membrane CD59.
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                  nses
              Modulating binding of CD59 to C9 complement component - uses that mimics or binds the C9-specific motif, used to activate complement in tumour therapy or to treat complement mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Margetts MB, Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; DB 18; Length 561;
Pred. No. 44;
0; Mismatches 0; Indels
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                                                                                                               Disclosure; Page 36–38; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphorymonas gingivalis protein PG36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY34495 standard; Protein; 891 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pamatches 6; Conservative 0;
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Webb EA;
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97AU-0000839.
97AU-0001182.
98AU-0001546.
98AU-0002564.
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98AU-0003338.
98AU-0003654.
98AU-0004917.
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Ross BC, Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-385613/32.
N-PSDB; AAX91713.
                                                                                                                                                                                                                                                                                                                                                                                                   561 AA;
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| 190 wdgntl
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10-DEC-1997;
31-DEC-1997;
30-JAN-1998;
10-AAR-1998;
05-AAY-1998;
05-MAY-1998;
23-AAY-1998;
22-MAY-1998;
29-JUL-1998;
                                                                           inflammation
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AAY34495
AAY34495
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The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia. The method involves detecting the presence of Schizophrenia. The method scalares (SFS) and SCH. Associated Protein isoforms (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of the nearly administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFS, SFIS and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the program of the discrete for the severity for the secondary messengers are studied to diagnose SCH, monitor the correlates of treatment and as a secondary messengers.
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AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 20; Length 899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                   100.08; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; IP Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorder; neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 32; 160pp; English.
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2000US-0750395.
                                                                                                                                                                                                                                                                                                                                                                                                    42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                   especially gingivitis
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Best Local Similarity
                                                                                                                                                                                                                                                                                         899 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 fawvdp 372
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28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiplatelet peptide; leech antiplatelet protein; collagen receptor; mimic; interaction site; constrained conformation; aggregation; moubatin.
disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of neuropsychiatric disorders. AAU15114 AAU15502 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention.
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide homologue or analogue with constrained conformation - has proline residues flanking the interaction site to impart greater, or more stable, biological activity
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                                                                                                                                                                                                   Indels
                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antiplatelet peptide (APCol~M2) contg. proline brackets.
                                                                                                                                                               DB 22; Le
. 4.3e+05;
                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                  Score 5; D
Pred. No.
                                                                                                                                                                                                                                                                                                                                                   AAR67105 standard; peptide; 13 AA.
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                                                                                                                                                                  35.7%; 8
100.0%;
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                                                                                                                                                     Query Match
Best Local Similarity 100.
Sanca 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evans HJ, Kini RM;
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                                                                                                                  9 AA;
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                                                                                                                                                                                                                                  9 DGNTL 13
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1 dgntl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                   AAR67105;
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                                                                                                                      Sequence
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     8888888888
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DB 15; Length 13;

35.7%; Score 5;

Query Match

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Nucleic acid encoding stereospecific nitrile hydratase and amidase also transformed cells expressing these enzymes, useful for conversion of racemic nitrile compounds to chiral amide(s) and acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides (AAW17821-25) were obtd. by subjecting the purified nitrile hydratase alpha subunit (AAW17886) of Pseudomonas putida NRRL 18668 to cyanogen bromide, TPCK-treated trypsin and AspN protease digestions. Peptides (AAW17856-29) of the beta subunit (AAW17817) were also obtd. PCR primers (AAW17843-44) based on the peptides were used to amplify 18668 genomic DNA. A partial nitrile hydratase sequence (AAM56443-45) was obtd. and used as a probe to identify the full-length coding sequence (AAM56440).
                                                                                                                                                                                                         Nitrile hydratase; stereospecific enzyme; chiral compound; amide
                                                                                                                                                                           Nitrile hydratase alpha subunit partial sequence.
                                                                                                                                                                                                                                       Pseudomonas putida strain NRRL 18668
                                                                                                                                                                                                                                                                                                                                                                                                       Ξ.
                                                                            AAW17823 standard; Peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 49; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson MJ, Payne MS;
                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Random biotinylation peptide 7.
                                                                                                                                                                                                                                                                                                                                                                       95US-0004914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-226208/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA;
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9 awvdp 13
                                                                                                                                                                                                                                                                                                                                      03-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                       06-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AWVDP 6
                                                                                                                                                                                                                                                                                                        10-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fallon RD,
                                                                                                              AAW17823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR65038;
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                                               11
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AAR65038
                                                                                                                q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of twenty overlapping peptides corresponding to the N-terminal 148 residues of the PrR27 adhesin from Porphyromonas gingivalis. Antibodies directed towards the Prt27 adhesin were found to provide protection against periodontitis in a human patient and found to immunoprotected mice. The peptides were used for epitope mapping of the PrR27 adhesin. Peptides comprising at least one P. gingivalis epitope particularly periodontitis, which is associated with P. gingivalis epitope particularly periodontitis, which is associated with P. gingivalis infection. They may lass be used to generate formulations protein specific and peptides are useful as immunogens in vaccine formulations protein specific and peptides per opticional or monoclonal antibodies. The peptides and antibodies against the peptides can be used in diagnostic tests to detect P. gingivalis infection. The antibodies can also be used in oral compositions such as toothpaste and mouthwash to neutralise the antigen and prevent disease.
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                                                                                                                                                                                                                                                                                                      Porphyromonas gingivalis; protective epitope; antiinflammatory; vaccine; periodontal disease; periodontitis; immunogen; infection; PrtR27 adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New compositions comprising at least one peptide with an epitope of Arg-specific proteinase associated with Lys-specific proteinase protein complex for treating and preventing periodontitis-associated Porphyromonas ginglyalis
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels
                              0; Indels
             Pred. No. 26;
Mismatches
                                                                                                                                                                                                                                                                        Porphyromonas gingivalis PrtR27 peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYME ) UNIV MELBOURNE.
(CSLC-) CSL LTD.
(VICT-) VICTORIAN DAIRY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 21; 62pp; English.
                                                                                                                                                                       AAB14944 standard; peptide; 13 AA.
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100.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000; 2000WO-AU00142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99AU-0008939
                                                                                                                                                                                                                                         (first entry)
             Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                      Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Brien-Simpson NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               API; 2000-579275/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
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7 dgntl 11
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                                                                                                                                                                                                         AAB14944;
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                                                                                                                                            RESULT 10
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Gaps
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0
                                                                                                                                                                                        biotinylation; peptide; recombinant; fusion protein; small; specific; defined; purification; BirA; enzyme; biotin.
Length 16;
                    0; Indels
35.7%; Score 5; DB 18;
100.0%; Pred. No. 30;
iive 0; Mismatches
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                          AAR65038 standard; Peptide; 27 AA.
                                                                                                                                                                                                                       Synthetic
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28-JUL-1994;

Schatz PJ;

WO9504069-A 09-FEB-1995

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derived from a library constructed to express peptides of the generic sequence AAM46623. The library was constructed using oligonucleotides AAV16118-20. The peptides contain a biotinylatable sequence motif, recognised by a biotinylation enzyme, e.g. biotini-protein ligase (BirA). The C or N terminus of the peptides can be covalently coupled to a protein that is incapable of being biotinylated by a biotin ligase. The peptides can be biotinylated in vitro or in vivo, especially with BirA biotin ligase, and used for the purification, immobilisation, labelling or detection of proteins.
                                                                                                                                         Peptides AAW46635-46 are non-naturally occurring biotinylation peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for the identification and biotinylation of proteins synthesized by recombinant DNA techniques in vivo with a biotinylation peptide of less than 50 amino acids. The method comprises: (a) on the surface of a substrate, providing a fusion protein comprising a recombinant protein and a peptide defined by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotinylation enzyme; biotin-protein ligase; BirA; labelling;
biotin carboxyl carrier protein; BCCP; Escherichia coli;
fusion protein; identification; purification; diagnosis; research.
                                       Peptide(s) that can be biotinylated by biotin ligase - and fusion proteins containing them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins synthesized by
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
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100.0%; Pred. No. 46;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification and biotinylation of recombinant DNA techniques in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biotinylation peptide SEQ ID NO:20.
                                                                                                 Claim 3; Column 65; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY24499 standard; peptide; 27 AA.
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97US-0959512.
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WPI; 1998-178542/16
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                           27 AA;
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|pgwdg 10
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                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      A library of small, efficient peptide biotinylation sequences (AAR65032-46) was generated by using a generic peptide (AAR65020) and a system known as the 'peptides on plasmids" system. At some positions in the sequences, no clear consensus is apparent. At other residues, however, clear trends emerge. A protein can be biotinylated by constructing a recombinant DNA expression vector encoding a fusion protein, comprising a protein and a biotinylation peptide. A host cell, eg. E. coli is transformed with the vector and is cultured in the presence of biotin and a biotinylation enzyme, eg. BirA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biotinylation peptide, biotinylation enzyme; biotin-protein ligase; BirA; biotin ligase; biotin; purification; immobilisation; labelling; detection; protein.
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                                                                                                                                                                                                                                                                                                                                      Production of biotinylated proteins by expression of a recombinant DNA vector - which encodes a fusion protein comprising a protein and a biotinylated peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biotinylation peptide isolated from random library 1.
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100.0%; Pred. No. 46;
tive 0; Mismatches
                  /note= "biotin-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 136; 146pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW46641 standard; peptide; 27 AA.
                                                                                                                                                                                                                        (AFFY-) AFFYMAX TECHNOLOGIES NV
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nes 5; Conservative
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Modified-site
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(AFFY-) AFFYMAX TECHNOLOGIES NV

Schatz PJ;

03-FEB-1995;

03-MAR-1998

US5723584-A

Synthetic.

28-MAY-1998

AAW46641;

AAW46641 ID AAW4

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Sequence

Query Match Best Local 3

Matches

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sequence given in AAY24492, where the peptide is capable of being blotinylated by a biotin ligase at the lysine residue adjacent to position 8 and is 13-50 as in length; (b) in a predefined region of the surface of the substrate, contacting the fusion protein with an enzyme; and (c) determining whether the fusion protein with an enzyme; the method allows the identification and purification of biotinylated enzymes e.g. BirA. The method is also useful in research and diagnostic applications. The method uses small but specific peptides, allowing the labelling of a protein at a defined site, this provides improved immobilization and avoids the use of antibodies. AAY2493 to AAY24548, and AAY2929 to AAY29312 represent specifically claimed examples of biotinylation peptides for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection;
colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                             35.7%; Score 5; DB 20; Length 27; 100.0%; Pred. No. 46; 0; Indels cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein SEQ ID NO:4329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 6175-6176; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG73565 standard; Protein; 41 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Barash SC, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0157137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
Matches 5; Conservative
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N-PSDB; AAH32996.
                                                                                                                                                                                                                                                    27 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         6 PGWDG 10
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-2001
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to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.

NB. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                    Query Match 35.7%; Score 5; DB 22; Length 41; Best Local Similarity 100.0%; Pred. No. 64; Matches 5; Conservative 0; Mismatches 0; Indels Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: January 31, 2002, 13:18:07
Job time: 168 sec
                                                                                                                                                                                                41 AA;
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20 dgnt1 24
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:37:38 ; Search time 130.99 Seconds (without alignments) 15.633 Million cell updates/sec Run on:

US-08-957-709-73 14 1 FAWVDPGWDGNTLM 14 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

473505 seqs, 146272329 residues Searched:

Word size :

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SPTREMBL\_17:\* Database :

sp\_phage:\*
 sp\_plant:\*
 sp\_rodent:\*
 sp\_virus:\*
 sp\_vertebrate:\*
 sp\_unclassified:\* sp\_arches:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_organelle:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description                   | P91585 ciona intes | Q9m031 arabidopsis | Q91vp4 arabidopsis | Q9y8v6 aeropyrum p | Q9ycc8 aeropyrum p | Q9kpw0 vibrio chol | Q9r414 helicobacte | Q27101 trichomonas | Q42130 arabidopsis | Q45127 bacillus fi | 062727 canis famil | P93074 bambusa sp. | Q27100 trichomonas | Q9kuel vibrio chol | Q9a8k7 caulobacter | Q9amn4 clostridium | Q9jr28 neisseria m | 006619 mycobacteri | 086213 enterococcu |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΙΩ                            | P91585             | Q9M031             | 09LVP4             | 09Y8V6             | Q9YCC8             | Q9KPW0             | Q9R4L4             | 027101             | 042130             | 045127             | 062727             | ) P93074           | Q27100             | Q9KUE1             | Q9A8K7             | Q9AMN4             | Q9JR28             | 006619             | 086213             |
|           | ogth DB                       | 190 5              | 401 10             | 412 10             | 687 1              | 785 1              | 803 2              | 21 2               | 51 5               | 64 10              | 92 2               | 93 6               | 104 10             | 116 5              | 122 2              | 131 2              | 147 2              | 153 2              | 169 2              | 171 2              |
|           | %<br>Query<br>Match Length DB | 42.9               | 42.9               | 42.9               | 42.9               | 42.9               | 42.9               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               |
|           | Score                         | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | ß                  | ស                  | S                  | S                  | 5                  | 5                  | S                  | S                  | Ŋ                  | S                  | S                  | Ŋ                  | S                  |
|           | Result<br>No.                 | 1                  | 7                  | e                  | 4                  | ស                  | 9                  | 7                  | 80                 | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 |

| Q9puf8 xenopus lae Q9fffy3 bacillus ha Q49088 mycoplasma Q9x2x0 rhodospiril Q9aqf5 clostridium Q471781 enterococcu Q97177 streptomyce C26239 methanobact Q9bx28 mycobacteri Q9bx28 mycobacteri Q923x2 pseudomonas Q923y9 streptomyce C53300 mycobacteri Q9r704 agrobacteri Q9r704 agrobacteri Q9x49 haltobacteri Q9x70 mycobacteri Q9x60 oncorhynchu Q9x60 arabidosceri | Q9cf98 lactococcus<br>Q41746 zea mays (m<br>Q41747 zea mays (m |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|
| 177 13 09PUFB<br>177 2 09KFV3<br>1178 2 0942088<br>190 2 094220<br>193 2 09408F5<br>199 2 094777<br>220 1 026239<br>223 4 094276<br>235 2 09477<br>235 2 09477<br>235 2 09470<br>236 2 097704<br>248 1 09CVB0<br>248 1 09CVB0<br>248 2 097704<br>248 1 09CVB0<br>248 1 09CVB0<br>248 1 09CVB0<br>255 2 094749<br>256 13 09W680<br>275 1 09H060<br>277 5 09U9F7<br>280 10 09XFB3                                                                                                                                                                                                                                   | 10 01                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | m m m                                                          |
| 22222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 6 4 4<br>73                                                    |

## ALIGNMENTS

|                  |              |                                       |          |                    | Phlebobranchia;                       |                  |       |                    | Tweedie S.;  |                                   |                           |                            |                  |                             |                       |                         |                        |                                | 0; Gaps         |            |    |        |        |              |             |                                                        |
|------------------|--------------|---------------------------------------|----------|--------------------|---------------------------------------|------------------|-------|--------------------|--------------|-----------------------------------|---------------------------|----------------------------|------------------|-----------------------------|-----------------------|-------------------------|------------------------|--------------------------------|-----------------|------------|----|--------|--------|--------------|-------------|--------------------------------------------------------|
|                  |              | Created) Last sequence update)        | apare)   |                    | Chordata; Urochordata; Ascidiacea; Ph |                  |       |                    |              | 3J databases.                     | ′                         |                            | 1.               |                             |                       | F8934267DADAD27E CRC64; | 100cth 100.            |                                | 0; Indels       |            |    |        |        |              |             | Last sequence update)<br>Last annotation update)<br>N. |
|                  | 190 AA.      | nce up                                | acton    |                    | ata; A                                |                  |       |                    | tgeb 9       | nk/DDI                            |                           |                            | UNKNOWN          |                             |                       | 7 DADAI                 | g                      | 7.8                            |                 |            |    |        |        | 401 AA.      |             | nce ug<br>ation                                        |
|                  |              | ed)<br>segue                          |          |                    | chord                                 |                  |       |                    | , Lei        | GenBa                             | (                         | . u                        |                  | 2; 1                        |                       | 93426                   |                        | Pred No.                       | Mismatches      |            |    |        |        |              | ed)         | seque                                                  |
|                  | PRT;         | Created)<br>Last seq                  |          |                    | ; Uro                                 |                  |       |                    | J.M.         | EMBL/                             | 4040                      | pilata                     | ATASE            | ATASE                       |                       |                         | 01000                  | 2                              | ;               |            |    |        |        | PRT;         | Created)    | st                                                     |
|                  | PRELIMINARY; | (TrEMBLrel. 03, 0) (TrEMBLrel. 03, 1) |          |                    | oa;                                   | ona.             | , 19; | M.A.               |              | EC-1996) to the EMBL/GenBank/DDBJ | EMBL; 283/60; CABU6U5I.1; | TPROUGS40; US_PHOSPHACASE. | 0383; TYR PHOSPH | PS50056, TYR_PHOSPHATASE_2; | 12; PTPc_DSPc; 1      | 190 AA; 21292 MW;       | . 00<br>00<br>00<br>00 |                                | 6; Conservative | 8          | 92 |        |        | PRELIMINARY; | 15,         | (TrembLrel. 13,<br>(TrembLrel. 17,<br>45 3 KDA PROTET  |
| LT 1<br>85       | 91585        | 01-MAY-1997<br>01-MAY-1997            | COS41.7. | Ciona intestinalis | Eukaryota; Metazoa;                   | Cionidae; Ciona. | [1]   | SEQUENCE FROM N.A. | Bird A.P., C | Submitted (DI                     | EMBL; 283/60              | InterPro; 1P               | 14               | PROSITE; PS5                | SMART; SM00012; PTPC_ | SEQUENCE 19             | W wood                 | Query March<br>Best Local Simi | es 6;           | 3 WVDPGW 8 | ~  | LT 2   | 31     | Q9M031       | 01-0CT-2000 | 01-0CT-2000<br>01-JUN-2001<br>HYPOTHETICAL             |
| RESULT<br>P91585 | O S          | 555                                   | D D      | SO                 | 8                                     | 88               | R C   | RP                 | RA           | R.                                | ž č                       | 2 5                        | Z Z              | DR                          | DR                    | ÖS.                     | ā                      | D A                            | W G             | οy         | QΩ | RESULT | Q9M031 | Q F          | PE          | 7 7 2                                                  |

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STRAIN-KI.

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M. BEDLINE-9910339; PubMed=10382966;

R. KAWATABAYSAI Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,

A. Jin.no K. Takahiashi M., Baka S.-I., Ankai A., Kosugi H.,

A. Hosoyama A., Fikui S., Nagai Y., Nishijima K., Nakazawa H.,

A. Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

A. Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

A. Takamiya M., Sako Y., Kikuchi H.,

Complete genome sequence of an aerobic hyper-thermophilic

T. Crenarchaeon, Aeropyrum pernix Kl.";

DNA Res. 6:83-101(1999).

I. DNA Res. 6:83-101(1999).

R. Brail, Hydantoinase_A.

R. InterPro: IPR003821; Hydantoinase_A.

R. Complete protecome.

Complete protecome.
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 785 AA; 85156 MW; 493F9D153A121FF7 CRC64;
      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
687AA LONG HYPOTHETICAL HYDANTOLNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APEJA2A LONG HYPOTHETICAL HYUA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             785 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; L
Pred. No.
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100.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                         Aeropyrum.
NCBI_TaxID=56636;
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NCBI_TaxID=56636;
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348 AWVDPG 353
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Q9YCC8;
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Q9YCC8
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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091VP4 PRELIMINARY; PRT; 412 AA.
091VP4 001 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
6B|AAD43172.1.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota: Viridiphantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosidas II; Erassicales; Brassicaceae; Arabidopsis.
T1008_130.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                             EBOUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 10; Length 401;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

42.9%; Score 6; DB 10; Length 412;
Best Local Similarity 100.0%; pract. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL161746; CAB81925.1;
Hypothetical protein
SEQUENCE 401 AA; 45306 MW; 9302E88BBB7D9F2B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:131-135(2000).
EMBL; AB018121; BAB01991.1; -.
SEQUENCE 412 AA; 47406 MW; 237AC10B0A67B44A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%; Scor.
100.0%; Pred. No. 10.
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MEDLINE-20277480; Pubmed-10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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235 DGNTLM 240
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392 FAWVDP 397
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Q9Y8V6;
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RESULT 4
09Y8V6
ID 09Y8V6
AC 09Y8V6

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Gaps

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Length 687; 0; Indels Page

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Gaps

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Matches

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=NIH-C1, ATCC 30001;
BEDLINE-506081479; Pubmed-7490769;.
Keeling P.J., Doolittie W.F.;
"Concerted evolution in protists: recent homogenization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                  0; Indels
Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=WHOLE SEEDLINGS OF A. THALIANA ECOTYPE COLUMBIA;
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Parabasalidea; Trichomonadida; Trichomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 51
51 AA; 947D7ED017FFF26C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GUANINE NUCLEOTIDE-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyubiquitin gene in Trichomonas vaginalis."; J. Mol. Evol. 41:556-562(1995).
EMBL; U28013; AAC46941.1; -...
35.7%; Score 5; DB 2; 100.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 5; DB 5;
100.0%; Pred. No. 40;
tive 0; Mismatches
                                                                                                                                                                                          51 AA.
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                                  0; Mismatches
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PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 2.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 226552; CAA81323.1; -.
Mendel; 16252; Arath;1350;16252.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    Trichomonas vaginalis
                                                                                                                                                                                                                                                                                UBIQUITIN (FRAGMENT).
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12 WDGNT 16
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STRAILNEL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
   Gaps
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Hughes N.J., Chalk P.A., Clayton C.L., Kelly D.J.;
"Identification of carboxylation enzymes and characterization of a
novel four-subunit pyruvate:flavodoxin oxidoreductase from
                                                                                                                                                                                                                                                                            Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY_2000 (TrEMBLrel. 13, Last sequence update)
01-MAY_2000 (TrEMBLrel. 14, Last annotation update)
PYRUVATE:FLAVODOXIN OXIDOREDUCTASE (EC 1.2.7.1) (FRAGMENT).
Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of both chromosomes of the cholera pathogen Vibrio
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.";
J. Bacteriol. 177:3953-3959(1995).
SEQUENCE 21 AA; 2319 MW; 127528027BAE8143 CRC64;
                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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100.0%; Pred. No. 26;
ive 0; Mismatches
                                                                                                                                                          803 AA.
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   Mismatches
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Pfam; PF01103; Bac_surface_Ag; 1.
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                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, SURFACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.98;
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Sina 6; Conservative
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448 AWVDPG 453
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                                  2 AWVDPG 7
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SEQUENCE FROM N.A.

MaDLINE-297019052; PubMed-8865668;

Mathews S., Sharrock R.A.;

"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot anglosperms.";
                                                                                                                                                                                                                                                                                                                                                                    Bambusa sp. (bamboo).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bambusoideae; Bambuseae; Bambusa.
NCBI_TaxID=48938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%; Score 5; DB 10; Length 104; Best Local Similarity 100.0%; Pred. No. 73; Matches 5; Conservative 0; Mismatches 0; Indels
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NON_TER 104

104 AA; 11473 MW; C42A5C80874EA01E CRC64;
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Eukaryota, Parabasalidea; Trichomonadida; Trichomonas.
NCBL_Taxnb=572:
                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PHYTOCHROME (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          027100 PRELIMINARY; PRT; 116 AA. 027100; 01-100-1996 (TEMBLEEL. 01, Created) 01-NOV-1996 (TEMBLEEL. 01, Last sequence update) 01-JUN-2001 (TEMBLEEL. 17, Last annotation update) UBIQUITIN (FRAGMENT).
                                                                                                                                     104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMOL BIOL EVOL 13:1141-1150(1996).

EMBL: U61199; AB441983.1;

MURCHOL 30961; Bamsp.2331; 30961.

MURCHOL 180619; Bytochrome.

InterPro: PR001294; Phytochrome.

InterPro: PR003018; GAF.

PROSITE; PS50046; PHYTOCHROME_1; 1.
                                                                                                                                     PRT;
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75 DGNTL 79
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027100
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P93074
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
1CA.
Canis familiaris (Dog).
Canis familiaris (Dog).
Canis familiaris (Dog).
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels
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Submitted (AUG-1955) to the EMBL/GenBank/DDBJ databases.
EMBL: U33209; AAA75478.1; -.
SEQUENCE 92 AA; 10041 MW; 7BDB64290196CFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFG14875; AAC05880.1; -1.
NON_TER 1 1 1
NON_TER 93 AA: 10416 MW; 36481D46FC8C8535 CRC64;
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1 1
64 AA; 6945 MW; 5735E41922E70993 CRC64;
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045127;
045127;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
SIMILAR TO VIBRIO PARAHAEMOLYTICUS MOTX PROTEIN.
Bacillus firmus
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.7%; Score 5; DB 6; Best Local Similarity 100.0%, Pred. No. 66; Matches 5; Conservative 0; Mismatches
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SEQUENCE FROM N.A.
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63 DGNTL 67
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56 PGWDG 60
NON_TER
SEQUENCE
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AC 045127
AC 045127
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STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Medlaberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                            116 116
116 AA; 13155 MW; 2DDF3A7CC4DFF75A CRC64;
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Complete proteome.
SEQUENCE 122 Aa; 14186 MW; 86F1A87329669BC2 CRC64;
                                                                                                                                                                                                                                                               01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROFEIN VCOS80.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MUTT/NUDIX FAMILY PROTEIN.
                                                                               35.7%; Score 5; DB 5;
100.0%; Pred. No. 80;
tive 0; Mismatches
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100.0%; Pred. No. 83;
Live 0; Mismatches
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Nuclear protein; Ubiquitin conjugation.
NON_TER 1 1 1 16
NON_TER 116 116
SEQUENCE 116 AA; 13155 MW; 2DDF3A7C
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EMBL; AE004143; AAF93748.1; -.
TIGR; VC0580; -.
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                                                                 Query Match
Best Local Similarity 100.00
--hes 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Caulobacter crescentus.
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                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae.
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|DGNTL 50
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09A8K7
1D 09A8K7
DT 01-JUN
DT 01-JUN
DE MUTT/NN
DE MUTT/NN
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OC CAULOD
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NY NEILTR
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MEDLINE-21173698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Ailey M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Avton W.S., Gybnen C., Phadke N.D., Ely B., DeBoy R.T., Dodson W.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
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                                                                                                                                                                                                                                                                                                                                         5CFDB4354DCF1491 CRC64;
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100.0%; Pred. No. 89;
tive 0; Mismatches
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Best Local Similarity
Matches 5; Conserv
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Thu Jan 31 13:32:40 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:39:16 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec Run on:

US-08-957-709-73 14 1 FAWVDPGWDGNTLM 14

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

0 Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description         | 09uxs8 pyrococcus 057706 pyrococcus P4831 mycobacteril P4831 mycobacteril P4892 lactococcus 09x14 thermotoga 09tum8 parietaria 006399 salmonella P48045 kluyveromyc P08792 pichia jadi 09nbz5 onchocerca 00469 ornithodoro 009169 r glucagon- P41534 g glucagon- P42706 branchiosto P42706 branchiosto P42706 branchiosto P42719 actinia equ 093109 actinia equ 093304 streptococc 074683 candida gla P42418 bacillus su 027434 leishmania P53306 leishmania P53306 leishmania P53306 leishmania P53306 pseudomonas P53430 monascus an P50160 zea mays (m |
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| SUMMARIES           | DCC_PYRAB DCC_PYRAB DCC_PYRAB CCO9_RABIT ACEA_MYCLE LCGB_LACLA RS11_THEMA PRO2_PARJU YEDD_SALTY RR25_PICJA OAZ_ONCYO MOUB_ORNWO MOUB_ORNWO MOUB_ORNWO MOUB_CRANRI PACA_CHICK SCP1_BRALA NHAA_PSECL NHAA_PSECL NHAA_PSECL NHAA_PSECU ORD_BOVIN NHAA_PSECU NHAA_PSECU ORD_BOVIN TRED_CANGA TOLL_BIMA ASSX_ECOLI TWOF_PSEME TS2_MAIZE YE91_SYNY3                                                                                                                                                                                                                         |
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| %<br>Query<br>Match | 78.66<br>42.99<br>9.85.7.7.99<br>9.85.7.7.7.99<br>9.85.7.7.7.7.99<br>9.85.7.7.7.7.99<br>9.85.7.7.7.99<br>9.85.7.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99<br>9.85.7.7.99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Score               | Η Η<br>Η Α Φ Φ Ρυ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| P46057 trichosporo<br>P25035 oncorhynchu | P11408 moraxella s<br>P08470 salmonella | P52605 escherichia<br>007035 mycobacteri | P24465 persea amer<br>P21948 escherichia | P19147 serratia ma<br>P75835 escherichia |           | P48770 equus cabal |
|------------------------------------------|-----------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|-----------|--------------------|
| MLE_TRICU<br>P53_ONCMY                   | MTM1_MORSP<br>PTSB_SALTY                | KLB2_ECOLI<br>YV30_MYCTU                 | CP71_PERAE<br>PPB_ESCFE                  | PPB_SERMA                                | NIR_PHOLA | CO9_HORSE          |
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| 373<br>396                               | 418                                     | 461<br>463                               | 471                                      | 475                                      | 510       | 547                |
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| 34<br>35                                 | 36                                      | 38<br>30                                 | 40<br>41                                 | 42                                       | 44        | 45                 |

### ALIGNMENTS

Gaps ; Query Match 78.6%; Score 11; DB 1; Length 154; Best Local Similarity 100.0%; Pred. No. 7.1e-06; Matches 11; Conservative 0; Mismatches 0; Indels

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91 FAWVDPGWDGN 101 1 FAWVDPGWDGN 11 οy qq

DCD\_PYRHO STANDARD; PRT; 156 AA. 057706; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) RESULT 2 DCD\_PYRHO ID DCD\_PYR AC 057706; DT 20-AUG-DT 20-AUG-DT 20-AUG-

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TYP TYPE-1.
LDL-RECEPTOR CLASS A.
POTENTIAL.
EGF-LIKE.
BY SIMILARITY.
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   C8, AND TO PERFORIN.
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ACEA_MYCLE
ACE STANDARD; PRT; 606 AA.

ACEA_MYCLE
ACEA_
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-:- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C8, AND TC
-:- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
-:- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-:- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 22-34.
STRAIN-NEW EZELAND WHITE; TISSUE-Liver;
MUEDLINE-95181293; PubMed-7533152;
Hueslar T. Lockert D.H., Raufman K.M., Sodetz J.M., Sims P.J.;
"Chimeras of human complement C9 reeveal the site recognized by
complement regulatory protein CD59."
J. Biol. Chem. 270:3483-3486(1995).
J. Biol. Chem. 270:3483-3486(1995).
B.ADDED IN THE ASEMBLY OF THE MEMBRANE ATTACK COMPLEX. IT IS
ABLE TO ENTER LIPID BILAYERS, FORMING TRANSMEMBRANE CHANNELS.
                                                             Pyrococcus horikoshii.
Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=53953;
   PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 34). Last sequence update)
01-FEB-1996 (Rel. 40). Last annotation update)
COMPLEMENT COMPONENT C9 PRECURSOR.
C9.
C9.
C0ryctolagus cuniculus (Rabbit).
Eukaryotes, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria: Lagomorpha; Leporidae; Oryctolagus.
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SEQUENCE 156 AA; 17871 MW; 96B2C2C50393A985 CRC64;
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InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
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ProDom; PD004900; dCTP_deaminse; 1.
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                      DEAMINASE).
DCD OR PH1997.
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P48747;
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(09_RABIT 1

(009_RABIT 2

AC P48747, 2

AC P48747, 2

AC P48747, 2

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEQUENCE FOUR 3109;
MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Haldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
"Evidence of Thermotoga maritima.",
Nature 399:323-329(1999).
                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
BACTERIOCIN LACTOCCOCIN G. BETA SUBUNIT.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRECT TRNA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LAI LOBE OF THE SMALL SUBUNIT (BY SIMILARITY).
SIMILARITY: BELONGS TO THE S11P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                               PIR; C44918; C44918.
Antibiotic; Bacteriocin.
SEQUENCE 35 AA; 4110 MW; 76109F8BB0C489D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY-2000 (Rel. 39, Last sequence update)
AUG-2001 (Rel. 40, Last annotation update)
RIBOSOMAL PROTEIN S11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 5; DB 1; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotogales; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity luv...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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RS11_THEMA
Q9X114;
30-MAY-2000 (Rel. 39, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                  STRAIN=LMG 2081;
                                                                                                                                        NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPSK OR TM1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AWVDP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AWVDP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                           "The Mycobacterium leprae genome: systematic sequence analysis identifies key catebolic enzymes, ATP-dependent transport systems and an novel polA locus associated with genomic variability."; MOI. Microbiol. 16:909-919(1995).
                                                                                                                                                                                                                                                                           MEDLINE-2112372; PubMed=11234002;
MEDLINE-21123732; PubMed=11234002;
Meeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M.,
Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                             Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00463; ICL; 2.
ProDom; PD001857; Isocit_lyase; 1.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
-i- CAUTION: REF. SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFT IN POSITION 569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 606;
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                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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R -> L (IN REF. 1).

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D82CCCADD6B6D384 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000918; Isocit_lyase.
                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96059637; PubMed=7476188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67600 MW;
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158
569
    Mycobacterium leprae.
                                                                                                                                        Fsihi H., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leproma; ML1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 VDPGWD 418
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CONFLICT
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0; Indels Length 35;

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EMBL; AE001798; AAD36542.1; -. TIGR; TM1474; -.

35 AA.

PRT;

STANDARD;

LCGB\_LACLA P36962;

LCGB\_LACLA

RESULT

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CONFLICT SEQUENCE

Matches

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella.
NCBI_TaxID=602;
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DGNTL 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KL25_KLULA
P48045;
                                                                                                                                                                               YEDD_SALTY
Q06399;
                                                                                                                    RESULT 8
YEDD_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RL25_KLULA
ID RL25_1
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Urticaceae; Parietaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Pollen;
Asturias J.A., Arilla M.C., Gomez-Bayon N., Martinez A., Martinez J.,
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                               Length 130;
                                                                                                                                                                                                                                                                                                       0; Indels
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PROSITE; PS0044; PROFILIN; 1.
Actin-binding; Cytoskeleton; Multigene family; Allergen.
SEQUENCE 131 AA, 13784 MW, 8A4FCC0BAC1565AB CRC64;
                                                                                                                       proteome.
1; E2D826640FE037CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROFILIN 2 (POLLEN ALLERGEN PAR J 3).
                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AA
InterPro; IPR001971; Ribosomal_S11.
Pfan; PF00411; Ribosomal_S11; 1.
ProDon: PD001010; Ribosomal_S11; 1.
PROSITE; PS00054; RIBOSOMAL_S11; FALSE_NEG.
                                                                                                                                                                                                                                               Query Match 35.7%; Score 5; DB Best Local Similarity 100.0%; Pred. No. 31. Matches 5; Conservative 0; Mismatches
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Pred. No. 31
0; Mismatches
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Best Local Similarity 100.0%; Pi
Matches 5; Conservative 0;
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InterPro; 1PR002097; Profilin.
Pfam; PF00235; Profilin; 1.
PRINTS; PR00392; PR0FILIN.
                                                                                                                           Complete p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                       Ribosomal protein;
SEQUENCE 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      39 DGNTL 43
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O9TOM8;
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DE PROQ_PARAUU

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DE PROG_LE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raha M., Kihara M., Kawagishi I., Macnab R.M.; "Organization of the Escherichia coli and Salmonella typhimurium chromosomes between flagellar regions IIIa and IIIb, including a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=28985;
                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 35.7%; Score 5; DB 1; Length 141; Best Local Similarity 100.0%; Pred. No. 33; Matches 5; Conservative 0; Mismatches 0; Indels Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L13280; AAA71971.1; -.
Stydene; SG10420; yedD.
Hypothetical protein.
SEQUENCE 141 AA; 15465 MW; A37E9E11ADCB8DD9 CRC64;
                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYPOTHETICAL PROTEIN YEDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
RPL25.
141 AA
                                                                                                                                                                                                                                                                                                                                                                                               large non-coding region.";
J. Gen. Microbiol. 139:1401-1407(1993).
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                                                                                                                                                                                                                                                                                                     MEDLINE-93381452; PubMed-8371104;
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STANDARD;
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9 DGNTL 13
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61 DGNTL 65
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                                                                                                OAZ_ONCVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                RESULT 11
OAZ_ONCVO
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CULT. Genet. 12:193-198(1987).
-!- FUNCTION: THIS PROTEIN BINDS TO A SPECIFIC REGION ON THE 26S RRNA.
-!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88210534; 'PubMed-3449224; Wassernaar G.M., Planta R.J.; Woudt L.P., Mager W.H., Beek J.G., Wassernaar G.M., Planta R.J.; Structural and putative regulatory sequences of the gene encoding ribosomal protein L25 in Candida utilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Pfam; PF00276; Ribosomal_L23; 1.
ProDom; PD001141; Ribosomal_L23; 1.
PROSTFE; PS00050; RIBOSOMAL_L23; 1.
SEQUENCE 142 AA; 15716 MW; E8F8EE77D344009C CRC64;
                                                                                                                                                                                                                                                                                                                                                                        DB 1;
o. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
60S RIBOSOMAL PROTEIN 1.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 5; DB 1;
Pred. No. 33;
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100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pred. No. 33;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pichia jadinii (Yeast) (Candida utilis).
                                                                                                                   or send an email to license@isb-sib.ch)
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InterPro; IPR001014; Ribosomal_L23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X05919; CAA29354.1; -.
                                                                                                                                                              EMBL; S53176; AAB24896.1; -.
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.00
5; Conservative
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Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 DGNTL 13
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P08792;
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AC PR25_P
AC PR25_P
AC PR25_P
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-FEB
DE 60S RI
GN RPL25.
OS SACCHA
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OC SACCHA
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OC CACCHA
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RR "SETUC
RR "SETUC
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CC -!-FU
CC -!-FU
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                                                                                                                                                                                                                                                                                                          MEDLINE-20237626; PubMed=10775274;
Ivanov I.P., Matsufuji S., Murakami Y., Gesteland R.F., Atkins J.F.;
"Conservation of polyamine regulation by translational frameshifting
from yeast to mammals.";
EMBO J. 19:1907-1917(2000)
-!- FUNCTION: BINDS TO, AND DESTABILIZES, ORNITHINE DECARBOXILASE.
-!- MISCELLANBOUS: A RIBOSOMAL FRAMESHIFT OCCURS BETWEEN THE CODONS
FOR SER-28 AND ASP-29, AN AUTOREGULATORY MECHANISM ENABLES
MODULATION OF POLYAMINES.
CONCENTRATION OF POLYAMINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connolly T.M.; "Cloning of the cDNA and expression of moubatin, an inhibitor of platelet aggregation."; J. Biol. Chem. 268:5450-5456(1993).
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Parasitiformes; Ixodida; Argasidae; Ornithodoros.
NCBL_TaxID=6938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-93194835; Pubmed-8449907;
Keller P.M., Waxman L., Arnold B.A., Schultz L.D., Condra C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ODC ANTIZYME FAMILY.
                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ORNITHINE DECARBOXYLASE ANTIZYME (ODC-AZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.7%; Score 5; DB 1;
llarity 100.0%; Pred. No. 34;
Conservative 0; Mismatches
145 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ornithodoros moubata (Soft tick).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF217279; AAF68270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002993; ODC_AZ.
Pfam; PF02100; ODC_AZ; 1.
PROSITE; PS01337; ODC_AZ; 1.
                                                                                                                                                                                                            Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
STANDARD;
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                                                                                                                                                          Onchocerca volvulus.
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Best Local Similarity
Local 5; Conserve
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=6282;
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MEDLINE-20273955; PubMed=10813784;

Alexandre D., Vaudry H., Jegou S., Anouar Y.;

Structure and distribution of the mRNAs encoding pituitary adenylate cyclase activating polypeptide and growth hormone-releasing hormone-like peptide in the frog, Rana ridibunda.";

J. Comp. Neurol. 421:234-246(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: PACAP PLAYS PIVOTAL ROLES AS A NEUROTRANSMITTER AND/OR A NEUROMODULATOR. STIMULATES ADENYLATE CYCLASE IN PITUITARY CELLS.
FUNCTION: SPECIFIC INHIBITOR OF COLLAGEN-INDUCED PLATELET AGGREGATION AT HIGHER CONCENTRATIONS IT MAY AFFECT MORE THAN ONE ASPECT OF PLATELET SIGNAL TRANSDUCTION INCLUDING THE THROMBOXANE A2 RECEPTOR.

CAUTION: THERE ARE 10 AA DIFFERENCES BETWEEN THE CDNA DEDUCED SEQUENCE AND THE DETERMINED PROTEIN SEQUENCE. THESE DIFFERENCES ARE NOT INDICATED IN THE PAPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
MEDLINE-92063899; PubMed-1720095;
MEDLINE-92063899; PubMed-1720095;
Chartrel N., Tonon M.-C., Vaudry H., Conlon J.M.;
Chartrel N., Tonon M.-C., Vaudry H., Conlon J.M.;
Primary structure of frog pituitary adenylate cyclase-activating polypeptide (PACAP) and effects of ovine PACAP on frog pituitary.", Endocrinology 129:3367-3371(1991).

- I- FUNCTION: PRIMARY ROLE OF GRF IS TO RELEASE GH FROM THE PITUITARY.

- PITUITARY.

- PITUITARY OF THE PACAP OF THE PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PACA_RANRI STANDARD; PRT; 171 AA.

101-009169; 0918R8; 0918R7;
01-00v-1995 (Rel. 32, Created)
20-40G-2001 (Rel. 40, Last sequence update)
20-40G-2001 (Rel. 40, Last sequence update)
GLUCAGON-FAMILY NEUROPEPTIDES PRECURSOR [CONTAINS: GROWTH HORMONE-RELEASING FACTOR (GRP) (GROWTH HORMONE-RELEASING POLYPEPTIDE-37)
[PACAP27]; PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-38
[PACAP28] (PACAP38)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kana ridibunda (Laughing frog) (Marsh frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea; Ranidae, Rana
VOEI_TaxID=8406;
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0
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MOUBATIN.
BLOCKED.
D -> DE (IN REF. 1; AA SEQUENCE).
79EC7B7E460FA74B CRC64;
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Pred. No: 39;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.7%; Sco
ilarity 100.0%; Pr
Conservative 0;
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16 171 MO
716 716 BL
54 54 D
171 AA; 18824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L04129; AAA29432.1; -. PIR; A46618; A46618.
HSSP; Q00422; 1AWC.
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Best Local Similarity
Thes 5; Conserve
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65 DGNTL 69
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phaslanidae; Phaslaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                             GROWTH HORMONE-RELEASING FACTOR.
PITUITARY ADENYLATE CYCLASE-ACTIVATING
POLYPEPTIDE-38.
PITUITARY ADENYLATE CYCLASE-ACTIVATING
POLYPEPTIDE-27.
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15-JUL.1998 (Rel. 36, Last sequence update)
20-AUG.2001 (Rel. 40, Last annotation update)
50-AUG.2001 (Rel. 40, Last annotation update)
GLUCAGON-FAMILY NEUROPEPTIDES PRECURSOR (CONTAINS: GROWTH HORMONE-
RELEASING FACTOR (GRF) (GROWTH HORMONE-RELEASING HORMONE) (GRRH);
PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-37 (PACAP-27)
(PACAP-37), PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-38
ADCYAP138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.; "Isolation and primary structure of chicken PACAP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97174314; PubMed-9022048;
MEXORY J.E., Parker R.L., Sherwood N.M.;
"Expression and alternative processing of a chicken gene encoding
both growth hormone-releasing hormone and pituitary adenylate
cyclase-activating polypeptide.";
DNA Cell Biol. 16:95-102(1997).
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION (BY SIMILARITY). RHADDLLINKAYRNLLGQLSARKYLHTLMAKHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN ISOFORM 2).
A9F0E841FA840907 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 39; Matches 5; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 AA; 19679 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 DGNTL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 DGNTL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PACA_CHICK
P41534;
                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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Cox J.A.;

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'Amino acid sequences of four isoforms of amphioxus sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                         InterPro; irravectory promote; 2.
Print Pr00123; hormone2; 2.
PRINTS: PR0075; GLUCAGON.
SMART; SM00070; GLUCAGON.
Andation family; Hormone; Cleavage on pair of basic residues; Signal; Alternative splicing.
Andation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                      FUNCTION: PACAP PLAYS PIVOTAL ROLES AS A NEUROTRANSMITTER AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-158 PROVIDE AMIDE GROUP).
AMIDATION (G-169 PROVIDE AMIDE GROUP).
RHADGIFSKAYRKLIGQLSARNYLHSLMAKRVG -> S
(IN ISOFORM GRF 33-46).
MISSING (IN ISOFORM GRF 1-43).
ODB54995F0AA9DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH HORMONE-RELEASING FACTOR 1-46. PITUITARY ADENYLATE CYCLASE ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
SARCOPLASMIC CALCIUM-BINDING PROTEINS I, III, AND IV (SCP I, III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takagi T., Konishi K., Cox J.A.;
"Amino acid sequence of two sarcoplasmic calcium-binding proteins from the protochordate amphioxus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; GRF 1-43, GRF 1-46 (SHOWN HERE) AND GRF 33-46; ARE PRODUCED BY ALTERNATIVE SPLICING. -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
           -! FUNCTION: PRIMARY ROLE OF GRF IS TO RELEASE GH FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (SCP III AND IV), AND REVISIONS (SCP I) MEDLINE-91006125; PubMed-2209593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%; Score 5; DB 1;
100.0%; Pred. No. 39;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYPEPTIDE-38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 25:3585-3592(1986).
                                                                                                                                                                                                                               EMBL; U71183; AAB51200.1; -.
EMBL; U71184; AAB51201.1; -.
EMBL; U71185; AAB51202.1; -.
PIR; A61070; A61070.
InterPro; IPR000532; Glucagon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19560 MW;
Regul. Pept. 37:326-326(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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80
128
168
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168
114
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                                                      A NEUROMODULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE (SCP I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
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46 DGNTL 50
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P04569;
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SEQUENCE
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Best Local S
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g
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Gaps
                                                                                                                                                      PROTOCHORDATES. MISCELLANEOUS: THIS PROTEIN HAS THREE FUNCTIONAL CALCIUM-BINDING
Eur. J. Biochem. 192:387-399(1990).

Eur. J. Biochem. 192:387-399(1990).

- FUNCTION: LIKE PARVALBUMINS, SCP'S SEEM TO BE MORE ABUNDANT IN FAST CONTRACTING MUSCLES, BUT NO FUNCTIONAL RELATIONSHIP CAN BE ESTABLISHED FROM THIS DISTRIBUTION.

- MISCELLANBOUS: THE SARCOPLASMIC CALCIUM-BINDING PROTEINS ARE ABUNDANT IN THE MUSCLE OF ARTHROPODS, MOLLUSCS, AND
                                                                                                                                                                                           SITES; POTENTIAL SITE 4 HAS LOST AFFINITY FOR CALCIUM.
-!- MISCELLANDOUS: THERE ARE 7 DIFFERENT SCP'S IN AMPHIOXUS. THE SEQUENCE SHOWN HERE IS THAT OF SCP I.
-!- SIMILARITY: TO OTHER EF-HNUD CALCIUM BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y -> M (IN SCP III).
D -> N (IN SCP IV).
92D556A663003FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANCESTRAL CALCIUM SITE 4.
                                                                                                                                                                                                                                                                                                                                          HSSP, P04570; 2SAS.
HSSP, P04570; 2SAS.
InterPro: IPR002048; EF-hand.
Pfam; PF00036; efhand; 3.

RPGSITE; PS00018; EF-HAND; 3.

Muscle protein; Calcium-binding; Duplication.

A CA_BIND 19 30 EF-HAND 1.

TO 81 EF-HAND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%; Score 5; DB 1;
100.0%; Pred. No. 41;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 31, 2002, 13:39:18 Job time: 78 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21418 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30
81
126
161
20
23
                                                                                                                                                                                                                                                                                               PIR; S13182; S13182.
PIR; S13184; S13184.
PIR; S13185; S13185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
150
20
23
185 AA;
                                                                                                                                                                                                                                                                             PIR; B24479; B24479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GNTLM 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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# This Page Blank (uspto)

us-08-957-709-72.rai

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:15:09; Search time 65.13 Seconds (without alignments) 4.492 Million cell updates/sec

US-08-957-709-72 13 Title: Perfect score: Sequence:

1 XGXXDXXXGXXXX 13

212252 seqs, 22503292 residues

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

Searched:

212252 Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_patents\_AA:\*
11. Cogn2\_6/ptodate/2/laa/5A\_COMB.pep:\*
22. /cgn2\_6/ptodate/2/laa/5B\_COMB.pep:\*
33. /cgn2\_6/ptodate/2/laa/6A\_COMB.pep:\*
43. /cgn2\_6/ptodate/2/laa/6B\_COMB.pep:\*
45. /cgn2\_6/ptodate/2/laa/PCTUS\_COMB.pep:\*
65. /cgn2\_6/ptodate/2/laa/PCTUS\_COMB.pep:\*
66. /cgn2\_6/ptodata/2/laa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result<br>No. | Score | %<br>Query<br>Match | Query<br>Match Length | 82  | SUMMARIES          | op                |
|---------------|-------|---------------------|-----------------------|-----|--------------------|-------------------|
| <b></b> 1 (   | ~     | 15.4                | Π,                    | ▼ , | US-09-021-247-16   | 16,               |
| 7             | 7     | 15.4                | -                     | Н   | 6 - 910 - 2        |                   |
| m             | 7     | 15.4                | 12                    | S   | PCT-US91-08497-29  | 29,               |
| 4             | 7     | 15.4                | 14                    | 4   | US-08-822-774-53   | 53,               |
| 2             | 7     | 15.4                | 19                    | m   | US-08-802-981-52   | 52,               |
| 9             | 7     | 15.4                |                       | 4   | US-08-669-304-2    | ς,                |
| 7             | 7     | 15.4                | 23                    | 4   | US-08-669-304-9    | Sequence 9, Appli |
| 80            | 7     | 15.4                | 40                    | Ŋ   | PCT-US95-10973A-77 | 77,               |
| 6             | 7     | 15.4                | 68.                   | 7   | US-08-511-485-2    | 7                 |
| 10            | 8     | 15.4                | 68                    | ٣   | US-09-212-971-2    | Sequence 2, Appli |
| 11            | 8     | 15.4                | 68                    | 4   | US-08-800-929A-2   | 7                 |
| 12            | 7     | 15.4                | 99                    | 4   | US-09-617-053A-2   | 7                 |
| 13            | 7     | 15.4                | 273                   | 4   | US-08-928-213B-10  | 10                |
| 14            | 7     | 15.4                | 455                   | -   | US-07-762-681A-2   | Sequence 2, Appli |
| 15            | 2     | 15.4                | 526                   | 4   | US-08-895-590-5    | 5, A              |
| 16            | 1     | 7.7                 | 7                     | Н   | US-07-820-154A-15  | 15,               |
| 17            | 1     | 7.7                 | 7                     | -   | US-07-820-154A-23  | 23,               |
| 18            | 1     | 7.7                 | 7                     | Н   | US-07-820-154A-33  | 33,               |
| 19            | -     | 7.7                 | 7                     | П   | US-07-820-154A-39  |                   |
| 20            | 1     | 7.7                 | 7                     | Н   | °                  | 39,               |
| 21            | 7     | 7.7                 | 7                     | -   | US-07-729-353-5    | ď,                |
| 22            | 1     | 7.7                 | 7                     | Н   | US-08-122-510-9    | 6                 |
| 23            | 1     |                     | 7                     | Н   | -08 - 12           | 14,               |
| 24            | 1     | 7.7                 | 7                     | Н   | w                  |                   |
| 25            | -     | 7.7                 | 7                     | Н   | -08 - 153          | 20,               |
| 36            | 7     | 7.7                 | 7                     | ~   | US-08-191-866D-69  |                   |
| 27            | -     | 7.7                 | 7                     | 7   | US-08-293-150A-39  | Sequence 39, Appl |
|               |       |                     |                       |     |                    |                   |

| 5, Appli<br>2, Appli<br>15, Appl                        | 23, Appl<br>33, Appl<br>39, Appl<br>15, Appl                                    | 16, Appl<br>17, Appl<br>69, Appl<br>4, Appli                                 | 1, Appli<br>2, Appli<br>15, Appl<br>23, Appl                                 | 33, Appl<br>39, Appl<br>4, Appli                           |
|---------------------------------------------------------|---------------------------------------------------------------------------------|------------------------------------------------------------------------------|------------------------------------------------------------------------------|------------------------------------------------------------|
| Sequence<br>Sequence<br>Sequence                        | Sequence<br>Sequence<br>Sequence<br>Sequence                                    | Sequence<br>Sequence<br>Sequence<br>Sequence                                 | Sequence<br>Sequence<br>Sequence<br>Sequence                                 | Sequence                                                   |
| US-08-470-837-6<br>US-08-272-255-2<br>US-08-097-554A-15 | US-08-097-554A-23<br>US-08-097-554A-33<br>US-08-097-554A-39<br>US-08-539-432-15 | US-08-539-432-16<br>US-08-539-432-17<br>US-08-185-949B-69<br>US-08-483-236-4 | US-09-060-455-1<br>US-09-327-424-2<br>US-08-480-640A-15<br>US-08-480-640A-23 | JS-08-480-640A-39<br>JS-08-480-640A-39<br>JS-09-039-308A-4 |
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| 7.7                                                     | r. r. r.                                                                        | r.r<br>r.r<br>r.r                                                            | <br>                                                                         | 7.7                                                        |
| ннн                                                     | пппп                                                                            | ਜਜਜਜ                                                                         | пппп-                                                                        | નતન                                                        |
| 28<br>29<br>30                                          | 332<br>332<br>34                                                                | 35<br>36<br>37<br>38                                                         | 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                      | 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                    |

### ALIGNMENTS

| RESULT 1<br>US-09-021-247-16<br>; Sequence 16, Application US/09021247<br>; Patent No. 622544 | GENERAL INFORMATION: APPLICANT: Shashoua, Victor E. TITLE OF INVENTION: NEUROPROTECTIVE PEPTIDES AND USES THEREOF NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: | ADDRESSEE: Wolf, Greenfield & Sacks, P.C.<br>STREET: 600 Atlantic Avenue<br>CITY: Boston | STATE: MA<br>COUNTRY: USA<br>ZTP: 0210 | COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk | COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COMMINDE: Datont To Dollogo #1 0 | ATA: | APPLICATION NUMBER: US/U9/U21,24/<br>FILLING DATE: OS/U9/U21,24/ | CLASSIFICATION: ATTORNEY/AGENT INFORMATION: | NAME: Van Amsterdam, John R.<br>REGISTRATION NUMBER: 40,212 | REFERENCE/DOCKET NUMBER: N0260/7023<br>TELECOMMUNICATION INFORMATION: | TELEPHONE: 617-720-3500 | TELEFAX: 617-720-2441<br>INFORMAUTON FOR SECTION OF 16. | <br>LENGTH: 11 amino acids | $\overline{}$ | .— | MOLECULE TYPE: peptide | NAME/KEY: Region |    | OTHER INFORMATION: /note= "Xaa = ASP, ASD, Thr Or Giu"<br>FEATURE: | NAME/KEY: Region | 1 10000 |      |
|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|----------------------------------------|--------------------------------------------------|----------------------------------------------------------------------------------------------|------|------------------------------------------------------------------|---------------------------------------------|-------------------------------------------------------------|-----------------------------------------------------------------------|-------------------------|---------------------------------------------------------|----------------------------|---------------|----|------------------------|------------------|----|--------------------------------------------------------------------|------------------|---------|------|
| REST<br>US-(                                                                                  |                                                                                                                                                                   |                                                                                          |                                        |                                                  |                                                                                              |      |                                                                  |                                             |                                                             |                                                                       |                         | ٠                                                       | <br>٠                      |               |    |                        | <br>             | ٠. |                                                                    |                  |         | )-SN |

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GENERAL LIGENT: HOLLY
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Batracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: And Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCES: and Methods for Purifying and Identifying Same
NUMBER OF SEQUENCE AND PL.L.C.
STREET: 1200 G Street, N.W. Suite 700
STREET: 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
       1755 Jefferson Davis Highway, Fourth Floor
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: The PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08497
FILING DATE: 19911121
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 05 07/616,910
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, Norman F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REDERBOCKET UMBER: 1126-069-0 PCT
TELECHONE: 701.062-21.4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 53, Application US/08822774
; Patent No. 6183997
; GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)486-2347
TELEX: 248855 OPAT
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.4 Best Local Similarity 100. Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide PCT-US91-08497-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
                                   CITY: Arlington
STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GXXD 10
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US-08-822-774-53
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                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fleming, Patrick J.
APPLICANT: Fleming, Patrick J.
APPLICANT: Fleming, Patrick J.
APPLICANT: Fleming, Patrick J.
TITLE OF INVENTION: Peptide Which Regulates Weight Gain in TITLE OF INVENTION: Manmals
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington
STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fleming, Patrick J.
APPLICANT: Fort, Ute M.
TITLE OF INVENTION: Peptide Which Regulates Weight Gain in TITLE OF INVENTION: Mammals
NUMBER OF SEQUENCES: 56
CORRESPONDENCES: 56
ADDRESSEE: 08LON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
       Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE: 5.2202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/616,910
FILING DATE: 19901121
CLASSIFTATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
RELEPHONE: (703)214-4500
TELEPHONE: (703)246-2347
TELECOMMUTCATION INCORMATION:
TELECOMMUTCATION 100: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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PCT-US91-08497-29
Sequence 29, Application PC/TUS9108497
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/07616910
Patent No. 5223484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.48; SUC-
100.08; Pre
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Query Match
Best Local Similarity
Matches 4; Conserval
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Best Local Similarity
Matches 4; Conserv
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7 GXXD 10
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APPLICANT: Peter Stougaard
APPLICANT: Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
TITLE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                 Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.4%; Score 2; DB 4; Best Local Similarity 100.0%; Pred. No. 0; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                               Query Match 15.4%; Score 2; DB 3
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches
                                                                                                                                                      ; LOCATION: 15
OTHER INFORMATION: /product= "Acp"
US-08-802-981-52
                        OTHER INFORMATION: /product= "Acp"
                                                                                                       OTHER INFORMATION: /product= "Acp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08669304
Patent No. 6251626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Hunton & Williams 1900 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                               NAME/KEY: Modified-site LOCATION: 14
                                                                                                                                          NAME/KEY: Modified-site LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-669-304-2
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STRANDEDNESS: un
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Reckard, Beverly S.
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Perancisco
STATE: California
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALLLULLAL
COUNTR: CALLLULLAL
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURBENT APPLICATION DATA: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELEPONE: (415) 576-0200
TELEFONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                      Pred. No. 0;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /product= "Aib"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 52, Application US/08802981
; Patent No. 6037137
                                                                                                                                                                                                                                                                                  Query Match 15.4%; Scr
Best Local Similarity 100.0%; P.
Matches 4; Conservative 0;
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site LOCATION: 3
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NAME/KEY: Modified-site
                                                                                                                                                                                                       internal
                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                         amino acid
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US-08-802-981-52
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Sequence 2, Application US/O8511485

Patent No. 591912

GENERAL INFORMATION:

APPLICANT: Mackenie, Alexander E.

APPLICANT: Baird, Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

COUNTRY: BOSCON

STATE: MA

COUNTRY: BEADABLE FORM:

MEDIUM TYPE: FLOPDY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: 025/08/511,485

FILING SYSTEM: PAUG-1995

CURRENT APPLICATION NUMBER: 07540/002001

REFERENCE/DOCKET NUMBER: 07540/002001

TELEBRAYICA FOUNDER: 07542-5070

TELEBRAYICA FORMSER: 07542-5070

TELEBRAYICA FOUNDER: 617/542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 40;
                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY disk
COMPUTER: IBM FC compatible
DERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: PAPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10973A
FILING DATE: 29 AuG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NOTEMBER: 39,317
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
RELEMENOR-POCKET UNMBER: 760100.413PC
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: peptide
FEATURE:
COTHER INFORMATION: /product- "SO-4"
PCT-US95-10973A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 2; DB 5;

y 100.0%; Pred. No. 0;

rvative 0; Mismatches
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Best Local Similarity
Matches 4; Conserv
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US-08-511-485-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                     RESOURT NO. 6251626

SEQUENCE 9, APPLICATION US/08669304

PAPLICANT: DECENT STOUGHAND THEXOSE OXIDASE, A TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A CORRESPONDENCE ADDRESS: 34

CORRESPONDENCE ADDRESS: 34

COUNTRY: WASHINGTON WILLIAMS

STREET: 1900 K Street, N.W.

COUNTRY: D.C.

IT.: WASHINGTON & STREET: D.C.

COMPUTER: IBM PC COMPATION

MEDIUM TYPE: PLOPPY disk

COMPUTER: IBM PC COMPATION

MEDIUM TYPE: PLOPPY disk

COMPATION SYSTEM: PC DOS/MS-DOS

COMPATION SYSTEM: DATA:

APPLICATION NUMBER: US 435

PRICESPERITATION NUMBER: US 435

REFERENCE/COCKET NUMBER: 320.00003

TELECAMICATION NUMBER: 320.00003

TELECAMINICATION NUMBER: 320.00003

TELECAMICATION NUMBER: 320.00003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unk
                                  14 DXXXG 18
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PCT-US95-10973A-77
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5 DXXXG 9
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DETECTION AND MODULATION OF IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT DISEASE
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; OTHER INFORMATION: Xaa can be any amino acid.
US-08-800-929A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOGTWARE: FASELSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
o. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 07891/009001
ELECOMMUTCATION:
TELEPHONE: 617-428-0200
TELEPHOXE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2; I
Pred. No.
                                                                                                                                                                    APPLICANT: Korneluk, Robert G
APPLICANT: Korneluk, Robert G
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MO
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                      RESULT 11
US-08-800-929A-2
Sequence 2, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
'ALCOMMENT CONTINGENT'S A PROPERTY OF THE CONTINGENT'S A PROPERTY OF THE CONTINGENT'S A PRESENTINGENT'S A PROPERTY OF THE CONTINGENT'S A PRESENT OF THE CONTINGENT'S A PRESENT OF THE CONTINGENT'S A PRESENT OF THE CONTINGENT OF THE CONTINGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%; 8
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRY: USA
02110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GXXD 5
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Xaa at positions 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MacKenzie, Alexander G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Patt, Chilstine
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER PAPLICATION NUMBER: 60/017,354
EARLIER PLING DATE: 1996-04-26
EARLIER PLING DATE: 1996-12-13
SAPILOR OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      Xaa at positions 1, 2, 3, 6, 9, 10, 14, 15, 18, 19, 20, 21, 24, 30, 42, 43, 44, 45, 46, 47, 49, 50, 51, 53, 5, 61, 62, 64 and 66 may be any amino acid or may be absent.
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o. 0;
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100.0%; Pred. No. 0;
tive 0; Mismatches
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100.0%; Pred. No. v,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/09212971B ; Patent No. 6107041
                         SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
Matches 4; Conserv
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COTHER INFORMATION:
US-09-212-971-2
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31 GXXD 34
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                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07762681A
Patent No. 5266475
GENERAL INFORMATION:
APPLICANT: Lee, Chanyong
APPLICANT: Bagdasarian, Michael
APPLICANT: Reikus, J. Gregory
APPLICANT: Meng, Menghsiao
TITLE OF INVENTION: Glucose Isomerases With Improved
TITLE OF INVENTION: Affinity For D-Glucose
NUMBER OF SEQUENCES:
ADDRESSEE: Thad Kryshak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 53202
ZIP: 53202
ZIP: 53202
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910919
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                           Query Match 15.4%; Score 2; DB 4; Best Local Similarity 100.0%; Fred. No. 0; Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad F
REGISTRATION NUMBER: 19,428
REFERENCE/FOCKET NUMBER: 66-336-9038-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5591
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERESTICS:
LENGTH: 455 amino acids
TYPE: AMINO ACID
TELEPHONE: 415-705-8410
TELEFAX: 415-397-8338
TELEFAX: 415-397-8338
TENGTH FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid a
STRANDEDNESS: not relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-928-2138-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Thad Kryshak
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
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242 GXXD 245
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                           APPLICANT: MacKenluk, Robert G
APPLICANT: MacKenluk, Alexander E
APPLICANT: MacKenluk, Alexander E
APPLICANT: MacKenluk, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Tang, Benjamin K
APPLICANT: True OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1907-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa at 1, 2, 3, 6, 9, 10, 14, 15, 18, 19, 20, 21, OTHER INFORMATION: 24, 30, 32, 33, 35, 37, 40, 42, 43, 44, 45, 46, OTHER INFORMATION: 47, 49, 50, 51, 53, 54, 55, 56, 57, 59, 60, 61, OTHER INFORMATION: 62, 64 and 66 can be any amino acid; xaa at 13, 16, OTHER INFORMATION: and 17 can be any amino acid; xaa at 13, 16, OTHER INFORMATION: Based on consensus from Homo sapiens and Mus US-09-617-053A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seville, Mark
Cull, Millard G.
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
HOLOENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER INCLUDED TOWN.

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/928,213B
FILING DATE: 12-Sep-1997
CLASSIFICATION: <u >CURROWN></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: ENZYCO-02550
""TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.4%; Score 2; DB 4; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08928213B
Patent No. 6238905
GENERAL INFORMATION:
APPLICANT: McHenry, Charles S.
Seville, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-928-213B-10
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31 GXXD 34
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RESULT 15

US-08-995-590-5

SGEWORCE A, Application US/08895590

SECURISAL INFORMATION

FAPLICANT: Ren, Dejian

APPLICANT: Bal, Linda M.

APPLICANT: Bold, Manuel Marcel Paul

TITLE OF INVENTOR: Genes Encoding an Insect Calcium Channel

CORRESPONDENCE ADDRESS:

ADDRESSES: BURNS, DOANE, SMECKER & MATHIS, LLP

STREET: 699 Prince Street

COUNTY: USA

COUNTY: USA

ILL. 22314-3137

COMMUTER TEALABLE FORM:

MEDILUM TYPE: LOPOPY disk

COMPUTER TEALABLE FORM:

MEDILUM TYPE: REPERVENCE PROSONALION:

PRINCE PRESENTATION NOTA:

MARIE: WECOMAN MILEDIAL SO SO TO NOTE:

TELEDRONE TO NOTE:

TELEDRONE TO NOTE:

TELEDRONE TO NOTE:

STRANDERS TO NOTE:

TELEDRONE TO NOTE:

STRANDERS: SIGHER

TELEDRONES: SIGHER

TO NOTE:

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Query Match 15.4%; Score 2; DB 4; Length 526; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps

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y 2 GXXD 5

Db 75 GXXD 78

Search completed: January 31, 2002, 13:15:10 Job time: 91 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

January 31, 2002, 13:18:05; Search time 140.03 Seconds Run on:

(without alignments)
6.877 Million cell updates/sec

13 1 XGXXDXXXGXXXX 13 US-08-957-709-72

Perfect score:

Title: Sequence:

Gapop 60.0 , Gapext 60.0 OFICO Scoring table:

0

Word size :

522463 seqs, 74073290 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

522463

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_1101:*

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/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1996 /gcgdata/geneseg/genesegp/AA1998 /SIDS2/gcgdata/geneseq/geneseqp/AA1999 /SIDS2/gcgdata/geneseq/geneseqp/AA1997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	Description	Octobus minor brai	Putative metal ion	[3H]BANA-CCK-8s (a	Neuroprotective ca	Weight regulating	Uridine binding mo	Amino acid sequenc	Wheat amyloplast A	ADP glucose transp	Fluorogenic protea	Fluorogenic protea
CHEMINAL	а	AAB74959	AAR75127	AAR86325	AAY45210	AAR24843	AAW72848	AAG62873	AAY42757	AAY39335	AAW82117	AAW82125
	DB	22	16	16	20	13	19	22	20	20	19	13
	% Query e Match Length DB I	4	σ	11	11	12	14	14	15	15	19	20
	& uery atch	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
	ŽÖ.	2	~	2	2	7	~	~		0	~	7
	Score						•					
	Result No.	1	7	m	4	S	9	7	8	σ	10	11

						RESULT 1
	ALIGNMENTS					
UGGT consensus seq	AAB72447	22	1626	15.4	7	45
Banana ripening fr	ω	20	197	15.4	7	44
	AAY05852	20	626		7	43
	AAR44236	14	455	15.4	~	42
Breast and ovarian	AAB58877	21	218		7	41
Human gene 7 encod	AAE03407	22	194		7	40
Human colon cancer	AAG75792	22	178		7	39
Human gastric canc	AAB63637	22	168		7	38
Arabidopsis thalia	AAG33832	2 7	166	15.4	N ()	37
Arabidopsis thalia	AAG33833	21	160	15.4	7	35
	AAY27137	20	150	15.4	7	34
Human colon cancer	AAG76477	22	130	15.4	7	33
Murine OR-like pol	AAG72675	22	123	15.4	7 (	32
SEQ ID NO 448 from	AAY19730		111	15.4	7	30
Hepatitis C virus	AAR84352		104	15.4	7	58
Sequence of endoge	AAP60952		98	15.4	7	28
	AAR84516		97		7	27
Zea mays protein f	AAG61652		74	15.4	7	26
Arabidopsis thalia	AAG24895		73		~	25
Mammalian inhibito	AAW19588		689		1 (1)	24
Human 5' EST relat	AAY65156		0 0		10	2.5
Human secreted pro	AAG00442	7 [	7 00	15.4	4 (	22
Human colon cancer	AAG74971	22	42		7	20
N-terminal of ribo	AAP81583	σ	40		7	19
Arabidopsis thalia	AAG15187	21	39		7	18
	AAB29933	21	24		4 (7	17
	0900CM44	1 C	9 6		4 C	71
Human endozepine-I Human endozepine-1	AAB81828 AAB81831	22	200	15.4	7 (	14 15
se binding	AAG73106	22	20	15.4	7	13
Human colon cancer	AAG76715	22	20	15.4	7	12

Octopus minor brain cardiotonic generic peptide. 4959 AAB74959 standard; peptide; 4 AA. (first entry) Octopus minor. 10-JUL-2001 AAB74959; 

Octopus minor; brain, cardiotonic; cardiant; mollusca; drug; neural transmission system; agricultural chemical. Location/Qualifiers Key Misc-difference 2

/label= Ser, Phe /note= "optionally D-form residue" Misc-difference 3

/label= Trp, Gly JP2000344795-A. 12-DEC-2000

99JP-0157700. 04-JUN-1999;

99JP-0157700.

04-JUN-1999;

(SUNR ) SUNTORY LTD.

WPI; 2001-268264/28

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9 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR86325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
  pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
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                                                                                            The present sequence represents a cardiotonic peptide (I) derived from the brain of Octopus minor. Cardiotonic peptides of Mollusca of formula H-Gly.x.-Y-Asp-OH (I), where X = L-Ser, D-Ser, L-Phe or D-Phe and used for drugs and agricultural brain of octopus minor, can be used as cardiotonic agents and agricultural chancals. (I) have cardiant activity. (I) can be used as cardiotonic agents and agricultural chancals. The peptides are useful as blochemical reagents for neural transmission system and structure and activity relationship in the molecular level leading to development of drugs and agricultural chemicals.
New neuropeptides from brain of Octopus minor are used as cardiotonics
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New glycosyl-phosphatidyl:inositol-specific phospholipase D gene used partic. for producing secreted recombinant proteins from . . .
                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Core sequence; metal ion binding domain; consensus; glycosyl-phosphatidylinositol; phospholipase-D; bovine; liver; integrin-alpha; EF-hand motif; calcium binding protein; signal peptide; recombinant protein; anchor; vector; cloning; fusion protein; protein secretion; purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative metal ion binding domain consensus core sequence.
                                                                                                                                                                                                                                                                                                                                           DB 22; Length 4; . 0;
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Amino acid not specified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-,"Amino acid not specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Amino acid not specified"
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                                                                                                                                                                                                                                                                                                                                                    15.4%; Score 2; DB 2
100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR75127 standard; Peptide; 9 AA.
                                                         Claim 1; Page 2; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF ) HOFFMANN LA ROCHE INC.
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90US-0588896.
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                                                                                                                                                                                                                                                                                                                                                    Query Match 15.4
Best Local Similarity 100.
Matches 4; Conservative
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Misc-difference
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27-SEP-1990;
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| gxxd 4
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Tsang TCH;
                                                                                                                                                                                                                                                                                             Sequence
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AAR70127
ID AAR70127
AZ AAR70127
XX AAR7
XX AAR7
XX IS-P
XX BOS

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regions of internal similarity in bovine liver regions of internal similarity in bovine liver regions of internal similarity in bovine liver (glycosyl-phosphatidylinosito] (GPI) specific phosphalipase-D (AAR75109). The regions show homology with metal ion binding domains of integrin-alpha subunits, and share an Asp-rich core sequence (AAR75109). The regions show homology with metal ion binding domains of integrins on the core sequence matches the EF-hand consensus motif characteristic of calcium and magnesium binding proteins. The presence of these colometred to a heterologous gene linked at the 3'-end to a C-terminal photologous gene linked at the 3'-end to a C-terminal peptide (e.g. AAR75130) gene to form a GPI-anchored molecule, where the C-terminal peptide directs attachment of a GPI anchored in a vector for expression in a host cell. The enzyme inserted in a vector for expression in a host cell. The enzyme selectively hydrolyses the inositol-phosphate linkage of GPI-anchored proteins, GPI lipids and related molecules, resulting in direct construct may be secretion into the medium and simple recombinant protein purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "[3H]4-(Biotin-epsilon-NH(CH2)5CO-oxymethyl)-3-
nitrobenzoyl-Gly; comprises carrier binding site,
spacer mol., photolytically cleavable linkage)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [3H]BANA-CCK-8s (affinity ligand specific for anti-CCK antibody).
                                                                                                                                                                  sequence represents a consensus core sequence derived from 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           photolytically cleavable affinity ligand; cholecystckinin; anti-CCk antibody ligand; carrier-binding; substance-binding; purification; affinity chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= OTHER
/note= "NH(CH2)5CO, 6-aminohexanoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
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/label= substance_binding_site
/note= "C-terminal octapeptide of CCK"
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0
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100.0%; Pred. No. 0;
iive 0; Mismatches
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GPI-anchored proteins expressed by cells
                                                                            Example 2; Column 21; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 100.
Matches 4; Conservative
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peptide, which comprises the amino acid sequence (1) or (Ta):

X1-XX3-XX5-XX7-XX9-XXX12 (1): X5-X6-X7-X8-X9-X10-X11-X12 (Ta): where

X1 = Asp, Gln, Gly or Tyr; X = any amino acid; X3 = Asp, Asn, Thr or Glu;

X5 = Asp, Ser, Gly, Asn or Leu; X7 = Ala, Asp, Phe, Lys, Thr, Tyr, Arg,

Val, Cys or Ser; X9 = Asp, Glu, Gly, Seer, Thr, Met or Asn; and X12 =

Glu, Gln, Ala, Leu or Asn. (I) and (Ia) are neuroprotective calcium

binding peptides. (I) is used to treat a condition characterized by

cerebral ischaemia. (I) reduces the neurotaxic effect of cerebral

ischaemia. (I) is used to increase neuronal cell Ap-1 or NF-IL6

transport across the blood brain barrier into the brain or it can be

calcium. The peptide can be conjugated with a compound which facilitates

transport across the blood brain barrier into the brain or it can be

administered with a compound that increases transport across the blood

brain barrier. Molecules that protect neurons against the ischaemic

effects of stroke will also be useful for treating Alzheimer's disease,

as well as the memory deficits that are characteristic of the aging

process. The present sequence represents a specifically claimed example

of a neuroprotective calcium binding peptide from the present invention.
                                                                                                                        Neuroprotective peptides, which bind calcium, are useful for treating stroke and other neurodegenerative diseases \,\cdot\,
                                                                                                                                                                                                                                present invention describes a composition comprising an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "cystine, hydroxylysine, hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cystine, hydroxylysine, hydroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "cystine, hydroxylysine, hydroxyproline"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEU, SER, THR,
GLN, LYS, HIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEU, SER, THR,
GLN, LYS, HIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.4%; Score 2; DB 20;
100.0%; Pred. No. 0;
tive 0; Mismatches (
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ASN,
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GLU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR24843 standard; Protein; 12 AA.
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GLU,
                                                                                                                                                                                       Claim 14; Page 56; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphetamine; appetite suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weight regulating peptide 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= GLY,
ASP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= GLY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1992 (first entry)
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Best Local Similarity 100.
  (NEUR-) NEUROMEDICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                WPI; 1999-610582/52.
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Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AA;
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                                           Shashoua VE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||
| gxxd 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GXXD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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  δ, q
                                                                                                                                                                                                                                                                                                                            compounds useful as affinity ligands for e.g. purifying substances are new, which comprise at least one carrier-binding site (CBS), egg.

biotin), at least one substance-binding site (CBS), and at least one biotoly, at least one substance-binding site (CBS), and at least one photolytically cleavable linkage (PCL) between a CBS and SBS. A spacer, a f-aminohexanoic acid gp. may be located between the CBS and SBS and the PCL is an o-nitrobenzyl ester linkage. AAR86325 peptide

(181]-BANA -CCK-88) is an affinity ligand for anti-CCK (cholecystokinin) antibodies. Biologically active substances can be isolated in pure form without damage to the substances by an "affinity chromatography" process in which the cpd. is incubated with a soln. of the target substance to form a complex; the complex is bound to a carrier through the CBS; the cubstance and a fragment of the cpd.; and the substance is recovered from this complex, e.g. by gel filtration, diaylsis or ultrafiltration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuroprotective; calcium binding; stroke; neurodegenerative disease; blood-brain barrier; cerebral ischaemia; Alzheimer's disease; memory deficit; aging.
                                                                                                                                                                                                          New photolytically cleavable affinity ligands - with photolytically cleavable linkage between carrier-binding and substance-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 11; . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuroprotective calcium binding peptide SEQ ID NO:15.
                                                                                  (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Asp, Asn, Thr, Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY45210 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                           Claim 10; Fig 1A; 13pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.4%; S
100.0%;
  94DE-4401135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US01786
                                         94DE-4401135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0021247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                          Fahrenholz F, Thiele C;
                                                                                                                                                                   WPI; 1995-312004/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
17-JAN-1994;
                                         17-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9940112-A1
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| gxxd 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY45210;
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RESULT AAY45210

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Gaps

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Length 11; 0; Indels CYS, ARG,

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Misc-difference 12
                                                                                                                                             lansen CJ,
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAG62873
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                                                                                                                                                                             The sequences given in AAR24818-61 are new peptides which comprise at least 6 amino acids from the sequence given in AAR24814. The remaining amino acids are each Gly, Ala, Val, Lew, Ser, Thr. Cys. cystine, Met, Asp, Glu, Asn, Gln, Lys, hydroxylysine, His, Arg, Phe, TYr, Trp, Pro or hydroxyproline. These peptides used for the regulation of weight gain in mammals and can be used instead of amphetamine, which is largely used as an appetite suppressor. These peptides can also be used to prepare antibodies. Such antibodies can be used to attenuate the effect of the peptides in a host or to detect, quantify or purify the peptides.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                  New dodeca:peptide cpds. - used for regulating wt. gain in mammals or for producing antibodies for attenuating such effects
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; sequencing; replication.
                                                                                                                                                                                                                                                                                                      Query Match 15.4%; Score 2; DB 13; Length 12; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note- "hydrophobic residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "hydrophobic residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "hydrophobic residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "any residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "any residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "any residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                           Disclosure; Page 10; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uridine binding motif (consensus).
                                                                                                                                                                                                                                                                                                                                                                                                     AAW72848 standard; Peptide; 14 AA.
                                           91WO-US08497.
                                                           90US-0616910
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                            (GEOU ) UNIV GEORGETOWN.
                                                                                                Kent UM;
                                                                                                                WPI; 1992-216791/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 9
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                                                                                                                                                                                                                                                                             12 AA;
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                Fleming PJ,
                                           20-NOV-1991;
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7 gxxd 10
                                                            21-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1999
                                                                                                                                                                                                                                                                                                                                         2 GXXD 5
        WO9209296-A
                         11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                              Sequence
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This is a consensus sequence of uridine-binding motifs of dUTPases and dCTP deaminases of Pyrococcus furiosus. Methanococcus of and address of Pyrococcus furiosus. Methanococcus of Jannaschii, Desulfurolobus ambivalens, Escherichia coli, yeast, human can herpesvirus (see AAM72850-57). A claimed method of enhancing and herpesvirus (see AAM72850-57). A claimed method of enhancing of nucleic acid polymerase reaction comprises performing the reaction in the presence of one or more of the following: a polymerase of the following: a polymerase a protein that turns-over dUTP and a protein selected from the sequences provided in AAW72848-57. A claimed protein having PEF activity comprises one or more of the sequences given in AAW72848-57. The invention provides novel extracts, proteins and complexes that improve the polymerisation activity of nucleic acid polymersses.

Also included are methods for identifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Kits are provided for replicating nucleic acids, for site-directed mutagenesis, for nucleic acids sequencing or for amplification (preferably PCR or PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fam35-lactase; fungus; foodstuff manufacture; lactose intolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 15.4%; Score 2; DB 19; Length 14; Best Local Similarity 100.0%; Pred. No. 0; Matches 4; Conservative 0; Mismatches 0; Indels
/note= "hydrophobic residue"
                                                                   /note= "hydrophobic residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 71; Page 47; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG62873 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                            97US-0957709.
                                                                                                                                                                                                                                                                                        98WO-US05497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hogrefe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-542284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STRA-) STRATAGENE.
                             Misc-difference 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 AA;
                                                                                                                                                                                                                                                                                        20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                            WO9842860-A1
                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
21-MAR-1997;
                                                                                                                                                                                                                    01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GXXD 5
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2 gxxd 5
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any amino acid'

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/note= "Xaa = any amino acid"
                    /note= "Xaa = any amino acid"
                                                                                                                                                                       (UYMA-) UNIV VICTORIA MANCHESTER.
                                             /note= "Xaa
12
                                                                                                                                 99WO-GB00728
           /label- Xaa
                                      /label= Xaa
                                                                 /label= Xaa
                                                                                                                                                                                        Tetlow IJ,
                                                                                                                                                                                                            WPI; 1999-590977/50
 Misc-difference 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                            Misc-difference 11
                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||
| 9 dxxxg 13
                                                                                            W09947682-A1
                                                                                                                                  19-MAR-1999;
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                                                                                                               23-SEP-1999
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                                                                                                                                                                                          Emes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY39335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY39335
ID AAY3
XX
AC AAY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                   Screening for DNA encoding enzyme of interest, involves obtaining DNA from microorganism, selecting PCR primers, performing PCR and screening PCR products, or selecting a probe for use in Southern blot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Starch biosynthesis; amyloplast; ADP-glucose; transport; import; amylopectin; amylose; branching; chemical structure; transgenic plant;
                                                                                                                                                                                                                                                                         AAG62871-77 represent conserved regions of Fam35-lactases. The specification describes a method for obtaining new Fam35-lactases of fungal origin. Primers designed from highly conserved regions of Fam35-lactases are used in the method of the invention. The Fam35-lactases are useful in the manufacture or processing of foodstuffs or feeds fit for consumption by lactose intolerant humans or animals. Fam35-lactases are also useful for treating lactose
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wheat amyloplast ADP-glucose transporter peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Xaa = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Xaa = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 2; DB 2
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           optimisation; industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers Misc-difference 7
                                                                                                                                                                                                                                                        Claim 19; Page 63; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY42757 standard; peptide; 15 AA.
          'label= Ala, Gly
                                                                                                                                                                               Lassen SF;
                           /label= Ala,
                                              /label- Phe,
                                                                                                                               13-MAR-2000; 2000DK-0000397.
                                                                                                                        99DK-0001888
                                                                                                     14-DEC-2000; 2000WO-DK00693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                   or animals. Fam35-lacta
Intolerance in mammals.
                                                                                                                                                                               Schnorr K, Lange L,
                                                                                                                                                            (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                 WPI; 2001-441894/47
Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                              14 AA;
                   Misc-difference
                                    Misc-difference
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                                                                WO200149878-A1
                                                                                                                      30-DEC-1999;
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5 gxxd 8
                                                                                 12-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                               Sequence
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ID AAY4
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This sequence represents a wheat amyloplast ADP-glucose transporter peptide, #5. The wheat amyloplast ADP-glucose transporter is associated with the amyloplast membrane and comprises at least two proteins; this sequence, along with peptides #4-#7 (AAY42756-Y42759) represent sequences within one of these proteins (AAY42756-Y42759) represent components of a second protein. The sugar nucleotide ADP-glucose is the immediate substrate for starch synthesis, which occurs in the amyloplast; however, ADP-glucose is mainly contributed the amyloplast in the cytoplasm. The ADP-glucose transporter is responsible for the import of ADP-glucose into the amyloplast and therefore plays a pivotal role in the regulation of starch camyloplasts. The transporter not only influences starch yield, but also quality as the starch synthases involved in amylose and amylopectin synthesis have different affinities for ADP-glucose. Variations in the chemical structure of starch are determined by the ratio of amylopectin camylopectin, and by the degree of branching in amylopectin in the starch committed the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and significantly alter the properties of transmission of starch and sig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plants in which the starch quality can be optimised for industrial applications in which starch is used. For example, transgenic plants which have an increased amylose content in starch are useful for production of starch with increased viscosity and gel strength, which prevents baked food going stale so quickly. Conversely, an increased amylopectin content in the starch produces waxy starch useful as thickening agents in food and coatings.
New transporter complex protein useful for modulating starch content in plants, especially useful in food production \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.4%; Score 2; 100.0%; Pred. No
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                                                                                                                                                                                                Claim 1; Page 3; 28pp; English.
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as as as

us-08-957-709-72.rag

(first entry)

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AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, and products can be used for the detection of polysaccharides, proteins, peptides, lipids, phopolipids, glycoproteins, steroids or polymers. In addition, attachment of a phycoproteins, steroids or polymers. In addition, attachment of a rhe composition is composed of P = peptide comprising a protease binding site for the protease, FI, F2 peptides = fluorophores where F1 is cartached to the amino terminal anno acid and F2 is attached to the artached and S1, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal and S2, when present, is attached to the amino terminal acid and S2, when present, is attached to the carboxyl terminal amino acid.
            Protease activity; fluorphore; detection; fluorogenic; cellular uptake;
conformation change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting procease activity in samples.
                                                                                                                  /label- Alb
/note- "alpha-aminoisobutyric acid, labelled as
amino acid B in the specification"
                                                                                                                                                                                                                                                                                                                 "epsilon-aminocaproic acid, labelled as amino acid J in the specification"
                                                                                                                                                                               "epsilon-aminocaproic acid, labelled amino acid J in the specification"
                                                                                                                                                                                                                                                                     "epsilon-aminocaproic acid, labelled amino acid J in the specification"
                                                                                                                                                                                                                           "epsilon-aminocaproic acid, labelled amino acid J in the specification"
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15.4%; Score 2; DB 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches
                                                                               Location/Qualifiers
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 24; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US03000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0802981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komoriya A, Packard BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ONCO-) ONCOIMMUNIN INC
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/note=
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/note=
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                           WO9837226-A1
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                                                             Synthetic.
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AAW82125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides AAV39331-Y39337 are fragments of an ADP glucose transporter protein. The protein contains at least one of the peptide sequences, and is capable of ADP glucose transport. A DAM molecule encoding an ADP glucose transporter protein can be used to transform plant cells. The production from a plant. The plants can then be used to regulate starch production from a plant. The plants can then be used to produce waxy starches that can be used as thickening agents in food and coatings. Alternatively the plants can be used to produce a starch with increased viscosity and gel strength, which can be incorporated in baked food which stays fresh for a longer length of time.
                                                        ADP glucose transporter; transform plant cell; wheat; starch production; waxy starch; thickening agent; food; coating; increased viscosity; stale; gel strength; baked food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP glucose transporter protein used for modifying plant starch production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2; DB 20; Length 15;
; Pred. No. 0;
0; Mismatches 0; Indels
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                                                                                                                                                                                                             note- "Any amino acid"
                                                                                                                                                                                                                                         'note- "Any amino acid"
                                                                                                                                                                                                                                                                     'note= "Any amino acid"
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                                                                                                                                                 Location/Qualifiers
                             ADP glucose transporter peptide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW82117 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowsher CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 15; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P. Matches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0005939
                                                                                                                                                                                                                                                                                                                                                                                         99WO-GB00727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-571841/48
                                                                                                                                                                                                                           Misc-difference 10
                                                                                                                                                                                                                                                         Misc-difference 11
                                                                                                                                                                                                                                                                                   Misc-difference 12
                                                                                                                     Triticum aestivum
                                                                                                                                                                 Misc-difference 7
                                                                                                                                                                                               Misc-difference 8
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| 9 dxxxg 13
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                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1998;
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Length 19; Indels ö

Gaps

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Indels

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Mismatches

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colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                             Human colon cancer antigen protein SEQ ID NO:7479.
                                                                                                                                    AAG76715
ID AAG76715 standard; Protein; 20 AA.
                                                                                                                                                                                                                          (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                 colorectal carcinoma
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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5 gxxd 8
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                                  GXXD 5
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                                                                                                                                                                                        AAG76715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, proteins, peptides, lipids, phopholipids, glycolipids, plycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to a molecule can be used to enhance uptake by cells. The composition is composed of P = peptide comprising a protease binding site for the protease, FI, F2 peptides = fluorophores where F1 is attached to the amino acid and F2 is attached to the artached to the amino acid and S1, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal amino acid, and S2, when present, is attached to the amino terminal acid, and S2, when present, is attached to the carboxyl terminal amino
                                                                                                                                    Protease activity; fluorphore; detection; fluorogenic; cellular uptake; conformation change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "tetrahydroisoguinoline-3-carboxylic acid,
labelled as amino acid O in the specification.
Can be L- or D- form residue"
                                                                                                                                                                                                                                                                                                                                                                                                   labelled as amino acid O in the specification.
Can be L- or D- form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease activity in samples.
                                                                                                                                                                                                                                                                                                                                                                                   "tetrahydroisoquinoline-3-carboxylic acid,
                                                                                                                                                                                                                                                         /label= Aib
/note= "alpha-aminoisobutyric acid, labelled as
amino acid B in the specification"
                                                                                                                                                                                                                                                                                                                             "epsilon-aminocaproic acid, labelled as amino acid J in the specification"
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amino acid J in the specification"
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                                                                                                    Fluorogenic protease indicator CPP32 substrate #14
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100.0%; Pred. No.
                                                                                                                                                                                                                          Location/Qualifiers
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AAW82125 standard; peptide; 20 AA
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                                                                  (first entry)
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∕note=
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Best Local Similarity
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                                                                                                                                                                                                                                         Modified-site
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                                                                  18-FEB-1999
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                                                                                                                                                                                        Synthetic
                                AAW82125;
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cancer-associated nucleic acid molecules (N) and proteins (P), where
the proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene
therapy and vaccine production. N and P may be used in the prevention,
diagnosis and treatment of diseases associated with inappropriate P
cepression. For example, N and P may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of P by expressing
in a patient's genome that affect the activity of P by expressing
the proteins or to supplement the patients own production of P.
Additionally, N may be used to produce the colon cancer-associated Ps,
by inserting the nucleic acids into a host cell and culturing the cell
to express the proteins. N and P can be used in the prevention, diagnosis
and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
cand AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                      Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 8904-8905; 9803pp; English.
                                                                                                                                                                                                                                                                  Birse CE,
                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                   99US-0157137.
99US-0163280.
28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conservat
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Human; endozepine-like protein; ENDO1; ENDO2; ENDO3; ENDO4; ENDO5; ENDO6; ENDO7; ENDO8; ENDO9; ENDO10; Desity; diabetes; dysliptdaemia; metabolic disorder; infection; anorexia; cachexia; syndrome X.
                                         Human endozepine-like ENDO proteins consensus peptide SEQ ID NO: 39
                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000; 2000WO-US41077
                    05-JUN-2001 (first entry)
                                                                                                                                                                                              misc_difference 10
                                                                                                                                                                                                                                                                     misc_difference 15
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                                                                                                                                                                                                                                                                                         misc_difference 17
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misc_difference
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22 - FEB - 2000;
22 - MAR - 2000;
19 - MAY - 2000;
30 - JUN - 2000;
20 - JUN - 2000;
22 - AUG - 2000;
                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1999
 AAB81828;
The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           New fluorogenic compositions whose fluorescence level increases in the presence of active protesses, useful for detecting and localizing protesses activity in biological samples, particularly in frozen tissue samples.
                                                                                                                        Protease detection; peptide cleavage; enzyme activity; fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis; haempphilas
                                                                                                                                                                                                                               6..7
/label= OTHER
/note= "tetrahydroisoquinoline-3-carboxylic acid,
D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.4%; Score 2; DB 22; Length 20; Ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                        /label= Aib
/note= "2-aminoisobutyric acid"
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 24; 86pp; English.
                                       AAG73106 standard; Peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                       11-SEP-2000; 2000WO-US24882
                                                                                                                                                                                                                                                                                                                                             99US-0394019
                                                                               (first entry)
                                                                                                   Protease binding site #40.
                                                                                                                                                                                                                                                                                                                                                                                     Packard BS;
                                                                                                                                                                                                                                                                                                                                                                (ONCO-) ONCOIMMUNIN INC.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-389573/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AA;
                                                                                                                                                                                                                                                                               WO200118238-A1
                                                                                                                                                                                    Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                           10-SEP-1999;
                                                                                 14-AUG-2001
                                                                                                                                                                 Synthetic.
                                                           AAG73106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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label= Met, Leu, Phe, Val, Thr, Ile, Ala, Trp

Met

label= Ala, Ile, Thr, Phe, Leu,

label= Ala, Ile, Thr, Val, Phe, Leu, Met

/label= Xaa /note= "Xaa=unknown"

'label= Lys, Arg

label= Lys, Arg, Asn

Location/Qualifiers

/label= Asp, Pro

Val, Thr, Ile, Ala, Pro

label= Lys, Met, Phe,

/label= Xaa /note= "Xaa=unknown"

/label= Lys, Arg

99US-0157786. 99US-016164. 2000US-0174505. 2000US-0183859. 2000US-0191133. 2000US-0206006. 2000US-0216143. 2000US-021649.

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The present invention provides the protein and coding sequences of 10 endozepine-like proteins, designated BNDOL-ENDOLO. The sequences are useful in the treatment of various diseases, including obesity, metabolic disorders, diabetes, infections, anorexia, syndrome X, cancer-associated cachexia and dyslipidaemlas. The present sequence is a protein fragment of the invention.
                                                                                                                                                                                                                                              Novel human endozepine-like polypeptide, polynucleotide for diagnosis, prevention, treatment of diabetes, metabolic disturbances associated with obssity, anorexia, cancer, dyslipidaemia and for identifying modulators
                                                                  Vernet C;
                                                                  Eisen A,
                                                                  Majumder K,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 115; 136pp; English.
                                                                  Shimkets RA,
(CURA-) CURAGEN CORP.
                                                                                                                                                                           WPI; 2001-266310/27.
                                                                  Prayaga SK,
Spaderna SK;
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Gaps

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RESULT 14 AAB81828 ID AAB81828 standard; Peptide; 20

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                                                                                                                                                                                        Human; endozepine-like protein; ENDO1; ENDO2; ENDO3; ENDO4; ENDO5;
ENDO6; ENDO7; ENDO8; ENDO9; ENDO10; obesity; diabetes; dyslipidaemia;
metabolic disorder; infection; anorexia; cachexia; syndrome X.
                                                  Gaps
                                                                                                                                                                         Human endozepine-like ENDO proteins consensus peptide SEQ ID NO: 42.
                                                 ö
                                DB 22; Length 20;
                                                 0; Indels
                               15.4%; Score 2; DB 2
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                          label= Thr, Ile, Met, Leu
                                                                                                                                                                                                                                                          'label- Asp, Asn, Pro
                                                                                                                                                                                                                                                                                                          /label= Xaa
/note= "Xaa=unknown"
                                                                                                                                                                                                                                                                                                                                                   /label= Met, Xaa
/note= "Xaa=unknown"
                                                                                                                                                                                                                                                                                                                                                                          /label= Xaa
/note= "Xaa=unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Xaa=unknown"
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                         AAB81831 standard; Peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                   label= Arg, Lys
                                                                                                                                                                                                                                                                                                                                                                                                   label= Phe, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157786.
99US-0164164.
2000US-0174505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0215684.
2000US-0219490.
2000US-0227072.
                                                                                                                                                                                                                                                                          label= Ile,
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2000US-0206006.
                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0190740
                                                                                                                                                         05-JUN-2001 (first entry)
                                        Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                 misc_difference 10
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09-NOV-1999;
04-JAN-2000;
22-FEB-2000;
20-MAR-2000;
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13 gxxd 16
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19-MAY-2000;
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
20-JUL-2000;
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                                                                2 GXXD 5
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                                                                                                                                         AAB81831;
                                Query Match
        Sequence
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The present invention provides the protein and coding sequences of 10 endozepine-like proteins, designated ENDO1-ENDO10. The sequences are useful in the treatment of various diseases, including obesity, metabolic disorders, diabetes, infections, anorexia, syndrome X, cancer-associated cachexia and dyslipidaemias. The present sequence is a protein fragment of the invention.
                                                                                                                     Novel human endozepine-like polypeptide, polynucleotide for diagnosis, prevention, treatment of diabetes, metabolic disturbances associated with obesity, anorexia, cancer, dyslipidaemia and for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Vernet C;
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Shimkets RA, Majumder K, Eisen A,
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                                                                                                                                                                           Claim 1; Page 116; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                        WPI; 2001-266310/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA;
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gxxd 16
Prayaga SK,
Spaderna SK;
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Nucleotide sequenc Nucleotide sequenc Genomic fragment # VISNA sheep lentiv Nsk2 receptor gene

Oligonucleotide D2 Oligonucleotide D2 Oligonucleotide D1

Mouse receptor tyr Probe #7790 for ge Probe #9627 used t Probe #11514 used

Nucleotide sequenc Nucleotide sequenc

Rice mature pullul Reporter gene SVS1 Pullulanase expres Rice mature pullul

Gene encoding a su Human polynucleoti Nucleotide sequenc Gastric cancer ass

Human gastric canc Gastric cancer ass Human telomere rep

Human secreted p Human secreted p Human secreted p FIV F14 clone.

Altered telomere

Human telomere rep Human TRF1 coding Mouse muscle-local

relomeric repeat

for

Score

Result . 02 Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB 9 Maximum DB 9

Database

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Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases,
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; sequencing; replication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymerase enhancing factor P45 (dUTPase) component DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                    AAV58053
AAF22679
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AAV59278
AAF63966
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AAX98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus strain DSM 3638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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                                                                                                              WO9842860-A1
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21-MAR-1997;
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Oligonucleotide Dl
Oligonucleotide Dl
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                                                                                                                                                                                    1 ATGCTACTTCCAGACTGGAA.......CAAAGAGAAAGAAACTCTAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqn/NN1982.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseqn/NN1987.DAT:*/SIDS2/gcgdata/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq
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/SIDS2/gcgdata/geneseq/geneseqn/NA1981.
          4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             930621 seqs, 428662619 residues
                                                                                             January 31, 2002, 10:53:12;
          GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAF58262
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seq length: 2000000000
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471
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                              This DNA sequence encodes the P45 component (see AAW72847) of the pulymerase enhancing factor (PEF) of Pyrococcus furiosus DSM 3638.

C PCR primers (see AAA668861-64) based on an N-terminal peptide (see CR PCR primers (see AAA668861-64) based on an N-terminal peptide (see CR PCR primers (see AAA668861-64) based on an N-terminal peptide (see CR PCR products and plasmid sequencing was carried out on purified PCR products and plasmid min-preps. P45 and P40 (see AAW72844) are the predominant components of PEF, which acts to enhance the activity of P. furiosus DNA preparase, thereby providing replication products of greater length and purity. P45 was identified as a dUTPase, and possesses polymerase enhancing activity. The invention provides novel activity of nucleic acid polymerases, as well as DNA constructs and activity for purifying and using these contribodies. Also included are methods for identifying compositions with polymerase enhancing activity, for purifying and using these compositions and pecific extracts, proteins and compositions and pecific extracts, proteins and composition composition are provided for replicating nucleic remanding activity. Risk are provided for replicating nucleic enhancing activity. Risk are provided for replicating nucleic enhancing activity. Risk are provided for replicating nucleic acid sequencing or amplification (preferably PCR or RT-PCR). Isolated DNA can be used in the recombinant production of P45.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 471; DB 19; Length 471; Best Local Similarity 100.0%; Pred. No. 6.2e-143; Matches 471; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAGAGAAAGTCTTAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 471 BP; 156 A; 80 C; 124 G; 111 T; 0 other;
          Claim 17; Page 43; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
AAF58252 Standard; DNA; 936 BE
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AC AAF58252;
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DT 24-APR-2001 (first entry)
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FW) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAACTTAACACTAATGCTC 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTTGCCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAAGGG
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                                                       Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                                                                                                                                                                                                                     26-JUL-2000; 2000WO-US20476.
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17-MAR-2000; 2000US-0190259.
Oligonucleotide D1835
                                                                                gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-159728/16.
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                                                                                                                                           Synthetic.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                   379 TTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
 present invention relates to a composition comprising two nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 TATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                            Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5%; Score 44.8; DB 2).9%; Pred. No. 0.00016;
                                                                                                              439 AGGTTAGCGTTTTCAAAGAGAAAGTCTCTA 470
                                                                                                                                          354 ИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМ 323
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                                                                                                                                                                                                               BP
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                            gene expression; ss.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTC 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 44.8; DB 22; Length 936; 0.9%; Pred. No. 0.00016; ve 258; Mismatches 190; Indels 0
                                                                                                                                                                                   mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
354 МИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                   EIM;
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17-MAR-2000; 2000US-0190259.
                                                                   AAF58254 standard; DNA; 936
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                                                                                                                                                                                   group;
                                                                                                                                                       Oligonucleotide D1875
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                                                                                                                                                                                                gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                    WO200107665-A2.
                                                                                                                          24-APR-2001
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                                                                                                                                                                                                                           Synthetic
                                                                                               AAF58254;
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GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAACTTAACACTAATGCTC 318
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                                                                                                                                                                                                                              TTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
                                                                                                                                                                                                                                                                                                                               AAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGT 78
                                                                                                                                                                       GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGATA
                                                                                                                                                     AAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAGGG
                                                                           AGGTTAGCGTTTTCAAAGAGAAAGAAACTCTA 470
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                                                                                                   TACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGAGTTTGTGTGCAGATCGCA 378
                                                                                                                                                    379 TITATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms; e.g. for genotyping, monitoring gene expression
AAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAGG
                                                259 GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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                                                                                                                                                                                                                              439 AGGTTAGCGTTTTCAAAGAGAAAGAAACTCTA 470
                                                                                                                                                                                                                                                  354 ИМИМИМИМИМИМИМИМИМИМИМИМИМИМ 323
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                                                                                                                                                                                                                                                                                          RESULT 5
AAF58259/c
ID AAF58259 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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allowing repeat analyses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping, a single surface
Example 6; Page 128; 159pp; English.
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gene expression; ss.
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17-MAR-2000; 2000US-0190259.
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ID AAF58262 standard; DNA; 936
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                                                                                                                                           GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGATA 198
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                                                                            19 AAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGGAGGT 78
                                                                                                                          379 TITATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGGAGCACA
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                                             Length 936;
and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                      Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                             Query Match 9.5%; Score 44.8; DB 22; Best Local Similarity 0.9%; Pred. No. 0.00016; Matches 4; Conservative 258; Mismatches 190;
                       6 T; 776 other
                                                                                                                                                                                                                                                                                                  439 AGGTTAGCGTTTTCAAAGAGAAAGAAACTCTA 470
                                                                                                                                                                                                                                                                                                            Sequence 936 BP; 5 A; 139 C; 10 G;
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         monitoring gene expression.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 TATGACCTCAGAGTGGGCAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligase, thermostable; thermostability; Desulfurolobus ambivalens; archaebacteria; detection; ligation; ATP; adenosine triphosphate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pDam-L3 plasmid fragment encoding thermostable ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%; Score 44.8; DB 22;
Local Similarity 0.9%; Pred. No. 0.00016;
les 4; Conservative 258; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "Open reading frame 4."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 ИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМ 323
                                                                                                                              Example 6; Page 127; 159pp; English.
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                                                                                                                                                                                                                                                                                                                                                 monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                       The DNA ligase is ATP dependent and is useful for detecting nucleic acids by Mybridising two oligonuclectides with adjacent sequences of the target nucleic acid, ligating the two oligonucleotides (using the ligase) and detecting the ligation product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ATTAATCGACGTGGAAAAGGAAAGGAAAAGTCGTTATTCCTÇCAAGGGAATACGCCTTAAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 CCTAACCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGATAAGGAG 239
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                                                                     2713..2722
/*tag= e
/note= "Potential transcription termination signal."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              598 ATTTATGAGATAGAGAAGGAGAATTCATCATTACCCTAACGAACATGTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 CAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGG
                                                                                                                  termination
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3382;
                                                                                                                                                                                                                                                                                                               Thermostable ligase from archaebacteria - and DNA coding for useful for nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 9.5%; Score 44.8; DB 14; Length Best Local Similarity 47.9%; Pred. No. 0.00029; Matches 161; Conservative 0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3382 BP; 1188 A; 512 C; 683 G; 999 T; 0 other;
                                                                                             2804..2811
/*tag= f
/note= "Experimental transcription
                                                                                                                                                                                                                                         (BOEF ) BOEHRINGER MANNHEIM GMBH.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                    WPI; 1993-378402/48.
P-PSDB; AAR44614; AAR51076; AAR51077; AAR51078.
         /*tag= b
//note= "Open reading frame 3."
878. 883
/*tag= c
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/note= "Open reading frame 2."
                                                                                                                                                                                                                                                                    Kletzin A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 AAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAA 455
complement (250..771)
                                                                                                                                                                                                                                                                    Kessler C,
                                                             Ligase
                                                                                                                                                                                                                                                                                                                                        Claim 11; Figure 1; 26pp; German.
                                                                                                                       signal.
                                 . .49 c
908..2707
/*tag= d
/product= Liv
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                                                                                                                                                                                                                                                                    Kaletta C,
                                                                                                                                                                                                      23-MAY-1992;
                                                                                                                                                                  DE4217134-A.
                                                                      terminator
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                           promoter
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FFM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 TATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electron-transfer group, useful as labels i
j. for genotyping, allowing repeat analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 ыштытытытытытытытысыптытытытытытытытытыты
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                                                                                                                                                                                                                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 9.4%; Score 44.4; DB 22; Best Local Similarity 1.3%; Pred. No. 0.00022; Matches 6; Conservative 255; Mismatches 191;
Example 6; Page 127; 159pp; English.
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17-MAR-2000; 2000US-0190259
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hybridization assays, e.g.
a single surface
                                                                                                                                                                                                                                           24-APR-2001 (first entry)
                                                                                                                                               AAF58252 standard; DNA;
                                                                                                                                                                                                                                                                                           Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-159728/16
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
              GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAGTTAACACTAATGCTC 318
                                                                                                                                                                                      TTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
                                                                                                                                                                                                                                                                                        The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                AAGTTGCCCGACGATGTTATGGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAAGGG
                                                                                                                                                    ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.4%; Score 44.4; DB 22; Best Local Similarity 1.3%; Pred. No. 0.00022; Matches 6; Conservative 255; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electron-transfer group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
            TTTATAAGGCTAGAGGTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
                                                                                                                TATGACCICAGAGIGGCCAGAGAGCCTTTTGTTAAGGGGAAATTAATCGACGIGGAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATA 198
                                              AAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGT
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Pred. No. 0.00022;
55; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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                                                                                                                                                    AGGTTAGCGTTTTCAAAGAGAAAGTCTCTA 470
                                                                                                                                                                                  573 WWWWWWWWWWWWWWWWWWWWW 604
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Best Local Similarity 1.3%;
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                          (first entry)
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                   139 GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATA 198
AAAATCAGAAAAGAAATACTTATAGAGCCATTTTTCTGAAGAATCGCTCCAACCAGCAGGT
                                       TATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAG
                                                          259 GITATIGGITCTITIGCITGGGITGACCCAGGATGGAAAGCTTAACACTAATGCTC
                                                                                                                                                                                379 TTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACA
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                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                  439 AGGTTAGCGTTTTCAAAGAGAAAGAAACTCTA 470
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                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide D2004.
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                                                                      Length 936;
                                                                                            Indels
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                                         Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                       DB 22;
                                                                       Query Match 9.4%; Score 44.4; DB 22; Best Local Similarity 1.3%; Pred. No. 0.00022; Matches 6; Conservative 25; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                      AGGTTAGCGTTTTCAAAGAGAAAGAAACTCTA 470
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17-MAR-2000; 2000US-0190259.
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         group, useful as labels in allowing repeat analyses on
                                                              The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                   Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
          containing electron-transfer
                  assays, e.g. for genotyping,
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 TATGACCTCAGAGTGGGCAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.4; DB Pred. No. 0.00022
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                                                                                                                                                                                                                                                                                                               Example 6; Page 127; 159pp; English
                                                                        (CLIN-) CLINICAL MICRO SENSORS INC.
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26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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The present sequence encodes a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                       New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                 Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma; ss.
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                                                                                                                                                                                                                                                                                                                  Chow TP, Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; Page 104; 402pp; English.
                                                                                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC.
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97US-0045107
                                                                       Helicobacter pylori.
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25-APR-1997;
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                                                           112 AAGGGGAAATTAATCGACGTGGAAAAGGAAAGGCAAAAGTCGTTATTCCTCCAAGGGAATAC 171
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Query Match
9.4%; Score 44.2; DB 20; Length 2006;
Best Local Similarity 47.6%; Pred. No. 0.00036;
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SUMMARIES

Score Match Length DB ID  280.8 89.6 26518 6 AX0 280.8 59.6 26518 1 CNS 280.8 59.6 26518 1 CNS 280.8 59.6 26518 1 CNS 280.8 19.6 26518 1 AEO 47.4 10.1 1390 1 AEO 47.4 10.1 139340 1 AEO 47.6 9.7 14286 1 AEO 47.8 9.1 923 14 AE 47.8 9.1 10922 1 AEO 47.8 9.2 167000 1 AEO 47.8 9.1 10922 1 AEO 47.8 9.1 1092 1 AEO 47.8 9.1 10922 1 AEO 47.8 10047 2 AEO 47.9 10047 AEO 47.0 10047 AEO 48.8 10047 2 AEO 48.8 10047 1	Description	AP000000 AP000000 AX041922 AX0419222 TF6404 F		·				9 402978 Caenorhabdi AC053469 Homo sapi AC026852 Homo sapi AC079680 Mus muscu AC0799285 Homo sapi AC083366 Mus muscu AC083366 Homo sapi AC079459 Homo sapi AC079459 Homo sapi	ALIGNMENTS DNA BCT 08-FEB-1999 3 genomic DNA, 1485001-1738505 nt. po	465 AB0009521 AB0009522 AB0009533 AB000953 527 AB009528 AB009529 AB009530 AB000953 AB00953 AB009531 AB000953 AB009531 AB000953 AB00953 AB009528 AB009528 AB009528 AB009528 AB009528 AB0009528 AB0009528 AB0009528 AB0009528	and Kikuchi,H.
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Shizuya, H. is at the California Institute of Technology, Pasadena, CA, USA, USA.

CA, USA.

The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nushihara, Shibuya, Tokyo 151-0066, Japan.

All the sequence with length 100 codons or more between ATG or GTG Homology analysis is performed by Smith-Waterman algorithm against release 34.0; PIR-Protectan release 52.0; Swissprot release 34.0; PIR-Protectan release 54.0; and OWL release 29.5.

E-mail address for comments and questions: genomeOr3@nite.go.jp Restriction map, ORF organization, sequence alignment and more information are available at W.W.W. site of Biotechnology Center, URL: http://www.blo.nite.go.jp/.

Festriction/Qualifiers

1. .253605

I. .253605

Acraim-Ora and Carrier and Garier 
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Masuchi,Y., Shizuya,H. and Kikuchi,H.
Complete sequence and gene organization of the genome of a
hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3
DNA Res. 5 (2), 55-76 (1998)
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298. .780
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3192. .4340
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                                                                                           09-SEP-1999
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                                                                                        CNSPAX06 265118 bp DNA BCT Pyrococcus abyssi complete genome; segment 6/6. AJ248288 AL096836 AJ248288.1 GI:5458960
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chromosome structure and
Unpublished
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Pyrococcus.
1 (bases 1 to 265118)
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Pyrococcus abyssi
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complement(3398. .4735)
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                                                                                                                                                                                   /note="similar to PIR:E64312 percent identity:60.870 in 444aa; owl:AAFFH1 percent identity:50.236 in 430aa; owl:SAFFH percent identity:50.611 in 415aa. motif=ATP/GTP-binding site motif A (P-loop); SRP54-type proteins GTP-binding domain signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to PIR:F64336 percent identity: 42.778 in 196aa. motif=ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 250975 TTAATTGATGTGGAAAAGAAGGGAAAGTAGTTATTCCTCCAAGGGAATACGCTCTAATT 251034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D 251095 AGCTTAGCTAGAGAGGGATTCTAGGTTCTTTGCCTGGGTTGACCCAGGATGGGATGG 251154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 251155 AACTTAACTCTAATGCTCTACAATGCTTCAAATGAACCAGTAGAATTAAAATAACAGAGAA 251214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 251215 AGGTTTGTGCAGATTGTCTTTATAAGGCTAGAGGATCCACCAAGGAATCCCTATAGTGG 251274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 251035 CTAACCCTCGAGAGAGAGAGATAACCTGATGAGGAGGATGGAGATATGAAGATAAGGAGC 251094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAGCCCTTACAGAGGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AACTTAACACTAAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="205aa long hypothetical thymidylate kinase"
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                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="445aa long hypothetical signal recognition
particle protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CTAACCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGC
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Pred. No. 1.5e-97;
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complement(4767..5384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4767. .5384)
                                                                                                                     complement(3398. .4735)
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                                                                                                                                                            /gene="PH1694"
                                                                                        /gene="PH1694"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.4%;
ilarity 87.2%;
Conservative
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Matches 410;
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Complement(10179. .10817)

Complement(10179. .10817)

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/ (Transl_tslaft=1)
/ (Transl_tslaft=1)
/ (Aransl_tslaft=1)
/ (Aran
                                                                                                                                             /protein_id="ca850455.1"
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Litalldpearkghronakryvotglolllkbylklgaskfrieaklegaagmeoniks
DELKIGERNVQTAKRELKKLGIRLVAEDTGGRGTTIYLDLSTGKVRMRKVJGGQVIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 262165 TTCATAGATGTTGAAAAGGAGGCAAAGTCATAATACCTCCAAAAGAATATGCCCTAATA 262224
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/transl_table=11
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1.7e-70;
ches 117; I
                                                              /transl_table=11
/product="CHEMOTAXIS_PROTEIN_CHED"
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/note="PAB1331"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein"
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VVMYKGKMLGTIRGGFICPFTTERIPDEVPOEFFXDNPNLILVGEMAGPESPYLVEGP
PYVKEDIOFFLEPVOEIKTGRSLPVEERLKIABEFGINHVEVFGKYTKDDVDELYQLI
FELSKERGREGTIMKSPDMKKIVXYYTPFANINITIKIGARVFEELPGYFTERRISFLADI
YLAERRIKGEEFERVAKELGSALLQPPVESIFPVNEOEBDIHELFKYRVKYTERTPGYTTATKKNY
THFEKLGLKIEIVDIEBIKDGMRITFKRLYPDATNEIRELIGGKAFVD"
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/translation="hypothetical protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypo
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/note="PAB1337"
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DEFINITION
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VERSION
KEYWORDS
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JOURNAL
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ORIGIN
   181
                                                                 241
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AF022221
LOCUS
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Forterre, P., Thierry, J.C., Prieur, D., Dietrich, J., Lecompte, O., Ouerellou, J., Weissenbach, J., Saurin, W., Hellig, R., Flament, D., Raffin, J.P., Henneke, G., Guequen, Y. and Rolland, J.L. Genome sequence and polypeptides of pyrococcus _1(abissy), fragment and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FR)
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                  262225 CTGACCCTAGAGAGGATAAAAGCTTCCAGATGATATTATGGGAGACATGAAGATAAGGAGC 262284
                                                                                262285 AGTCTAGCTAGGGAAGGTGTTCTAGGCTCCTTTGCATGGGTAGACCCGGGATGGGACGGT 262344
                                                                                                                                                                                                              262405 AGGTTTGTCCAGATAGCCTTCCTAAGGCTTGAGGCTCCCGCCAAGAATCCATACAGGGGC 262464
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                                                               241 AGTTTAGCAAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGA
                                                                                                                                                           262345 AATCTAACCTTGATGCTTTACAATGCATCGGAAAAGGAGGTAATTTTAAGGTACAAAGAG
CTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGGAGC
                                                                                                                               301 AACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAG
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                                                                                                                                                                                             361 AGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGA
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                         Patent: WO 0065062-A 817 02-NOV-2000;
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INSTITUT FRANCAIS DE RECHERCHE POUR L'EXPLOITATI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pyrococcus abyssi"
/db_xref="taxon:29292"
/note="Original length of seq 1: 1765118
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Pred. No. 1.7e-70;
0; Mismatches 117;
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Sequence 817 from Patent WO0065062.
AX041922
AX041922.1 GI:11340687
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Viruses: unclassified viruses.
1 (bases 1 to 600)
Prangistivili,D., Klenk,H.P., Jakobs,G., Schmiechen,A.,
Hanselmann,C., Holz,I. and Zillig,W.
Biochemical and phylogenetic characterization of the dUTPase from
J. Biol. Chem. 273 (11), 6024-6029 (1998)
                                                262225 CTGACCCTAGAGAGGATAAAGCTTCCAGATGATATTATGGGAGACATGAAGATAAGGAGC 262284
                                                                                                                                                                                                                                                            262285 AGTCTAGCTAGGGAAGGTGTTCTAGGCTCCTTTGCATGGGTAGACCCGGGATGGGACGGT 262344
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                                                                                                                                                                                                      AACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAG
CTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGATAAGGAGC
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/function="hydrolysis of dUTP to dUMP"
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Archaeal virus SIRV dUTPase gene, complete cds.
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/db_xref="taxon:66287"
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501 ACTITAACGCCGGTAGAAAGCCTTATAACGAAAATATCAGAAAACAGAGAGGCGTCAA 560
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                                                                                                                                                                              328 TCAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCATTTATAAGG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 AGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAAGGAAAAGTCGTTATT 156
                                                                                                                           268 TCTTTTGCTTGGGTTGACCCAGGATGGAAACTTAACACTAATGCTCTACAATGCC 327
                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1997
                         148 GTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCC
                                                                                                                                            264 ITTATAATTTATCCAAATGAACATGTACTTTTAACAACAAGAATATATAAAATTATCA
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                                                                          208 GACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGT
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
166494.1 GI:2724471
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DD 1151 REMERRER 1092

Oy 437 ACAACAAA 465

DD 1091 REMERRER 1093

RESULT

RECORDS 4 10130 DD DNA CLICA 1199 DD DNA CLICA 114 of the Complete genome. ACCESSION ACROSS 4 11390 DD DNA CLICA 1199

RESULT 6 ACAACAAA 465

DECURS 100554 ACROSS 11990 DD DNA CLICA 1199 DD DNA CCESSION ACROSS 4 101301 THE COMPLETE TO COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 4 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 4 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 4 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 4 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO CLICA 11990 DD DNA CCESSION ACROSS 5 101301 THE COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE TO COMPLETE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLRWYVSGHSPWSNAYESMLYIAWASVIAGFILRSKLALSASSFLAGIALFVAHLGF
MDPQIGHLVPVLKSYWLNIHVSVITASYSFLGLCFVLGILSLVLFILRKQGRFNLDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILSISAINEMSMILGLFMLTAGNFLGGVWANESWGRYMGWDPKFTWALISICVYALIL
HLRFLGSHNWPFILASSSVLGFYSVLMTYFGVNYYLSGLHSYAAGDPLPIPTFLYFLV
AIPFALVILAYFKRHLSLPKLA".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLNHTNFFNRLTLPYILLGLLLFIVVISSLVKNTIPNIWLTKILYFAILLCALAHSMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKENHPNLCAVVNDESDLLKRGFASFVASNANAPMRNAFYDALNSIEPVTGGGSVRNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Contingency gene; similar to GB:X78031 SP:011130 PID:516293 PID:520464 PID:520525 percent identity: 39.22; identified by sequence similarity; putative"
                                                                                                               fuote="similar to GB:X76687 SP:P39691 PID:495244 percent identity: 26.45; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AAGGGGAAATTAATCGACGTGGAAAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="thiol:disulfide interchange protein (dsbC),
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.larity 48.7%; Pred. No. 0.002;
Conservative 0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="fucosyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAD07447.1"
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/gene="HP0379" •
8693. .9970
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/gene="HP0378"
5873. Ren
                       /gene="HP0377"
5198. .5863
                                                          5198. .5863
/gene="HP0377"
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                                                                                                                                                                                                                                                                                      putative"
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Matches
        gene
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TOTREDYITYOR IYERPLITHPOTREDPREDARSDFANPOGANGRY Y POSTILKNATA
LPTTDKIENGLIFYSONPYANHVIGSYTIONFLPYNLINVELSEKDAGKYVNLGVI
ETTDKIENGLIFYSONPYANHVIGSYTIONFLPYNLINVELSEKDAGKYVNLGVI
ETTRKOSOTILLAFSENDSEFROADSFNYGOLGAFAYOFSDANTGGLFOKLSKITTHN
EMSYENGADTRINFKGNCHDCYSDFTPOTAEELTNLMLDMIANFESTRIANENENTILKSGFYG
INSTSERCGSDFPRCVNPRNGRYAPTRYNDIVERDIIHAFSTRINLENNTILKSGFYG
IGYELDDNIOGNIGIEBAALNESKLEGKTINKYDIYELRDIIHEFSTRYGNNTY
QRYRLCOENGALOECGGKEELVNGKEELKFTNGKEVKDODGYTYDVCSFYKDNHOY
QRYRLCOENGALOGSTTSTLYKRSSKNERSPILGSNNYK IGYOHYPNDY IGLAY VGI
IKYNYAKTNDEKIQOLSYGGGMDVLFDFITTYANKKONPTKKVFASSFGVFGGLRGII
IKYNYAKTNDEKIQOLSYGGGMDVLFDFITTYANKKONPTKKVFASSFGVFGGLRGI
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KKSLEYADESQRNEKIDIAKLERFQKILIHSCEQCGRSALMELEVESYTKEALKAYPK
ASVLDFKGETLPASADFEKGVILGPEGGFSEPERGYFKEREIYRIPLDMVLKSESACV
FVASIAQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mlemSLQALNTODSSVMAQSLLIHAFFAALLALAFWINLYTLFK
EKNFIQLNKKIYLVMPAIYILLSIALLSGIFIWAWQQFAFSFSVVAMLLGLLLMLIAE
IKRHKSVKLAITKKERMEAYIKKAKILYFLETILIVVLMGL"
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FDDPFILTIKNNFMRKMVGKMIVNSRIEKSKKIYEKLGGKSPLTPITFALTERLNKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSRFYTYAMRYTPPYASMVLQDLALKEVESLVFFSMYPQYSSTTTLSSFNDAFNALKS
LETFRPYVRVIERFYASKKLNKIILNTILNTLNNRKSQDFVLIFSVHGLPKSVIDAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YNSYYVFNQVKGSGNLDIVTGFNYRYKHSKYSVGISVPLIQSGIKIASNNGIYANSVV
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IYPLAFTIDNSETLYELDMQYRLMAERLAVKEYLVCPCLNDSIEFAQFIIERVKNLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SP:P22830 PID:219656 percent
by sequence similarity;
                                                                            Anote="similar to GP:1800185 percent identity: 31.40; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="H. pylori predicted coding region HP0375"
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identity: 33.44; identified
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Kawashima, T., Yamamoto, Y., Aramaki, H., Nunoshiba, T., Kawamoto, T.,
Watanabe, K., Yamazaki, M., Kanehori, K., Amano, N., Ohya, Y., Makino, K.,
and Suzuki, M.
Determination of the complete genomic DNA sequence of Thermoplasma
volvanium GSS1
                                                                                                                                                                                                                                                                                                                                                                                 AP000993 239340 bp DNA BCT 07-JUN-2001
Thermoplasma volcanium genomic DNA, complete sequence, section 3/6
AP000993 BA000011
AP000993. GI:14324830
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Direct Submission

Submitted (20-DEC-1999) Masashi Suzuki, National Institute of
Blostlence and Human Technology, Core Research for Evolutional
Science and Technology, Centre of Structural Biology; Higashi 1-1,
Tsukuba, Ibaraki 305-0046, Japan (F-mail:namano@nibh.go.jp,
URL:http://www.aist.go.jp/RIODE/archaic/, Tel:81-296-61-6582,
On Jun 6, 2001 this sequence version replaced gi:11990452.
The most recent annotation is available at
http://www.aist.go.jp/RIODE/archaic/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Jpn. Acad. 75, 213-218 (1999)
2 (sites)
Rawashima.T., Amano,N., Koike,H., Makino,S., Higuchi,S.,
Rawashima-Ohya.Y., Watranebe,K., Yamazaki,M., Kanehori,K.,
Kawamoto,T., Nunoshiba,T., Yamamoto,Y., Aramaki,H., Makino,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium Proceedings of the National Academy of Sciences of the United States of America. 97 (26), 14257-14262 (2000)
                                                                                                                                                           GCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAG 231
                                                                                                       419 GGCAAAAGCACTTAGGCTAGGTGTGGGATTATTGTGAATGTTAGGCCTTTTGAGCCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoplasma volcanium (strain:GSS1) DNA.
Thermoplasma volcanium
Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
                                                                               232 ATAAGGAGCAGTTTAGCAAGAGAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGA

    .239340
    /organism="Thermoplasma volcanium"

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                                                                                                                                                                                                                                             352 TATGGAGAGAGTTTGTGCAGATCGCATTTATA 384
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TPVSSSDTIAADICNALGAKLIKTKVGAPIVARAMIDNGATIGGEENGVIYGKHOYCR
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7987. :10302
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Ruepp, A. Graml, W., Santos-Martinez, M.L., Koretke, K.K., Volker, C., Mewes, H.W., Frishman, D., Stocker, S., Lupas, A.N. and Baumeister, W. Direct Submission

Direct Submission

Luct Submission

Submitted (28-SEP-2000) Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG Bioinformatics, Smith Kline Beecham Pharmaceuticals, Collegeville, Pennsylvania 19426, USA GSF-Forschungszentrum fuer Unwelt und Gesundheit, Munich Information Centre for Protein Sequences (MIPS) am Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FKG Project Coordination: Andreas Ruepp and Wolfgang Baumeister E-mail: ruepp@biochem.mpg.de, baumeister@biochem.mpg.de Information on performance of analysis and a more detailed annotation can be viewed at:
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Ruepp.A., Graml.W., Santos-Martinez,M.L., Koretke,K.K., Volker,C.,
Mewes,H.W., Frishman,D., Stocker,S., Lupas,A.N. and Baumeister,W.
The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                   22761 GGCTACGAIGTTAGAGTAGAATCTATACTTGCAGACGAAGGAAGTTGATGAAGTATT 22820
                                                                                                                                                                                                                                                                                                                                    22821 GTTGGGACGATGAAACATTTCTTGTGTCAACCTTGGAAGTATTGAGGCTTCCCGAGAAT 22880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22881 GICATCGCCAATATTTGGATTCGTTCAAGTTACGCCAGGCGTGGAGTAATAGGCTCTTTT 22940
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                                                                                                                                                                                                                                                                    213
                                                                                                                                  94 GGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAAAGTCGTT 153
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AL445064 AL139299
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                                                                                                                                                                                                                                                                    154 ATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGGGATAAAGTTGCCCGACGAT
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
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   DB 1;
Score 47.4; DB Pred. No. 0.0093
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NNIYVNBORTIDPSMGKYNARIEDDMAADIYALEGIHIAKMHRAGIAHGDLIV
1697. 2260.
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3747. .4019
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Thermotoga maritima (strain MSB8); PIR:A72242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="FIXA (related to carnitine metabolism) related
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/note="similarity to known protein:
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HAMI [validated] - yeast (Saccharomyces cerevislae);
PIR3:557088
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2450. :3736
2450. :3736
2450. :3736
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                                                                                                                                                                                                                                                                                                                                             /gene="Ta0325"
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4044. .4820
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/gene="Ta0328"
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SVVVVSTADQSPILKVKGAISAVVHAHHFASQGKDVLLLMDSITRLALAQREIGLAAG
EPPTLAKETPSFPQLLTRIAESCGAFKKGSITGIFYULVEGDDISLDPIADSLMGVLD
GHILLSRRRAVRGLFPAVDPVRSLSRLMPKLVSEBHFWKANFFKEVLSKFEDVBELVR
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COMPLEMENT (2004. .2687)
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KGQKIGIFAGAGVGKSTLLGMITRHSKADVVVLALIGERGREVKFFLEEVLGEEGLKK
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/db_xref="G1893955"

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SNLKEEYREKVEEFLKTFLLEFSYYVPQVKVLKEDLRNIIDELIKFKTNLKLYINPED
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SLIAIHARTAKQGFSGKALWHRIKEAKKVASVPIIGSGDVKSWRDIERMFEETECDGV
MVGRAALSNPWIFKEFKEKRDIEVGLKERMDFILEELSMMTEYMSREKACAEIKSQIV
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KIPRDKKVIVICRSGARAIAATFALRSAGFDNVYALKGGIAALADYVTPKTTLGIK"
complement (4364. .5128)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKEFWPYLAVFLFGLILGSFYNVLIYRLPRNISIVFPSSHCPBC
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IPFVIYLYYVRFRIEGLGFGDVILLGFIGSVGGVYGYFSALFIGSFLGLLYALDMII
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complement(5125, .5991)
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                                                                                                                                                                                                                           /product="flagellar export protein"
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LPPEGVGADELRKKLLSFGVRVAGGGGKLKGKIFRISHMGMDVLDMVHAISAVELALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative indicates no similarity to known proteins Hypothetical indicates similarity to a protein of unknown function. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286236 ACCATTGAAATACTGAAGATACCAGACGACGTTGTCGGCCATGATATGGACAAGGTCAAGC 286295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286296 TTCGCTCGCAAGGGTATCTTTGGATCCTTCGGTGCCATAGATGCCGGTTATCATGGCAAT 286355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286356 CTCACCCTATCCTTCAACGCCGGATCG---CGGTTAACCTTAGGAGGGGAAGA 286412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lenox, A.L.,
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(Dassa 1 to 14286)

Deckert, G., Warren, P. V., Gaasterland, T., Young, W.G., Lenox, A.L., Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., Aujay, M., Huber, R., Feldman, R.A., Short, J. M., Olsen, G.J. and Swanson, R.V. The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 TTAGCAAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 ACCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGATAAGGAGCAGT 243
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Aquifex aeolicus section 79 of 109 of the complete genome.
AE000747 AE000657
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                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                             0; Mismatches 105; Indels
                                                                                                                                                                                                                                                               DB 1;
0.025;
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                                                                                                                                                                                                                                                               Score 46;
Pred. No.
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68. .427
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68. ^^7
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                                             /codon_start=1
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                                                                                                                                                                                                                                                               9.88.
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PIR: D69316"
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Best Local Similarity
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Sulfolobus solfataricus.

Sulfolobus solfataricus

Sulfolobus solfataricus

Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.

1 (bases 1 to 11922)

She, O., Singh, R.K., Confalonieri, F., Zivanovic, Y., Allard, G.,

Awayaz, M.J., Chan-Weiher, C.C., Clausen, I.G., Curtis, B.A., De

Moors, A., Erauso, G., Fletcher, C., Gordon, P.M., Heikamp-De Jong, I.,

Beffrias, A.C., Kozeraz, C.J., Medina, N., Peng, X., Thi-Iwgoc, H.P.,

Redger, P., Schenk, M.E., Theriault, C., Tolstrup, N., Charlebois, R.L.,

Ragan, M.A., Sensen, C.W. and Van Der Oost, J.

The complete genome of the crenarchaeon Sulfolobus solfataricus P2

L. Proc. Natl. Acad. Sci. U.S.A. 98 (14), 7835-7840 (2001)

142726

L. bases 1 to 11922)
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S She,O., Singh,R.K., Confalonieri,F., Zivanovic,Y., Allard,G.,
S She,O., Singh,R.K., Confalonieri,F., Zivanovic,Y., Allard,G.,
S She,O., Singh,R.K., Confalonieri,F., Zivanovic,Y., Allard,G.,
Awayez,M.J., Chan Welher,C.C.-T., Clausen,I.G., Curtis,B.A., De
Moors,A., Erauso,G., Fletcher,C., Gordon,P.M.K., Heikamp-de
Jong,I., Jeffries,A.C., Kozera,C.J., Medina,N., Peng,X.,
Thi-Ngoc,H.P., Redder,P., Schenk,M.E., Theriault,C., Tolstrup,N.,
Charlebois,R.L., Doolittle,W.F., Duguet,M., Gasterland,T.,
Garrett,R.A., Ragan,M.A., Sensen,C.W. and Van der Oost,J.
Direct Submission
L Submitted (24-APR-2001) Europe/Canada joint project: Copenhagen
University, The Netherlands; Institute for Marine Biosciences &
University, The Netherlands; Institute for Marine Biosciences &
Location/Qualifiers
Location/Qualifiers

rce /organism="Sulfolobus solfataricus"
//db_xref="Laxon:2287"
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Sulfolobus solfattaricus section 16 of 272 of the complete genome.
AE006657.1 GI:13813325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8230 TTAACGCAAACGACAGACCTATAAGACTTTACAGAGGTATGAGGATATGCCAGCTCGTTT 8171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
                                                                                                                                                                                                                                                                                                                                                                                                                                          9.7%; Score 45.6; DB 1;
llarity 54.1%; Pred. No. 0.02;
Conservative 0; Mismatches 79;
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COMPLement (8061. 8603)
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/conplement (8061. 8603)
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CDS

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDRDEIVTLISKEGKAIIVATDVNPLPDTVKKIASKFNAKIFIPEKSLSIDEKQRLID
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NEKQIEKLREVLYKLLNGKAIVVKKDSRVGDIAFDGNNIYIGEEKVNNEIAEYADKEI
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| GOKKUMPDEGGEPTRENDARAESISPROTERRYKYSODIGGVAPDIKOKO
| GSASILAFLGAOKASKPLTVEKYYDDIAKVATSTGGSRDIKIRLAGILKDASPLEA
| KYLVRFVDGRIRKOGIOPTILDALAITFGGGONFRPIVERAYNIRADIGNIAKILANG
| GIBOLKNIRPOGETPRENDARSTSOPARAESKVORGNETYOPERGENGPIKAGNET
| FIFSRRLENITNOYPOVAET-EDLMYYEGEDYTVKPKLESTVENDINOYHIRAGDKI
| FIFSRRLENITNOYPOVAET-EDLMYYEGEDYTVKRESTYPORGNETGENRPFOELMHRKRK
| SDIHBATKEYPVNYTHPODWYTFTDLMYYEGEDYTVKRESTYPORGNETGENRPFOELMHRKRK
| FIPSRRLENITNOYPOVAET-EDLMYYEGEDYTVKRESTYPORGNETGENRPFOELMHRKRK
| SDIHBATKEYPVNYTHPODWWITPALVAETIGAETISPLATCKOOYAEGGLSIRFPRRIRWR
| PDRSREDBATTNREILEMYKSOLKKIEBERPSDGSV"
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| // gene="ORRE" | 23382
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Pred. No. 0.028;
); Mismatches 172;
                                                                                                                                                      878. .883
/note="lig box A"
906. .909
/note="lig box B"
/evidence=experimental
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47.9%; Pred
                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
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908. .2710
/gene="lig"
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TYTOTSABHGIDGANGKGNRGVGLITPMRPMSLEATAGKNPVNHVGKLYNVLANLIA
NKTAQEVRDVKFSGVOVLGQIGRPIDDPLIANVDVITYDGKLTDETKNEISGIVDEML
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Submitted (06-DEC-1991) A. Kletzin, Max-Planck-Institut
Blochemie, Am Klopferspitz 18a, D-8033 Martinsried, FRG
2 (bases 1 to 3382)
Kletzin,A.
                                                                                                                                                                                                                    Score 45.4; DB 1; Length 11922;
Pred. No. 0.022;
0; Mismatches 171; Indels 3;
                                                                      complement(9603...9866)
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/note="SSO5410"
complement(9603..9866)
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/note="Transcription, RNA modification"
/codon_start=1
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complement(250. .771)
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Best Local Similarity 48.1%;
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IQKKUMPPETGMPELGJGFKFLIRASIATSYSDDEIRKWKSKSGLGQVAFDIKQKO
GSASILAFLGAQKASFLTVBKVYDDLAKYATSTGEGSRDIKIRLLAGLLKDASPLEA
KYLVRFVDGRLRKGIGDATILDALAITFGGGQNFRPIYERAYNLRADLGNIAKILANG
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FIFSRRLENITNQYPDVAEYISKYVKGNEFIVEGEIIPVDPETGEMRPFQELMHRKRK
SDIHEAIKEYPVNVFLFDLMYYEGEDYTVKPLSERRKKLESIVEDNDYVHIATHITD
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MYGAFHGKGRKGGKYSSFLMAAYNPDKDVFETYCKVASGFTDAELDDLQKKIAELKRD
TPHPRVVSTMVPDVWLTPALVAEIIGAEITISPLHTCCKDQYAEGGLSIRFPRFIRWR
361 TCGCTTTCTTCACCTCATTTTCGCCAGAACATTAACACCCAGTAGAGAATCCTTATCATGG 302
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                                                                                                                                                                                                                                                                                      unclassified.

1 (bases 1 to 3382)
Rletzin,A.D. and Rueger,R.D.
THERMOSTABLE LIGASE FROM ARCHEOBACTERIA
Patent: EP 0571880-A 5 01-DEC-1993;
BOEHRINGER MANNHEIM GMBH (DE)
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                                    420 AAACTATCAGGGGGGGCACAAGGTTAGCGTTTTCAAA 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="unidentified"
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Sequence 5 from Patent EP0571880.
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Kawarabayssi, Y. is officially affiliated with the National Institute of Bioscience and Human-Technology, Tsukuba, Ibaraki 305-0046, Japan.
Nomura, N. and Sako, Y. are at Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan
The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
All the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS codons or more between ATG or GTG and stop codon are defined by Smith-Waterman algorithm against GenBank and GenPept release 109; EMBL release 56.0; SwissProt release 36.0; PIR-Protein release 57.0; and OWL release 31.0.
E-mail address for comments and questions: genomeAPB@hite.go.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayasi, National Institutte of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:kyutaka@kazusa.or.jp, Tel:+81-3-3481-8951, Fax:+81-3-3481-8424)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi,Y., Hino,Y., Horikawa,H., Yamazaki,S., Haikawa,Y.,
Jin-no,K., Takahashi,M., Sekine,M., Baba,S., Ankai,A., Kosugi,H.,
Hosoyama,A., Fukui,S., Nagai,Y., Nishijima,K., Nakazawa,H.,
Takamiya,M., Masuda,S., Funahashi,T., Tanaka,T., Kudoh,Y.,
Yamazaki,J., Kushida,N., Oguchi,A., Aoki,K., Kubota,K.,
Nakamura,Y., Nomura,N., Sako,Y. and Kikuchi,H.
Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl
DNA Res. 6 (2), 83-101 (1999)
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361 TCGCTTTCTTCACCTCATTTTCGCCAGAACATTAACACCAGTAGAGAATCCTTATCATGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeropyrum pernix
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                          06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka,T., Hino,Y., Kawarabayasi,Y. and Kikuchi,H.
Direct Submission
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AP000059 BA000002
AP000059.1 GI:5103911
                                                                       420 AAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAA 455
                                                                                                                                          301 CAAATACCAAGGACAACAAGGCGTAACTTTACCAAA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Aeropyrum pernix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aeropyrum pernix (strain:K1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:56636""
complement(422, .595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1152. .1490)
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/qene="APES009"
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COMPLEMENT (4516 . 4842)
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complement (4516 . 4842)
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"SEPDSFFTCASRTSIAASSAVVSALPPTPFATILTSSTKLYLGLYFSSPHDKIRKAW
                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 TTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 GGGAAATTAATCGACGTGGAAAAGGAAGGAAAGGCATTGTTCCTCCAAGGGAATACGCC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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9.2%; Score 43.4; DB 1; Length 167000;
Best Local Similarity 48.3%; Pred. No. 0.13;
Matches 153; Conservative 0; Mismatches 161; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                            KROMAP"
                                                                                              gene
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AFTSERALHEIDEHLEERAKRKVSYBELRAAIRILLINVNMYEKGTYNAYYEKAGEC
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complement(3301. 3669)
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MDDRDARNLAKKLGLQVMGTLGVIALAKYKGLTSKAKPIIDKLIESGEWISRRTLEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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KVILVGDEAYFRIAVEIALGSRGADSYYLGLAKTLNLPVATSDKVQAQNAKKAGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="WSLSIIGFALEVNPLYLANAITPSVPITCNPSFLARFLASRSI
SSKPALRSKARTIASASPVSTNSSKRDTSLLSTTSSTRIKPALTTFSLPGLPATVISA
OTVSGTRTSPKSFSRRSRRHTLASAMIMLELETTRSLSSSSLLLCKLLGDLQIILLQLL
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LAELARRIRRRLSQEREEPSEILSRERSRLA"
                          /gene="APE0276"
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complement(1152. .1490)
/gene="APE0276"
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4028. ,440?
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YKSQGNWKTKEVYGYETPGBYKERRQFWFHWRVAICSCKKEKWDIREFLIGRHRWDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 9203)
Sargan,D.R., Bennet,I.D., Cousens,C., Roy,D.J., Blacklaws,B.A., Dalziel,R.G., Watt,N.J. and McConnell,I.
Nucleotide sequence of EV1, a British isolate of maedi-visna virus J. Gen. Virol. 72 (Pt 8), 1893-1903 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Maedi-Visna-like virus EVI
Viruses; Retrold viruses; Retroviridae; Lentivirus; Ovine/caprine
                                                                                                                                                                                                                                                                                                                                       S51392 9203 bp RNA VRL 24-JUL-2000 gag. . .rev [maedi-visna-like virus EV1, Genomic RNA Complete, 6 genes, 9203 nt].
38201 CTCCTCCACACCCAAGAGTACATCAGGCTCCCGGGCTACGTGGCGGGCTGGTGAACCTC 38260
                                                           GenBank staff at the National Library of Medicine created this entry (NCBI glubbsq 51392) from the original journal article. This sequence comes from fig 2. Location/Qualifiers
                                                                                                        GATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1785. :5045
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1785. :5045
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<5691. .5978
/ote-"This sequence comes from fig 2"

    9203
    /organism="Maedi-Visna-like virus EV1"
    /db_xref="taxon:12750"
    11848

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S51392.1 GI:234046
                                                                                                                                                                                                                               415 AGAGGAAACTATCAGGG 431
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EERQGLVTGKRKPWVSIEILGTKHDOEKEKVNWAEPCEKWFGOLVWYTSRYIRLULWG
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Helicobacter pylori, strain J99 section 90 of 132 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="This sequence comes from fig 2; conceptual translation presented here differs from translation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3869 AGAGGTAAGTATCCCAGCAGGACAAGTAAAGAAGATTCCAATTGATTAAGAATAAATTT 3928
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AE001529 AE001439
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VERSION KEYWORDS SOURCE

REFERENCE

COMMENT

TITLE

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  gene
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25;397(6721):719]]

2 (bases 1 to 10922)

2 (bases 2 to 10922)

2 (bases 2 to 10922)

2 (bases 3 to 10922)

2 (bases 2 to 10922)

2 (bases 3 to 10922)

3 Extract Submission

3 Street. Cambridge, MA 02139 USA

Address all correspondence to: Me@arcb.us.astra.com or Richard

A. Alm, Astra Research Center Boston, 128 Sidney Street. Cambridge,

MA, 02139. Loc See L. Ling, Donald T. Moir, Douglas R. Smith,

Braydon C. Guild, Gilles Garmel, Anthony Caruso, Debra M. Mills,

Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics

Comporation, 100 Beaver Street, Waltham, MA, 02453. Gill Jiang and

Diane E. Taylor are with the University of Alberta Department of

Medical Microblology and Immunology, Edonotron, Alberta, Canada, TGG

2H7 and the Canadian Bacterial Diseases Network All other authors

are with Astra Research Center Boston, 128 Sidney Street,

Cambridge, MA, 02139. Putative identifications, sequence

alignments, and name and sequence search capabiblity are available

http://www.astra-boston.com/hpylori).

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                                                                                                                                                                                                                                                              Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori Nature 397 (6715), 176-180 (1999) 99120557
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Helicobacter pylori J99
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
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Mark A. Ling, L. S., Moir, D. T., King, B. L., Brown, B. D., Doig, P. C., Smith, D. R., Noonan, B., Guild, B. C., deJonge, B. L., Carmel, G., Tummino, P. J., Caruso, A., Uria-Nickelsen, M., Mills, D. M., Ives, C., Gibson, R., Merberg, D., Mills, S. D., Jiang, Q., Taylor, D. E., Vovis, G.F. and Trust, T. J.
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Clones are available from Research Genetics (info@resgen.com). BAC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cohter: Mark Adams
Department of Eukaryotic Genomics
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Maximum DB seq length: 200000000
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Database :

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Result

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i EST.

Chicken.

ISM Gallus gallus

Rukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

ICE 1 (bases 1 to 697)

IRS An expressed sequence tag database of T-cell-enriched activated chicken splenocytes; sequence analysis of 5251 clones

INE 20318616

Molecular Endocrinology

University of Delaware

40 Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-341

Email: joan@UDel.Edu, www.chickest.udel.edu

Seq Primer: T7.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               A1982253 697 bp mRNA EST 07-MAY-2001 att. PROVINGS 92.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0078.92.f 5' similar to MITOCHONDRIAL CARNITINE O-PALMITOYLTRANSFERASE II, mRNA sequence.
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/organism="faulus gallus"
/do_arei="fauxon:9031"
/do_arei="fauxon:9031"
/clone="pat.pk0078.g2.f"
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/cs="male"
/cell_type="Con A-activated splenic T cell"
/lab_host="E.coli TOP10 F/"
/lab_host="E.coli TOP10 F/"
/lab_host="faulus"
/l
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Pred. No. 6.1;
0; Mismatches 0; Indels
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Fax: 217 244 5617

Email: h-lewinGuluc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

for A. Lewin and J. E. Womack, Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trimmi g:

Cross_match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.
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1 (bases 1 to 592)

Lewin, H.A., Soares, M.B., Rebelz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine ESTS

Unpublished (2000)

Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF041541 592 bp mRNA EST 10-OCT-2000 BP250026A10A11 Soares normalized bovine placenta Bos taurus CDNA clone BP250026A10A11 5', mRNA sequence. BF041541 GI:10758596
                                                                                                                                                                                                                                                                                                                                                                                Gaps
/db_xref="GDB:5362141"
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/csx="Male="CIT"+HSP"
/coll_Ltype="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
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Gaps ; 0 100.0%;

TITLE COMMENT

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                                                        Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Murinae; Lio 222)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukudishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishiawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawal, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabo, M., Matsuyama, T., Miki, R., Mizuo, Y., Nakmura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, J., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Watanishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)

Londatic Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frote—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGACCAAGAGCTCTTTTTTTTTTTTTYN 3'], cDNA was prepared by using trehalose themo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand CDNA was prepared size themo-activated reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawal, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
WL.http://genome-gsc.riken.go.jp,
Sasaki,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Garnind, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/clone="4921501122"
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//doc="Next-"Dutub (Life Technologies)
//doc="Next-"Dutub (Life Technologies)
//doc="Next-"Carl (Tayl)-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the UI-R-C0 library.

UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, audit lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 norlectides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library of origin of a clone within
the mixture as follows: PCR amplified CDNA inserts from
UI-R-C1 clones from which 3' ESTS had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacterial (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1787230
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammålia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 413)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
1E1: 319 335 9250
Fax: 319 335 9565
                                                                                                                                                                                                                                                         BESS1925 413 bp mRNA EST 12-DEC-2000 UI.R-C2p-ob-f-12-0-UI.rl UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-ob-f-12-0-UI 5', mRNA sequence.
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/clone_lib="UI-R-C2p"
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
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                                                                CTGGAAAATCAGAAAAGAAA 34
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Query Match

LOCUS RESULT 6 BE503276/c

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ACCESSION VERSION KEYWORDS SOURCE

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REFERENCE AUTHORS TITLE

JOURNAL COMMENT

FEATURES

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Tourse mouse.

ENKATYORIA MATERIAGOS CHORDATA; Vertebrata; Euteleostomi; Musmusculus.

ENKATYORIA; Metrazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 530)

Ano, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

AL Upublished (1999)

Other GSSS: RPCI-23-307F24.TV

Contact: Shaying 2hao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Fax: 307 700x; F column: 24

Seq primer: SP6

Class: BAC ends

Class: BAC ends
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/lab_host
AQSB3242 530 bp DNA GSS 30-JAN-2000
RPCI-23-307F24.TJ RPCI-23 Mus musculus genomic clone RPCI-23-307F24
, DNA sequence.
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4.2%; Score 20; DB 13; Length 530;
Best Local Similarity 100.0%; Pred. No. 20;
Mátches 20; Conservative 0; Mismatches 0; Indels
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Eukaryota; Metazoa; Chordata; Cancer Genome Anatomy Project (CGAP),

In (bases 1 to 517)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: Gapba: remail.nih.gov/ncicgap.

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CEAP clone distribution information can be infodimage. Inl.gov Requence stop: 463.

Clone distribution: Sequence stop: 463.

Infodimage. Inl.gov Requence stop: 463.

Infodimage. Inl.gov Requence stop: 463.

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//organism="Homo sapiens"
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                                                                                     Score 20; DB 11; Length 413;
Pred. No. 20;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                       mRNA sequence.
BE503276
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Query Match Best Local Sir Matches 20;

RESULT AQ983242

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BASE COUNT

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ORGANISM

REFERENCE AUTHORS

TITLE

MEDLINE PUBMED

REFERENCE AUTHORS

REFERENCE AUTHORS

JOURNAL PUBMED

TITLE

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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fi/Tetraodon.
                                                                                                    /tissue_type="testis"
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384. .935
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holofternktolldyksemfkeeptktrkgosonkskykiedskoflpksdyd
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodontidae: Tetraodon.
1 (bases 1 to 1172)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius,H. Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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Tetraodon nigroviridis genome survey sequence T3 end of clone
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Pred. No. 19;
Mismatches
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                     /note="putative"
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1048
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ative 0;
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
IIOh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                Shibate, K. Itoh, M. Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN Integrated sequence analysis (RISA) system-184-format Genome research. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 1048)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 (bases 1 to 1048)
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
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JOURNAL REFERENCE AUTHORS

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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

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JOURNAL

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/strain="C57BL/6J

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RIRBN Genome Exploration Research Group Phase II Team and the Fahrom Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-680 (2001)
S (bases to 1504)
Adachi,J., Alzawa, K., Akahira,S., Akimura,T., Aono,H., Arai,A., Hanawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanawa,T., Carninci,P., Tido,M., Izawa,M., Kato,H., Kawai,J., Kolima,Y., Konno,H., Kouda,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okkido,T., Owa,C., Saito,H., Saito,H., Sakai,K., Sakai,K., Sani,H., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,X., Shinagawa,A., Shiraki,T.,
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Musaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmanla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus
I (pases 1 to 1504)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Mathods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKO15811 1504 bp mRNA HTC 05-JUL-2001 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930517G15, full insert sequence. AKO15811 GI:12854293
/organism="Tetraodon nigroviridis"
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/clone=11b="C"
/note="Genoscope sequence ID : COBCO06DH04T1-end : T3"
/ 243 c 231 g 356 t 13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAP trapper.
Mus musculus (strain:C5/BL/6J) adult male testis cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:4930517615.
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                                                                                                                                                                                                                                 Length 1172;
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Pred. No. 19;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Yanaka, T., Tejima, Y., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshina, Y., Muramatsu, M. and Hayashizaki, Y. Direct Submission and Jul-2000, Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Presearch Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suchiro-cho, Tsurumi-tu, Yokohama, URL: http://genome.psc.riken.go.jp/, Tel:81-45-503-922, Pax:81-45-503-9216, Pax:81-45-503-922, Pax:81-45-503-922, Pax:81-45-503-922, Pax:81-45-503-9216, Pax:81-45-503-922, Pax:81-45-503-9216, Pax:81-45-503-922, Pax:81-4504, Pax:81-45-503-922, Pax:81-4504, Pax:81-4504, Pax
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/protein_id="Bh829987.1"
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/translation="MKCAKHPSTISMKLTSVPELPYKKGLLNSSPRPKEKHNAKSKYG
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CYDNGEKAAEKSEAEGISIODDVSSTLLCCSOFTSOLEBAVREECGALESLYKMPCOO
WNOMEEISKDOSNLEELOSDGKTASLNIVOIAKLARKFEDFKSRLKTRKEWWQTKNED
KETMAETLKHYGLMEKOIEEFITSHSALAESOTEFESSOGTPSVYTRMARMIKIFENOS
TMLEKALNOOOTIESKYKOLETDFOMLIMEKTLLEAEIRRIERPKSAAKEEOTKK
SGKSEKKKFKEKEKSYDMKICYLFIPQLVKMYLNHGLF"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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377. .1492
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/db_xref="MGD:MG1:1907906"
/db_xref="MGD:MG1:1921953"
/clone="4930517G15"
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100.0%; Pred. No. 19;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 20; Conservative
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Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

'N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAGGGCGCGCAACTCGAGTTTTTTTTTTTTV 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
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MOL129F24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCZM0129F24 R, DNA sequence.
AZ835592
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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/dome_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.rtc.riken.go.jp) for
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="0 day.neonate"
/lab_host="DH10B"
                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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  Tel: 81-45-503-9222
Fax: 81-45-503-9216
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RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishl, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawal, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kagawa, J., Kal, C., Kawal, J., Kikuchi, N., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Wataniki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, K., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Shida, K., Yoshiki, A., Yoshino, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                    1 (bases 1 to 240)
Schwerin,M., Dorroch,U. and Goldammer,T.
Mapping of differenially expressed hepatic and intestinal EST's in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                  Score 19; DB 10; Length 240;
Pred. No. 66;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="XL1-blue"
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24 c 60 g 60 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Intestine"
/dev_stage="lactation"
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                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female"
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                                                                                                                                                                                                   Unpublished (2000)
Contact: Schwerin M
Molecular Biology
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Best Local Similarity 100.
Matches 19; Conservative
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444 AGCGTTTTCAAAGAGAAAG 462
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AV760824/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. :310
/organism=Mus musculus"
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musculus G7BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess: The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWNA2 (gill/372114/191A129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Rm. 310, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Rm. 310, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Rm. 310, SSS 5606
Fax: 801 585 5707
Email: ddunn@genetics.utah.edu
Insert Lenghhi: 1000 Std Error: 0.00
Plate: 0129 row: F column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 310.
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Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases I to 349)
Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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AU221733 unpublished oligo-capped cDNA library, stage L1
Caenorhabditis elegans cDNA clone yk897e04 3', mRNA sequence.
AU221733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 TGGAAAATCAGAAAGAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
AU221733/c
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Homean.

Eukaryota: Metacoa: Chordata; Craniata: Vertebrata: Euteleostomi; Homeania: Eutheria; Primates; Catarrhini: Hominidae; Homo.

Eukaryota: Metacoa: Chordata; Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini: Hominidae; Homo.

Exp. 1 (bases 1 to 374)

In (bases 1 to 374)

RS (du,Y., Zhao,M., Huang,O., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Xiao,H., Xiao,H., Xiao,H., Xiao,H., Xiao,H., Ziao,M., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Zhang,Q., Chen,S., Han,Z., and Chen,Z., Xu,S., Gao,W., Zhang,Q., Chen,S., Han,Z., and Chen,Z., Contact: Zequang Han Chinese National Human Genome Center at Shanghai

Contact: Zequang Han Chinas Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

This 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzgechgc.sh.cn

This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                             /strain="N2"--
/db_xref="taxon:6239"
/clone="yk897e04"
/clone_lib="unpublished oligo-capped cDNA library, stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV760824 374 bp mRNA EST 19-OCT-2000 AV760824 MDS Homo sapiens cDNA clone MDSEDE05 5', mRNA sequence.
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0
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4.0%; Score 19; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 others
A complementary view of the C.elegans genome Unpublished (2001)
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata Ill, Mishima Shizuoka 411, Japan
Tel: 81-559 81-6854
Fax: 81-559 81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. 349
Corganisma Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
102 c 80 g 95 t
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ô 0; Gaps Query Match
4.0%; Score 19; DB 10; Length 374;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 19; Conservative 0; Mismatches 0; Indels

δ QQ

Search completed: January 31, 2002, 11:49:22 Job time: 1204 sec

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R.Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A: Omplete sequence and gene organization of the genome of a hyper-thermophili A; Reference number: A71000; MUID:98344137
A; Reference number: A71000; MUID:98344137
A; Accession: E71216
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-156 < KAW>
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A; Residues: 1-156 < KAW>
A; Resperimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBa C; Genetics:
i pol polyprotein - Maedi/Vis
i pol polyprotein - Maedi/Vis
i pol protein - Maedi/Visna v
probable duTP pyrophosphatas
deoxycytidine triphosphate
                                                                                                                                                                                        seq_documentation_block:
dCTP deaminase (EC 3.5.4.13) PH1997 [similarity] - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGGGATAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 GTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAA 250
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Gaps: 0
Percent Identity: 93.590
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165
  0.0024
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0.0056
0.0050
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183.95
178.34
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pir1:B45390
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pir2:S26429
pir2:F84406
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dCTP deaminase [imported] - Chl
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dCTP deaminase (EC 3.5.4.13) dc
probable dCTP deaminase (EC 3.5
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nucleoside-triphosphatase (EC 3
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probable dCTP deaminase (EC 3.5
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-Q=Cqqn2_L/USPTQ.pmodel -DEV=x1h
-Q=Cqqn2_L/USPTQ.pmodel -DEV=x1h
-Q=Cqqn2_L/USPTQ.pmodel -DEV=x1h
-Q=Cqqn2_L/USPTQ.ppod_L/USB957709/runat_30012002_133258_9503/app_query.fasta_1.536
-DB=PIR_68 -QFMT=fastan -SUFFIX=rpr -GAD-PD=12.000 -GAPEDT=4.000
-DGAPEDT=6.100 -LOOPECL=0.000 -LOOPEXT=6.000
-GCAPEDT=6.050 -KGAPOP=10.000 -KGAPEXT=0.500 -FCAPOP=6.000
-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOPOP=6.000
-DELDEY=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOPOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=DLOSUMG2 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -TRX_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE_LOCAL -OUTFWT=PIS NORM=-XR -HEAPSIZE=500
-ALIGN=6 -KGPU=3 -LONICG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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                                                                                              Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 219241
Database length: 76144552
Search time (sec): 39.880000
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pir2:E71860
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pir2:T44356
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D.E.;

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Nature 392, 353-358, 1998
A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MUID:98196666
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Most accoule type: DNA
A; Residues: 1-180 < AQDP>
A; Residues: 1-180 < AQDP>
A; Exess references: GB:AE000747; NID:g2983944; PIDN:AAC07499.1; PID:g2983951; GB:AE00
C; Genetics:
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probable dCTP deaminase (EC 3.5.4.13) dcd [similarity] - Aquifex aeolicus
brobable dCTP deaminase (EC 5.5.4.13) dcd [similarity] - Aquifex aeolicus
C.Species: Aquifex aeolicus
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86 TCAGAGTGGGCAGAGGG...GCTTTTGTTAAGGGGAAA...TTAATCGAC 129
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51 ValLysLysGlyThrLysGlyValArgIleLeuGluPheGluGluTyrPh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 GTGGAAAAGGAAAGGTCGTT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 162
Gaps: 5
Percent Identity: 37.654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: A70439 from: 1 to: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: dcd
C;Superfamily: dCTP deaminase
C;Keywords: hydrolase
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2.229
67.284
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US-08-957-709-70 x A70439
                                                                                                                        451 TCAAAGAGA 459
                                                                                                                                                                                 151 SerLysArg 153
                                                                                                                                                                                                                                              seq_name: pir2:A70439
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                        seq_documentation_block:

GCTP deaminase (EC 3.5.4.13) PABI164 [similarity] - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: G75030

R; anonymous, Genoscope
R; anonymous, Genoscope
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R; Accession: G75030
R; Reference number: A75030
R; Reference number: A75030
R; Resture: DNA
R; Resture: DNA
R; Resture: DNA
R; Resture: DNA
R; Resture: Strain Orsay
R; Corsa-references: GB:AJ248288; GB:AJ096836; NID:g5458960; PIDN:CAB50685.1; PID:g545919
C; Genetics:
C; Genetics:
C; Genetics:
C; Cepperfamily: GCTP deaminase
C; Keywords: hydrolase
TTCTGAAGAATCGCTCCAACCAGCTTATGACCTCAGAGTGGGCAGAG 100
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Gaps: 0
Percent Identity: 85.621
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                                                                                                                 703.00
4.718
97.386
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US-08-957-709-70 x G75030
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Alternate names: hypothetical protein 3 lig-region classifications ambivated acceptance of the cannings (E. 3.7.4.1) [Similarity] and Alternate names: hypothetical protein 3 lig-region classification by the conversion 21-Jul-1995 #text_change 31-Mar-2000 [Species: Desulfurolobus ambivalens and 1-Jul-1995 #text_change 31-Mar-2000 [Skretzin, A. Accession: S26382] [Skretzin, A. Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and the conversation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extremely thermophility and second in S26382 [Aritle: Molecular characterisation of a DNA ligase gene of the extrem
                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
probable dCTP deaminase (EC 3.5.4.13) [similarity] - Desulfurolobus ambivalens
380 TTATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTAT... 426
                                           .....AGAGAGGCTT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 TIGITAAGGGGAAA.....TTAATCGACGTGGAAAAGGAAGGA 144
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100 heAlaArgLeuGlyLeuPheValProProThrIleValAspAlaGlyPhe 116
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117 GluGlyGlnLeuThrIleGluValLeu...GlySerAlaPheProValLy 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 GATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTT 244
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Percent Identity: 35.897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 173
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163 PheGlnLysGlyAlaThr 168
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US-08-957-709-70 x S26382
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                                                                                                                                     427
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deoxycytidine triphosphate deaminase BH0368 [imported] - Bacillus halodurans (strain C-1 C.) Species: Bacillus halodurans
C.) Species: Bacillus halodurans
C.) Species: Bacillus halodurans
C.) Species: Bacillus halodurans
C.) Species: Bacillus halodurans
C.) Species: Bacillus halodurans
C.) Sacession: H83695
Narakani, M.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A; Reference number: A83650; MUID:20263314
A; Accession: H83695
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-17, CSTO>
A; Residues: 1-17, CSTO>
A; Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04087.1; GSPDB:GNOC
A; Experimental source: strain C-125
                         347 TAAGATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGT 396
                                                                           .A 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 lyArgSerSerValGlyArgLeuGlyLeuPhelleGlnAsnAlaGlyTrp 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 AACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 TAAGGAGCAGTTTAGCAAGAGAGGGGTT...ATTGGTTCTTTTGCTTGG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 GTTGACCCAGGATGGGAAGCTTAACACTAATGCTCTACAATGCCTC 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCT
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Gaps: 6
Percent Identity: 37.179
                                                                                                                                                                                                             CCGCCAAGAACCCTTACAGAGGAAACTATCAGGGG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 TTATGACCTCAGAGTGGGCAGAGGCTTTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: BH0368
C;Superfamily: dCTP deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242.50
2.310
67.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: H83695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-957-709-70 x H83695
                                                                                                                                                                                                                                                                                                           seq_name: pir2:H83695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics
                                                                                                                                                                  397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
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395 GTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTA 444

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seq_documentation_block:
probable dCTP deaminase (EC 3.5.4.13) SCH35.46 [similarity] - Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Dec.1999 #sequence_revision 03-Dec.1999 #text_change 31-Mar-2000
C.Accession: T56613
R.Oliver. K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, June 1999
A.Reference number: 221610
A.Reference number: 221610
A.Scatus: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: references: EMBL:AL078610; PIDN:CAB44381.1; GSPDB:GN00070; SCOEDB:SCH35.46
A.Experimental source: strain A3(2)
                                   |||||||:::|||
| 135 roValLysLeuTyrProGlyAspArgPheLeuHisLeuValLeuValLys 151
                                                                                                                      338 CTGTCGAATTAAGATATGGAGAGAGTTTGTGCAGATCGCATTTATAAGG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GGTTCTTTTGCTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|||||||||:::|||
101 LysSerSerLeuGlyArgLeuGlyLeuValThrHisSerThrAlaGlyPh 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTCTACAATGCCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 AAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 .CTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|||::: ||||
34 alargLeuAspargTyrPheArgValPheGluAsnHisArgTyrProHis 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 uGlyAspGluProPheIleLeuHisProGlyGluPheValLeuAlaSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 CCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 TCAGAGTGGGCAGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 31.361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: T36613 from: 1
                                                                                                                                                                                                                                                                 438 AAGGTTAGCGTTTTCAAAG 456
                                                                                                                                                                                                                                                                                                                     168 gGlyValArgLeuProLys 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Gene: SCOEDB:SCH35.46
C)Superfamily: dCTP deaminase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216.00
2.077
61.538
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US-08-957-709-70 x T36613
                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:T36613
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                         seq_documentation_block:

C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
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C:Species: Aeropyrum pernix
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A: Aeropyrum per
111 ......TAAGGGGAAATTAATCGACGTGGAAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 GGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 TCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 uValValGluProLeuSerGlyAspThrValArgGluAsnGlyLeuAspL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 euAspProArgAlaProGlySerProGlyGluPheTyrGluCysGlyGlu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGCTACTTCCAGACTGGAAAATCAGAAAA......GAAAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 ACTIATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235.00 Length: 174
2.136 Gaps: 5
63.218 Percent Identity: 34.483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: D72724 from: 1 to: 181
                                                                                               445 GCGTTTTCAAAGAGAAG 462
                                                                                                                                                          166 ThrLeuProLysPheLys 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Gene: APE0333
C,Superfamily: dCTP deaminase
C,Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-957-709-70 x D72724
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Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                          seq_name: pir2:D72724
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to: 191

67

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Cypecies: Mycobacterium tuberculosis
Cyspecies: Mycobacterium tuberculosis (Cyspecies)
Cyspecies: Mycobacterium tuberculosis (Cyspecies)
Cyspecies: Mycobacterium tuberculosis (Cyspecies)
Cyspecies: Mycobacterium tuberculosis from the complete geno
A;Accession: B70526
A;Accession: B70520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
Residuca: 1-190 <COL>
A;Cross-references: GB:296800; GB:AL123456; NID:93261800; PIDN:CAB09605.1; PID:921939
                                                                                                                                                                                                                                                                                                                                                         451
                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 yHisProSerArgAspSerLysTyrIleGlyGlnThrArgProGlnThrS 187
                       GATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GG 266
                                                   367 GTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTAC.. 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
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                                                                                                                                                                                                                                                         .....AGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....ATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 uGlylleAspProPheAspAspThrLeuValGlnProSerSerlleAspV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 TCAGAGTG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 169
Gaps: 3
Percent Identity: 30.178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198.00
1.941
60.355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: dCTP deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: B70526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-957-709-70 x B70526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAAGAGAAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:B70526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Óuality:
Ratio:
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                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T. X
                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
dCTP deaminase (EC 3.5.4.13) MTH1847 {similarity} - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec.1997 #sequence_revision 05-Dec-1997 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000937; GB:AE000666; NID:g2622974; PIDN:AAB86313.1; PID:g262298
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A69114
R; Smith, D.R; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
CAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCA 378
                                                                                                                    134 laThrLeuProlleLysLeuTrpProGlyMetLysIleGlyGlnLeuCys 150
                                                                                                                                                                      TTTATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 ACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATC..... 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . AAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||
|aLeuAlaThrThrHisGluTyrIleAlaLeuProGluAspLeuValAla 103
                                                                                                                                                                                                  ::::::||||||| :::|||||||:::::|||||||
151 LeuPheArgLeuThrSerProAlaGluHisProTyrGlySerGluArqTy 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 rIleAspProLeuAspAspProGluArgGlnIleGlnProSerSerValA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 LysProCysIleAspProLysAspProSerAspIleGluSerTyrMetGl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...ATACT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......GACGTGGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATAGAGCCATTTTCT....GAAGAATCGCTCCAACCAGCAGGTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 uThrPheHisValGluAspGlyProPheIleIleHisProGlyGluPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 7
Percent Identity: 31.551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A69000; MUID:98037514
A; Accession: A69114
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to
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1.860
57.219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: dCTP deaminase
C;Keywords: hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-957-709-70 x A69114
                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:A69114
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Quality:
Ratio:
                                                                                                                                                                                                                                                                        GGGGAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                       167 rGlySer 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-200 <M
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                    117
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seq_documentation_block:

decytytidine triphosphate deaminase [imported] - Halobacterium sp. NRC-1

Geoxycytidine triphosphate deaminase [imported] - Halobacterium sp. NRC-1

C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 16-Peb-2001

C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 16-Peb-2001

C;Accession: G84184

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky

Jung, W.V.; Kennedy, S.P.; Mahairas, T.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jan, J., Reithauser, B.; Pan, M.; Freiters, T. Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;

A;Reference number: A84160; MuID:20504483

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-195 <STO>
A;Residues: 1-195 <STO>
A;Conso: references: GB:AE004437; NID:g10579885; PIDN:AAG18843.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                                                                                                                                                    225
                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 CGTGGAAAAGGAAGGAAAGTC...GTTATTCCTCCAAGGGAATACGCCT 175
                                                                                                                                                                                                                                                                                                                                                       326 CCTCAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTTATGACCTCAGAGTGGGCAGAGG......102
                                                                                                                                                                                                                                                       pPhe.....GluGlyAspValCysIleValProAlaAsnSerPheAlaL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
                                                   AsnSerThrValValAspProLysAsnPheValGluGluAsnValValAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGGGTTGACCCAGGATGGGATGGAACTTAACACTAATGCTCTACAATG
                                                                                                                      ..........GCTTTTGTTAAGGGGAAATTAATCGA
                                                                                                                                                                                                                                                                                                                       176 TAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                      226 ATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATTTATAAGGCTAGAGGTCCGGCAAGAAACCCTTAC.....AG
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Gaps: 7
Percent Identity: 31.214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 AGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 195
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1.724
61.850
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C;Superfamily: dCTP deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: G84184
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US-08-957-709-70 x G84184
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Ratio:
Percent Similarity:
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                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

probable dCTP deaminase (EC 3.5.4.13) Cj1292 [imported] - Campylobacter jejuni (strain N C.Species: Campylobacter jejuni
C.Species: Campylobacter jejuni
C.Species: Campylobacter jejuni
C.Species: 31-Mar-2000
C.Species: 31-Mar-2000
C.Species: 31-Mar-2000
C.Species: 31-Mar-2000
C.Species: 31-Mar-2000
R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.N.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A.;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp.
A.;Reference number: A81250; MUID:20150912
A.;Retus: prellminary
A.;Residues: 1-186 cPAR>
A.;Cross.references: GB:AL139078; GB:AL111168; NID:G6968723; PIDN:CAB73719.1; PID:G696872
A.;Experimental source: serotype 02, strain NCTC 11168
C.;Genetics: dcd; CJ1292
C.;Superfamily: dCTP deaminase
C.;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                          AGGAGCAGTITAGCAAGAGAGGGGTTATT.....GGTTCTTTTGCTTG 278
                                                                                                                                                                                                                                                                                                                                                                                               GGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTCTACAATGCCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                         CAAATGAACCTGTCGAATTAAGATATGGAGAGATTTGTGCAGATCGCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .......GGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGA 134
                                                                                               135 AAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
                                                                                                                                                                                                 CCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCA 428
                                  51 IleAspProAlaLysGlnGlnAspGluLeuThrSerLeuValGlnProVa 67
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| eCysGluAlaAsnIleGlyLySGlyValValSerTyrGlyLeuSerSerT 39
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                                                                                                                                 67 lAspGlyGluProPheValLeuHisProGlyGluPheValLeuGlySerT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 7
Percent Identity: 29.444
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Quality: 189.50
Ratio: 1.788
Percent Similarity: 58.889
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US-08-957-709-70 x A81272
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us-08-957-709-70.rpr

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dcTP deaminase (EC 3.5.4.13) dcd [similarity] - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A; Variety: strain J99
C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Mar-2000
C.Accession: E71860
C.Accession: B71860
C.Accession: B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-188 -ARN>
A; Cross-references: GB: AE001529; GB: AE001439; NID: g4155590; PIDN: AAD06585.1; PID: g415
A; Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 IleValAsnValThrProPheGluProGluPheGluGlyTyrIleThrIl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 .....TTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 ATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 TACAGA......GGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTC 452
                                                                                                                                                                                                                      :::|||:::||||||||| ||||:::
20 MetIleSerProPheCysGluLysGlnValGlyLysAsnValIleSerTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||::::::
53 euPheAspAsnLysAsnAlaLeuIleAspProLysAsnPheAspProAsn
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                                                                                                                                                                                                                                                                                                                                                                                                            :::|||:::
36 rGlyLeuSerSerTyrGlyTyrAspIleArgValGlySerGluPheMetL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 AsnAlaThrLysIleAspAlaSerLysGluGlyTyrPheIleLeuProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 ATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTT
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                                                                                                                                                                                                                                                                                                                                               61 .TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 .....GCTTTTGTTAAGGGGAAA....
                                                                                        to: 190
                                                                                        from: 1
                                                                                                                                                                            37 CTTATAGAGCCATTTTCTGAAGAA.
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                                                                                   Align seg 1/1 to: D64566
US-08-957-709-70 x D64566
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dCTP deaminase (EC 3.5.4.13) HP0372 [similarity] - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 31-Mar-2000
C;Accession: D64566
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467
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A;Molecule type: DNA
A;Residues: 1-190 <TOM>
A;Cross-references: GB:AE000554; GB:AE000511; NID:92313475; PIDN:AAD07441.1; PID:9231347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 TTCTTTTGCTTGGGTTGACCCAGGATGGAAACTTAACACTAATGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 euSerAsnLeuGlyLysValProValAlaLeuThrProGluMetArgIle 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 SerGlnLeuValPheThrGluLeuThrSerProAlaAspArgProTyr. 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 GATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 GTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAG 416
                                                                                                                                                                                                                                                           80 ATGACCTCAGAGTGGGCAGAGAG.....GCTTTTGTTAAGGGGAAATTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......GTGGAAAAGGAAAGTCGTTATTCCTCCAAGGGAATACG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 CCTTAATCCTAACCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 aThrAlaGlyPheIleAspProGlyPheAsnGlyArgValThrLeuGluL 134
                                                                                                                                                                                                                                                                                                              ||||:::||||:::||||||||||:::
34 alAspValArgLeuGlyArgArgArgPheLeuGluPheGluArgAlaAsnVal 50
                                                                               36 ACTIATAGAGCCATTITCIGAAGAATCGCTC.....CAACCAGCAGGTT 79
                                                                                                                                  1 MetileLeuSerAspGlnAspIleLeuAlaArgLeuAlaAspGlyAspLe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 uThrValValGluAspGlyAspGluPheIleLeuHisProGlyAspPheV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ProCysIleHisProAsnArgGluAspGluValAspGluTyrValThrGl
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Percent Identity: 27.976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codon: GTG
C;Superfamily: dCTP deaminase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181.00
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us-08-957-709-70.rpr

A;Gene: dcd; BU108 C;Keywords: hydrolase

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211
                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spThrLeuAlaIleCysLeuGlyLysSerThrTyrAlaArgCysGlyIle 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 ATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 AATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 GATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 TACAGA......GGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                          68 AsnalaThrLysIleAspAlaSerLysGluGlyPhePheIleLeuProAl
                                                                                                                                                                        61 TCGCTCCAACCAGCATATGACCTCAGAGTGGGCAGAGAG.....
                                                                                                                                                                                                                                   103 ......GCTTTTGTTAAGGGGAAA....
                                                                                                                                                                                                                                                                                                                                            .....TTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                    162 AAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACG
                                                                                                                                                      37 CTTATAGAGCCATTTCTGAAGAA.....
            Length: 168
Gaps: 4
Percent Identity: 27.976
                                                                                                                         to: 188
                                                                                                                       Align seg 1/1 to: E71860 from: 1
            180.00
1.782
60.119
                                                                          alignment_block:
US-08-957-709-70 x E71860
              Quality:
Ratio:
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                                       Percent Similarity:
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alignment_scores
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seq_documentation_block:

dCTP deaminase (EC 3.5.4.13) [imported] - Buchnera sp. (strain APS)

Mylternate names: decxycytidine triphosphate deaminase
C; Species: Buchnera sp.
C; Species: Buchnera sp.
C; Species: Buchnera sp.
C; Species: Buchnera sp.
C; Species: Buchnera sp.
C; State: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C; Accession: C84942
A; Statember: A84930; Mulp:20445173
A; States: preliminary
A; States: preliminary
A; Molecule type: DNA
A; Residues: 1-206 cSTO
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104 ysSerThrPheGluSerIleLysMetProAsnAsnLeuValGlyTrpLeu 120 137 aHisArgIleAspProGlyTrpAsnGlyAsnIleValLeuGluMetPheA 154 102 132 133 ....GAAAAGGAAAGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAA 178 179 TCCTAACCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGATATG 228 273 IGCTIGGGTIGACCCAGGATGGGATGGAACTTAACACTAATGCTCTACA 322 154 snalaGlyLysLeuThrLeuValLeuArgProLysMetArglleAlaAla 170 87 7 CTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGA 57 AGAATCGCTC...CAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG. 37 nLysThrLeuIleAsnGlyIleThrValAspIleHisLeuGlyAsnLysP 103 .....GCTTTTGTTAAG......GGGAAATTAATCGACGTG...... 54 heArgPhePheTyrGluHisThrGlySerCysIleAspLeuSerAsnSer 71 Lys1leIleGlyGlyLeuSerLeuThrGluIleMetSerAsnGluIleIl 229 AAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GGTTCTTT 323 ATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGATTTGTGCAG Length: 164 Gaps: 5 Percent Identity: 29.268 373 ATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTAC 414 from: 1 174.00 1.812 58.537 Align seg 1/1 to: C84942 alignment_block: US-08-957-709-70 x C84942 Quality: Percent Similarity: alignment_scores

seq_name: pir2:A83210

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C,Genetics:
A,Gene: PA3480
C,Superfamily: dCTP deaminase
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Gaps: 4 Percent Identity: 26.316 Length: 172.00 1.737 57.895 alignment_block: US-08-957-709-70 x A83210 alignment_scores:
 Quality: 1
 Ratio: 1
 Percent Similarity: 3

Align seg 1/1 to: A83210 from: 1 to: 188

::||| |||||||:: 100 lebroArgAspValLeuThrIleCysLeuGlyLysSerThrTyrAlaArg 116 303 CTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGAT 352 TGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCCAAGA 252 253 GAAGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAA 302 117 CysGlyIleIleValAsnValThrProLeuGluProGluTrpGluGlyHi 133 353 ATGGAGAGAGTTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCA 402 403 AGAAACCCTTACAGA......GGAAACTATCAGGGGAGCACAAAGGTT 443 68 AsnPheAspGluLysSerPheValAspIleAsnSerAsp...ValCysIl 83 51 laGluPheLysValPheThrAsnIleHisSerAlaValValAspProLys 67 444 AGCGTTTTCAAAG 456 98 GAGAG..... ::::::: ||| 183 lThrLeuProLys 187 203

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156 TCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGGATAAAGTTGCCCGACGATGT 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-822-774-42
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2737.966 Million cell updates/sec
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Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                 1 ATGCTACTTCCAGACTGGAA.......CAAAGAGAAAGAAACTCTAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
Sequence 1,
                                                                                              January 31, 2002, 12:14:38; Search time 38.96 Seconds
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Sequence 10
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Sequence 1
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/cgn_2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn_2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn_2_6/ptodata/2/ina/RD_COMB.seq:*
/cgn_2_6/ptodata/2/ina/RD_CTUS_COMB.seq:*
/cgn_2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-822-774-40
US-08-822-774-40
US-08-822-774-36
US-08-458-218-99
US-08-450-497-101
US-08-861-289-4
US-09-293-273-4
US-09-134-596-4
US-08-188-583-5
US-08-188-583-5
US-08-88-51B-1
US-08-88-51B-1
US-08-848-760B-33
US-08-646-538-35
US-09-66-538-35
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US-09-046-247-80
US-09-329-796-2
US-07-791-61A-32
US-07-791-122
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PCT-US91-05801-32
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US-08-951-648-1
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APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
TITLE OF INVENTION: and Methods for Purifying and Identifying Same
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
STREET: D.C.
STATE: D.C.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 740;
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
TELECOMMUNICATION INFORMATION:
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US-09-114-437-5

US-09-114-437-5

US-08-261-663A-3

PCT-US95-07754A-5

PCT-US95-07754A-5

US-08-911-648-3

US-08-911-648-3

US-08-211-653A-1

PCT-US95-07754A-1

US-08-388-353-800
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PCT-US91-03680-9
US-08-840-316-17
                                                        US-09-268-140-1
US-09-268-140-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/08822774 Patent No. 6183997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 316; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-822-774-36

US-08-822-774-36

Sequence 36, Application US/08822774

Patent No. 6183997

GENERAL INFORMATION:

TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBERS OF SEQUENCES: 61

ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C.

ADDRESSEE: Lanahan, P.L.L.C.

STREET: 1200 G Street, N.W. Suite 700

STATE: D.C.

21F: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-WAR-1997
CLASSIFICATION: 436
ATORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 1486/43163
REGISTRATION NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-8844
INFORMATION FOR EQ. ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TTELENGTH: 84 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ET AL. NEUTROPHIL INHIBITORS
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Patent No. 5747296
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHINGMEN OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
-822-71
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| Sequence 40, Application US/08822774
| Patent No. [613397]
| GENERAL INFORMATION:
| APPLICANT: HOGREFE, Holly
| TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: AUXIE, Evenson, MCKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C.
| CORRESPONDENCE ADDRESSE: Lenahan, P.L.L.C.
| ADDRESSEE: Lenahan, P.L.L.C.
| ADDRESSEE: Lenahan, P.L.L.C.
| CITY: Washington STREET: 1200 G Street, N.W. Suite 700 CITY: Washington STATE: DC.
| ZIP: 20005 COMPUTER: FIDPPY disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURREMT APPLICATION DATA:
| PTLING DATE: 21-MAR-1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                              61 TATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTTTGC 120
                                                                                                                                                                                        276 TIGGGITGACCCAGGATGGGAACTTAACACTAATGCTCTACAATGCCTCAAATGA 335
                                                                                                                                                                                                                                                                                                                                                                        241 TCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAA 300
                                                                                                                                                                                                                                                                                                                                               396 TCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAAGGTTAGCGTTTTCAAA 455
1 TCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGT 60
                                                                   216 TATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGC
                                                                                                                                                                                                                                                      336 ACCTGTCGAATTAAGATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGG
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Ilarity 100.0%; Pred. No. 1.2e-2;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, DAVId J.
RECISTRATION NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8800
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1486/43163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GAGAAAGAAACTCTAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 129 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      456 GAGAAAGAAACTCTAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADCLECULE TYPE: DNA (
HYPOTHETICAL: NO
ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 61; Conserv
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US-08-822-774-40
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US-08-822-774-40/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Sequence 101, Application US/08450497

Sequence 101, Application US/08450497

GENERAL INFORMATION:

APPLICANT: MATTHEW MOYLE, ET AL.

TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS

NUMBER OF SEQUENCES:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700
                              IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                         APELICALIAN

EILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:
PELING DATE:
IO-NOVEMBER-1993

APPLICATION NUMBER: 08/151,064

FILING DATE: 11-MAY-1993

APPLICATION NUMBER: 07/881,721

FILING DATE: 11-MAY-1992

APPLICATION NUMBER: 07/896,972

FILING DATE: 11-MAY-1992

APPLICATION NUMBER: 07/896,972

FILING DATE: 10-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 203/226

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 499-1600

TELEFAN: (213) 955-0440

INFORMATION FOR SEQ ID NO: 99:
                                               SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/450,497
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Scilarity 100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Coding Sequence LOCATION: 3...725
       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GTGGAAAAGGAAGGAAAA 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserva
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APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                  COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.0 For Dos 5.0 SOFWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,510B FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/151,064 FILING DATE: 11-NOV-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/991,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/991,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/991,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/891,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 205/073
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 99, Application US/08458218 Patent No. 5789178
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.8%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: Coding Sequence; LOCATION: 3...725
US-08-173-510B-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 GTGGAAAGGAAGGAAA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 GTGGAAAAGGAAGGAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: NUCLEIC
                           Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
                                                  Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                  U.S.A.
                                                                                                                      90071
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                                                                   STATE: C.
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US-08-458-218-99
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DB 1; Length 1197;
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                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-134-290-4

Sequence 4, Application US/09134596
Patent No. 592318
GENERAL INFORMATION
APPLICANT: Bandman, Olga
APPLICANT: CATLEY, Neil C.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STARE: 3174 Porter Drive
CITY: Palo Alto
STARE: USA
COUNTRY: USA
CONDUTER RADABLE FORM:
MEDIUM TYPE: DISABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,596
FILING DATE:
PR.OR APPLICATION DATA:
APPLICATION NUMBER: 08/861,269
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: B111,108; LUCY
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0302 US
TELEPHONE: 415-85-0555
                                                                                                                                                                                                                                                                                                      3.6%; Score 17; DB 100.0%; Pred. No. 11; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%; Score 17; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1197 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                               834 GAAAATCAGAAAAGAAA 850
                                                                                                           TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOTO9
; CLONE: 2151473
                                                                                                                                                                                                                                                                                                                                                                                        18 GAAAATCAGAAAAGAAA 34
                                                                                                                                                                                                                                                                                                      Query Match 3.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 2; Length 797;
Pred. No. 3.2;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Carley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,269
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
PILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY CACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0302 US
TELECOMMUNICATION INFORMATION:
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
ATORNEY AGENT: 12-MAY-1993
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATORNEY AGENT: NUMBER: 205/073
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 205/073
TELEPONMINICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION POR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-861-269-4
Sequence 4, Application US/08861269
Patent No. 5817494.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.8%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: Coding Sequence;
; LOCATION: 3...725
US-08-450-497-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GTGGAAAGGAAGGAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR MOLECULE TYPE: NUCLEIC FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 797
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94304
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Gaps
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Sequence'5, Application US/08188583
Patent No. 5851813
GENERAL INFORMATION:
APPLICANT: Desrosiers, Ronald C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WORDERICATION DATA:
APPLICATION NUMBER: US/08/188,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                     FILING DATE: 07-APR-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,849
FILING DATE: 28-AUG-1992
ATTORNEV ARCHION: 526
ATTORNEV ARCHION: 526
                                      MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17;
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                          36,459
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                           SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 7399 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 TGGAAAAGGAAGGAAAA 147
                                    ADDRESSEE: MORGAN & FIN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts COUNTRY: U.S.A.
                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                          U.S.A.
                                                                         NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                     10154
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TELEX: 42
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0
     Gaps
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCHUBERT, MANFRED, HARMISON II,
APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANJERJEA, AKHIL
TITLE OF INVENTION: DEFECTIVE, INTERFERING
TITLE OF INVENTION: HIV PARTICLES
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Freeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: UBLQUITIN CONJUGATION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,273
   Mismatches
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Mismatches
                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0302 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-418-848A-9; Sequence 9, Application US/08418848A; Patent No. 5847096; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.00.
100.08; Pic
                                                                                                                       RESULT 9
US-09-293-273-4
: Sequence 4, Application US/09293273
; Patent No. 6057112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1197 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GAAAATCAGAAAAGAAA 34
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17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: BRAINOT09
CLONE: 2151473
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CITY: Palo Alto
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                         94304
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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   Matches
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Length 9709;
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                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION

APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDEMES: 841
CORRESPONDEMES: SCOTT, MURPHY & PRESSER
STATE: NEW YORK
COUNTRY: US.A.
ZIP: 11530-0299
COMPUTER: NEW YORK
COMPUTER: NEW PORK
COMPUTER: DALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DALE FORM:
MEDIUM TYPE: PLOPSY/MS-DOS
SOFTWARE: PACTOR NOTA:
COMPUTER: DALECTON NOTA:
SOFTWARE: DALECTON NOTA:
APPLICATION NOTA:
PRILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: DATO:
APPLICATION NUMBER: PM3021/95
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM3021/95
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
                                                                                     Score 17; DB 3;
Pred. No. 11;
0; Mismatches
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Pred. No. 11;
0; Mismatches
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100.0%; Pre
                                                                                          Query Match 3.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (516) 742-4343
                                                                                                                                                                                                                                      2671 TGGAAAAGGAAGAAAA 2687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9709 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 TGGAAAAGGAAGGAAAA 147
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE:
US-08-488-551B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08388353
Patent No. 6010895
GENERAL INCEMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Coper. Dale A.
APPLICANT: COOPE: SUzanne
APPLICANT: COOPE: David
APPLICANT: COOPE: David
APPLICANT: COOPE: David
COOPERSONDENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 400 Garden City Plaza STRY: Garden City Plaza STREET: 37ATE: New York STRATE: New Y
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/551,945
FILING DATE: JULY 12, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman John W
REGISTRATION NUMBER: 00246/079002
REFERENCE/DOCKET NUMBER: 00246/079002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPA: 200154
INFORMATION FOR SEQ.
INFORMATION FOR SEQ.
SEGUENCE CHARACTERISTICS:
LEGGRAPHICATICS:
LEGGRAPHICATION: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,56
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2671 TGGAAAAGGAAGGAAAA 2687
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nucleic acid
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United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-188-583-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United State ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-388-353-1
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Patent No. 6248721
GENERAL INFORMATION:
APPLICANT: Chang, Lung-Ji
APPLICAF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·:
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11;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,312
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
Sequence 13, Application US/08935312.
Patent No. 6207455
GENERAL INFORMATION:
TITLE OF INVENTION: LENTIVIRAL VECTORS
NUMBER OF SEQUENCES:
CORRESPONDENCE S. 20
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W.
CITY: Washington
STATE: D.C.
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FILING DATE: 25-Jan-2001
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Mismatches
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COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVET P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: CHANG
TELEPOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 12494 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Sequence encoding
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improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
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P-PSDB; AAW72847.
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WO9842860-A1.
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Polymerase enhancing factor; PEF; dUTPase; DNA polymerase; PCR; amplification; ligation independent cloning; primer; ss.

Synthetic. Pyrococcus furiosus.

WO9842860-A1.

20-MAR-1998; 24-OCT-1997; 21-MAR-1997;

01-OCT-1998

Polymerase enhancing factor P45 primer #1.

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Compositions, and sequence encodes the P45 component (see AAW72847) of the P45 component (see AAW72847) of the P45 component (see AAW72847) of the P45 component (see AAW72847) of the P45 component (see AAW72847) of the P45 component (see AAW72846) of P45 components (see AAW72846) of P45 ware used to amplify P. furiosus genomic DMA, and CC AAW72846) of P45 and P40 (see AAW72844) are the predominant components of P45 and P40 (see AAW72844) are the predominant components of P45 and P40 (see AAW72844) are the predominant components of P45 and P40 (see AAW72844) are the predominant components of P45 and P40 (see AAW72844) are the predominant components of P45 and P40 (see AAW72844) are the predominant components of P45 and P415 and P415 and AAW72844) are the predominant components of P45 and P415 and Complexes that improve the P4019 mersase enhancing and complexes that improve the P4019 mersase of Also included are methods for identifying and using these compositions, and specific extracts, proteins and compositions and specific extracts, proteins and compositions compositions and specific extracts, proteins and compositions compositions can be enhanced (claimed) by mixing a nucleic acid polymerase composition and a composition and complete composition and a composition and complete composition and a composition and a composition and complete composition and a composition of P45.

C sequence at least 1 polymerase acid in the recombinant production of P45.

S sequence 471 BP; 156 A; 80 C; 124 G; 111 T; 0 other;

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Ouery Match

Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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97US-0957709. 97US-0822774.

Hansen CJ, Hogrefe H;

(STRA-) STRATAGENE.

WPI; 1998-542284/46.

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AAV63865 standard; DNA; 33

AAV63865;

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DT 01-M

01-MAR-1999 (first entry)

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Gaps

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4.5%; Score 21; DB 19; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels

Sequence 33 BP; 12 A; 8 C; 8 G; 5 T; 0 other;

coligonucleotides #1 and #2 (see AAV63866) are designed to amplify a portion of a genomic clone encoding the P45 protein (see AAW72847) of Pyrococcus furiosus DSM 3638. They include P45 and vector specific sequences. Oligo #1 includes the ATG start codon and 5° end of the P45 coding region (see also AAV63860). The primers were designed to function with the Stratagene Affinity Protein Expression and Purification System, which uses ligation independent cloning. Recombinant P45 was expressed in E. coli independent cloning. Recombinant P45 was expressed in E. coli independent cloning. Recombinant P45 was expressed in E. coli curlosus DNA polymerase, thereby providing replication products of greater length and purity. A claimed method of enhancing a nucleic acid polymerase reaction involves adding P45 protein to the reaction. A claimed DNA encoding a polymerase encinon involves adding P45 protein C (EEF) may include oligonucleotide #1, or a hybridisable or degenerate variant, and a claimed method for cloning a PEF activity may utilise the complement of oligonucleotide #1.

Polymerase enhancing factor proteins, extracts and complexes - improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

Claim 84; Page 48; 161pp; English.

Yamamoto J;

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Sequence 405 BP; 98 A; 84 C; 93 G; 128 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA clone (3'-primer) SEQ ID NO:6201.
                                                                                         Wildung MR;
                                                                                                                                                Claim 1; Page 237; 251pp; English.
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2000JP-0118776.
2000JP-0183767.
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Matches 18; Conservative
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                                                             (CROT/) CROTEAU R B. (LANG/) LANGE B M.
                                                                            (WILD/) WILDUNG M R.
                                                                                                       WPI; 2001-488706/53.
      WO200153319-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1074617-A2
                    26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001.
                                                                                                                                  proteins
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                     AAH09366;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprises a least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the partients and and oligonosis of the primers are also useful for the country of the full-length cDNAs. The primers are also useful for the hall the full-length cDNAs. The primers are also useful for the AMH13633 to AAH13633 to AAH13632 to AAH13632 to AAH13632 to Febresent thuman anno acid sequences; and AAH13632 to AAH13632 to fe the process to the process and the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the p
                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peppermint; plant oil gland cell; terpenoid essential oil; resin; genetic mapping; antisense suppression; recombinant expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 571;
17;
                                                                            Saito K, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 571 BP; 144 A; 162 C; 152 G; 106 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID 6201; 2537pp + CD ROM; English.
                                                                            Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peppermint plant oil gland expressed cDNA 402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18;
Pred. No.
                                                                                                         Wakamatsu
                                                                         ogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH88046 standard; cDNA; 638 BP.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 GTGGAAAGGAAGGAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 gtggaaaaggaaggaaaa 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the present invention.
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Les 18; Conservative
                         (HELI-) HELIX RES INST.
                                                                                                                                                         WPI; 2001-318749/34
                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                    full-length cDNAs
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                                                                                                         Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acid molecules (AAH87645-AAH88116) that correspond to all or part of a mRNA molecule expressed in plant oil gland cells, especially peppermint and plant oil glands that produce terpenoid essential oils and resins. The nucleic acids are useful for genetically mapping a plant genome for genes expressed in plant oil gland cells and to suppress (for example by antisense suppression) or enhance their expression (for example by genetically transforming a plant cell with a replicable expression vector that expresses one or more proteins naturally expressed in plant oil gland cells). The nucleic acids are also useful for recombinant expression of plant oil gland proteins required for terpenoid essential oil and/or resin production in bacterial and/or yeast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer, detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules corresponding to mRNA molecules expressed in peppermint oil glands for enhancing expression of plant oil gland cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 17;
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Gaps

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19-JAN-2001; 2001WO-US02567. 20-JAN-2000; 2000US-0177264

26-JUL-2001

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                                                                                                                                                                                                                               New nucleic acid molecules corresponding to mRNA molecules expressed in peppermint oil glands for enhancing expression of plant oil gland cell proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vascullits; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canine hookworm neutrophil inhibitory factor AcaNIF18 polynucleotide
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Pred. No. 17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 638 BP; 168 A; 144 C; 126 G; 200 T; 0 other;
                                                                                                                          Wildung MR;
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 224; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%; Scc_
100.0%; Pre
0;
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92US-0881721.
92US-096972.
93US-0060433.
93US-0151064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX85547 standard; DNA; 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 AGATATGGAGAGAGATTT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0450497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
les 18; Conservative
                                                                                                                      Croteau RB, Lange BM,
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(CROT/) CROTEAU R B.
(LANG/) LANGE B M.
(WILD/) WILDUNG M R.
                                                                                                                                                                                    WPI; 2001-488706/53
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11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1995;
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AAX85547

AAX85547

AAX85547

AAX85547

AAX85547

AAX8548

AAX87

AAX8648

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                                                                                                                                                                                                        The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137, or 223 in the wild type sequence (see AAY23591) is replaced by a Given to 223 in the wild type sequence (see AAY23591) is replaced by a Given to 233 in the wild type sequence (see AAY23591) is replaced by a Given to 234 in the wild type sequence (see AAY23591) is replaced by a Given to 245 in the material of the sequence (AROS), is the constant of an activities of the sequence (AROS), is the seperation injury following myocardial infarction, and acute inflammation caused by for a parasitic worm as sepsis or bacterial meningities. NIFs or NIF fragments may be used as vaccines against parasitic worm infection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may a parasitic worm, as antihnelminic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mind. So a rangonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAX85537-47 encode canine hookworm NIF proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirhomatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; cancer; cardiovascular disorder; infection; cerebrovascular disorder; anglogenesis; nervous system disorder; conclar disorder; wound healing; skin aging; food additive; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
                                                                                            Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 18; DB 20; Length 797;
100.0%; Pred. No. 17;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 797 BP; 262 A; 178 C; 177 G; 180 T; 0 other;
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                                                                                                                                                                        Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC59749/c
ID AAC59749 standard; cDNA; 878 BP.
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99US-0138626.
99US-0168662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 GTGGAAAAGGAAGAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                  WPI; 1999-403975/34.
P-PSDB; AAY23610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200056751-A1.
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11-JUN-1999;
03-DEC-1999;
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Matches
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WO200076530-A1

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The polynucleotide sequences given in AAC59738 to AAC59787 encode the human secreted proteins given in AAB34577 to AAB34626. AAB34627 to AAB34626 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: cardiant; vasotropic; cerebroprotective, nootropic; cardiant; vasotropic; cerebroprotective, nootropic; cytostatic; cardiant; vasotropid; or provent, treat or amelorate a medical condition in e.g. humans, mice, prevent, treat or amelorate a medical condition or susceptibility to a pathological condition or susceptibility to a cancers of the breast or liver, cardiovascular disorders, angiogenesis, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. Infections caused by bacteria, viruses and fungi and ocular disorders. Infections caused by bacteria, viruses and fungi and coular disorders. Corepensation, to prevent skin aging to submurn, to maintain organs before transplantation, for supporting cell culture of primary tissues, coreparative to preservative to increase or decrease storage capabilities. AAC59729 to AAC59739 and AAB34576 represent sequences used in the exemplification of the present invention.
                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
   Komatsoulis G;
                                                                                                                                                                                                                           Claim 1; Page 348; 419pp; English.
Ruben SM,
                                                      2000-579482/54
                                                                                 P-PSDB; AAB34588
Rosen CA,
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Sequence 878 BP; 192 A; 215 C; 249 G; 222 T; 0 other;

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                   Gaps
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0
Score 18; DB 21; Length 878;
                   0; Indels
                   Mismatches
          Pred. No.
 100.08; Pr
3.88;
                                  130 GTGGAAAGGAAGGAAAA 147
                                              Best Local Similarity 100.
Matches 18; Conservative
Query Match
                                                                                 RESULT
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dermatological; immunosuppressive; antiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; anti-Intiinflammatory; antiaconvulsant; vulnerary; antialzhelmers; antiparkinsonian; antimicrobial; immune disorder; antiparkinsonian; antimicrobial; immune disorder; hyperproliferative disorder; cancer; dancher's disease; wound healing; cardiovascular disease; Scinitar syndrome; Chaga's cardiomyopathy; corneal graft neovascularisation; neurological disorder; regeneration; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease; chemotaxis; ss. secreted protein; diagnosis; immunomodulatory; antisclerotic; Human secreted protein gene 39 SEQ ID NO:49. AAF33251 standard; cDNA; 1057 BP. 23-MAR-2001 (first entry) AAF33251; AAF33251/c 

Homo sapiens

and certs the years are expressed in Examples of activities include:
annunomodulatory; antisclerotic; dermatological; annunosuppressive;
antiinflammatory; antisclerotic; dermatological; mnunosuppressive;
c vascular; anticonvulsant; nootropic; antialzheimers;
antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can
be used in the prevention, diagnosis and treatment of diseases associated
with inappropriate polypeptide expression. Disorders that may be
prevented, diagnosed and/or treated by the above methods include immune
disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
human immuno-deficiency virus (HIV) infections), hyperproliferative
disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
c e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary
arteriosclerosis), angiogenic disorders (e.g. corneal graft
neovascularisation and diabetic retinopathy), neurological disorders
(e.g. Huntington's chorea, Alzheimer's diseases and Parkinson's diseases),
infectious diseases and/or for promoting wound healing, regeneration and
control of the coronary and ARPSI212 and ARBS(88) represent sequences The polynucleotide sequences given in AAF33213 to AAF33261 encode the human secreted proteins given in AAB64882 to AAB64930. AAB64931 to AAB64991 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: transferase; amylase; Sulfolobus; production; alpha, alpha-trehalose; malto-oligosaccharide; hydrolysis; ss. Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's ô DB 22; Length 1057; 17; Indels Sequence 1057 BP; 238 A; 259 C; 292 G; 268 T; 0 other; used in the exemplification of the present invention. ; DNA encoding Sulfolobus solfataricus amylase. 3.8%; Score 18; DB 100.0%; Pred. No. 17; ive 0; Mismatches Komatsoulis GA; Claim 1; Page 476; 554pp; English. preventing, diagnosing and/or tre disease and diabetic retinopathy AAT12325 standard; DNA; 2691 BP (HUMA-) HUMAN GENOME SCI INC 01-JUN-2000; 2000WO-US14933. 99US-0138572. 130 GTGGAAAAGGAAGGAAAA 147 970 GTGGAAAAGGAAGGAAAA 953 (revised)
(first entry) Conservative Rosen CA, Ruben SM, WPI; 2001-071147/08 Local Similarity tes 18; Conserv ROSEN C A. P-PSDB; AAB64920 11-JUN-1999; 24-JUL-1997 29-JUN-1996 21-DEC-2000. AAT12325; Query Match ROSE/) Best Loca Matches RESULT 9 q δλ

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Gaps

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29-JUL-1999; 99JP-0248036.
27-ANG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-RAX-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3068 GTGGAAAAGGAAGGAAAA 3051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GTGGAAAAGGAAGGAAAA 147
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                                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dengue 2 virus genome.
                                                                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dengue virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ12787
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    οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes an amylase derived from Sulfolobus solfataricus. The amylase acts on a saccharide having at least three sugar units, which are pref. glucose units at the reducing end (the linkage between the first and second glucose units is alpha-1, while the linkage between the second and third glucose units is alpha-1, alpha-1, stopha-1, sea alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alpha-1, alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sulfolobus spp. derived transferase and amylase - for production of alpha, alpha-trehalose from malto-oligosaccharide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 17; Length 2691; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2691 BP; 925 A; 387 C; 596 G; 783 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 109; Page 235-240; 357pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:16450.
                                     Location/Qualifiers
639..2318
                                                                               /*tag= a
/product= amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.8%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                    95JP-0120673.
94JP-0133354.
94JP-0194223.
94JP-0290394.
94JP-0286917.
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                                                                                                                                                                                                                   95WO-JP01189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AAAATCAGAAAAGAAATA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.8
Best Local Similarity 100.
Matches 18; Conservative
Sulfolobus solfataricus.
                                                                             /*tag•
                                                                                                                                                                                                                                                                                                                                                                                                 (KIRI ) KIRIN BEER KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-049671/05.
P-PSDB; AAR90619.
                                                                                                                                                                                                                                                    21-APR-1995;
15-JUN-1994;
18-AUG-1994;
31-OCT-1994;
21-NOV-1994;
                                                                                                                                                                                                                 14-JUN-1995;
                                                                                                                                   WO9534642-A
                                                                                                                                                                         21-DEC-1995
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The present invention describes primer sets for synthesising 5602

[ull-length CDMsA defined in the specification. Where a primer set

[ull-length CDMsA defined in the specification. Where primer set

[under comprises: (a) an oligo-dr primer and an oligoucleotide comprises one of

the 5602 nucleotide sequences defined in the specification, where the

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprises as 1'-end sequence complementary to a

polynucleotide which comprises a 3'-end sequence where the

oligonucleotide comprises a 1-end sequence which combination of

the 5'-end sequence/3'-end sequence is selected from those defined in

the specification. The primers are useful for synthesising polynucleotides,

particularly full-length combxs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

che full-length cDMAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

CMABS683 represent human annino acid sequences; AAB92446 to

AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

AAH13632 to AAH13632

cepresent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Suglyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 16450; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
97..10272
/*tag= a
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100.0%; Pro
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The present invention provides the sequences of 184 cDNA fragments which are differentially expressed in cancer cell depending on the age of the patient. They can be used to diagnose and identify treatments for cancers, particularly brain cancers as as a particularly brain cancers as haemangioblastoma, teratoma, haemangiona, glioblastoma, schwannoma, osteoma and pinealoma. The present sequence is a cancer-associated cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid molecules differentially expressed in brain cancers, useful for ascertaining propensity of cell for malignant phenotype or ascertaining suitability of anti-neoplastic drug candidate -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 285; 55;
                                                                            Human; cancer specific gene expression; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer specific gene expression; gene therapy; age related differential expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 285 BP; 77 A; 69 C; 45 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 55;
Mismatches
                                                                                         age related differential expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.6%; Score 17;
100.0%; Pred. No.
ive 0; Mismatc
                                              Human tumour associated cDNA #159.
                                                                                                                                                                                                                                                                                           (NYXI-) NYXIS NEURO THERAPIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 28; Page 62; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour associated cDNA #65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH50736 standard; cDNA; 309
                                                                                                                                                                                                                                              99US-0166056
99US-0166106
                                                                                                                                                                                                                17-NOV-2000; 2000WO-US31809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 TCAAAGAGAAAGAACT 253
                 23-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 TCAAAGAGAAAGAAACT 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                          Kroes RA, Moskal JR,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-355647/37.
                                                                                                                                                      WO200136685-A2.
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                                                                                                                         Homo sapiens.
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17-NOV-1999;
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                                                                                                                                                                                   25-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection and identification of Flaviviridae in biological sample - by amplifying consensus sequence then hybridisation opt. followed by typing, e.g. sequencing amplified prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The dengue 2 virus is an example of a member of the Flaviviridae which can be identified using the probe pair of the invention. A species-specific sequence can be amplified using the claimed oligonucleotides as primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses which can be identified include Japanese encephalitis virus and yellow fever virus.
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0
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Pred. No.
                      /product= M protein 937..2421
                                                           /*tag= c
/product= E protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 24pp; French.
                                                                                                                                                     /*tag= e
/product= NS2A
4132..4518
                                                                                                                                                                                                              /product= NS2B
1519..6375
                                                                                                                                                                                                                                                                                                                                                     'product= NS4B
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/product= NS3
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                                                                                                                     'product= NS1
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77.8%;
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/*tag= d
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                                            ..2421
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712..936
                /*tag=
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P-PSDB; AAR13166.
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nes 14; Conserv
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mat_peptide
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Gaps

0;

Indels

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99US-0166056.

17-NOV-1999; 17-NOV-1999;

2000WO-US31809

17-NOV-2000;

AAH50830 standard; cDNA; 285 BP

Matches

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AAH50830/c ID AAH50 XX AC AAH50 RESULT

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16-SEP-1987
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                                                                                                                                             The present invention provides the sequences of 184 cDNA fragments which part of differentially expressed in cancer cell depending on the age of the patient. They can be used to diagnose and identify treatments for cencers, particularly brain cancers such as haemangioblastoma, teratoma, haemangioma, glioblastoma, scheama, osteoma and pinealoma. The present sequence is a cancer-associated cDNA of the invention.
                                                                          Novel nucleic acid molecules differentially expressed in brain cancers, useful for ascertaining propensity of cell for malignant phenotype or ascertaining suitability of anti-neoplastic drug candidate -
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid interferons comprising a fragment of an alpha-interferon and a fragment of an omega-interferon, and their N -terminal Met or N-formyl-Met derivs. and N-glycosylated derivs, are new. The hybrid interferons are useful as antiviral and antitumour agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybrid alpha/omega interferon; antiviral; virucide; antitumour;
cytostatic; ss.
                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                          Score 17; DB 22; Length 309;
Pred. No. 55;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hauptmann R, Swetly P, Meindl P, Gunther A, Falkner E;
Bodo G, Maurer-Fogy I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding IFN-alpha-2 (Arg) on plasmid parpER33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybrid interferon prods. useful as antiviral agents alpha and omega interferon fragments
                                                                                                                                                                                                                            Sequence 309 BP; 83 A; 75 C; 51 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 382 BP; 111 A; 91 C; 99 G; 80 T; 1 other;
          (NYXI-) NYXIS NEURO THERAPIES INC
                                                                                                                         Claim 28; Page 46; 82pp; English
                                 Moskal JR, Yamamoto
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                    AAN71175 standard; DNA; 382 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BOEH ) BOEHRINGER INGELHEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87EP-0103030
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                                Kroes RA,
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                                                Gaps
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cytostatic; ss.
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Pred. No. 55;
0; Mismatches 0; Indels
ore 17; DB 8; Length 382;
red. No. 55;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoding IFN-alpha-2 (Arg) on plasmid parpER33.
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  Score 17;
Pred. No.
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Job time: 126 sec
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Bodo G, Maurer-Fogy I;
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Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
  Query Match 3.6%; So
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
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                                                                                                                     102 cagactggaaaatcaga 118
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Description

DB

AP000007 Pyrococcu AC084454 Caenorhab AC091338 Rattus no AC091336 Rattus no AC021666 Arabidops AC01266 Arabidops AC012124 Homo sapi AC021224 Homo sapi AC03229 Homo sapi AC0975 HIV-1 patie AC0975 HIV-1 patie AC0975 HIV-1 patie AC00380 HIV-1 iso AY00038 HIV-1 iso AY00038 HIV-1 iso AY00038 HIV-1 iso AY001380 HIV-1 iso AY001380 HIV-1 isol AF314059 Homo sapi AF314059 Homo sapi AF314059 Homo sapi AF314059 Homo sapi AF314056 Homo sapi AF314056 Homo sapi AF314056 Homo sapi AF314056 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF31408 Homo sapi AF3181 Homo sapi AC092286 Homo sapi AC092286 Homo sapi AC091284 Mus muscu AC091284 Homo sapi

AC081454 AC091338 AC091338 AC021666 AC021666 AC012124 AC012124 AC082190 AC022390 AC022390 AC022390 AC023084 AY000384 AY000384 AY000384 AY000384 AY000386 AC0873180 AC0873180 AC0873180 AC0873180 AC01360 
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	GenCore version	Result No.	Score	Query Match	Query Match Length
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OM nucleic - nucl	nucleic search, using sw model	3.12	21 21	4.4 3.0	59777 102195
Run on:	January 31, 2002, 11:49:27; Search time 1331.66 Seconds (without alignments)		2000	4 4 4 4 vi vi vi v	162041 1686 93859
Title: Perfect score: Sequence:	US-08-957-709-70 1 ATGCTACTTCCAGAACAAAGAGAAAGAAAGAAAAGTGTAG 471	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	00000	. 4 4 4 4 i u u u u	1046393 146393 164935 175291
Scoring table:	OLIGO_NUC Gapext 60.0	13	20 20 10	444 240	190174 192725 380
Searched:	1472140 segs, 8248589755 residues	15	19	4 4	418
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-	13: gb_un:* 14: ab vi:*	40	19	4.4	146810
	15: em_ba:*		19		150478
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	18: em_in:*		19		163136
7	19: em_om:* 20: em_or:*				
CA (					
10	23: em_phr:* 23: em_ph:*		•		
(4)		RESULT	<b>→</b>		
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7		DEFINITION	•	Pyrococcus	
(2) (2)				7).	
4 m	29: em_v1:* 30: em_htgo_hum:*	ACCESSION		APUUUUU/ ABUU9464 AB009525 AB009526	B009464 B009526
מי ני		VERSION		AP000007.1	GI:32
·1 (m)		SOURCE		Pyrococcus boriko	horiko
i en t		ORGANISM	Σ	Pyrococcus horiko	horiko
- <i>)</i> (1)	35: em_ntg_roo:* 36: em_htg_other:*			Archaea, Euryarch Pyrococcus	uryarch
Pred. No. i	is the number of results predicted by chance to have a	AUTHORS		ı (bases ı to 25 Tanaka,T., Kawara	I to 25 Kawara
score great and is deri	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	TITLE JOURNAL	ij	Direct Submission Submitted (11-JUN	mission (11-JUN
			300	arabaya	

Homo sapi Homo sapi Human DNA Homo sapi Homo sapi

AL035258 H AC028828 C AC006052 H AC024342 H AL159170 H AP002505 H AC03413 H AC09419 H AC018639 H AL031599 H

Homo sapi Human Chr Human DNA

ALIGNMENTS

Human DNA Caenorhab

SUMMARIES

05 bp DNA BCT 08-FEB-1999 coshii OT3 genomic DNA, 1485001-1738505 nt. position Direct Submission Submission Submitted (11-700-1998) to the DDBJ/EMBL/GenBank databases. Yutaka Kawarabayasi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tckyo 151-0066, Japan (E-mail:genomeOT3@nite.go.jp, Tel:+81-3-3481-8951, 54 AB009465 AB009521 AB009522 AB009523 AB009524 26 AB009527 AB009528 AB009529 AB009530 AB009531 3236134 oshii :haeota; Thermococcales; Thermococcaceae; abayasi, Y. and Kikuchi, H. oshii (strain:OT3) DNA. 53505)

TITLE

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                                       Tax:Hol. 3-3801-8444)

Sa Kawarabayasi, Y., Sawada, M., Horikawa, H., Haikawa, Y., Hino, Y., Yamanoto, S., Sekine, M., Baba, S., Kosugi, H., Takamiya, M., Nagai, Y., Sawada, M., Daba, S., Kosugi, H., Takamiya, M., Nagai, Y., Sakal, M., Ogura, K., Otuka, K., Nakazawa, H., Takamiya, M., Ohitku, Y., Sakai, T., Kudoh, Y., Yamazaki, J., Kushida, N., Ohitku, Y., Roki, K., Nakamura, Y., Robb, T.F., Horikoshi, K., Masuchi, Y., Shizuya, H. and Kikuchi, H.

Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3

ND Ress. 5 (2), 55-76 (1998)

ND Ress. 5 (2), 55-76 (1998)

ND Ress. 5 (2), 55-76 (1998)

On Mar 17, 1999 this sequence version replaced gi:3131896

gi:3132139 gi:3131974 gi:3132233 gi:313303 gi:313203 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nishthara, Shibuya, Tokyo 151-0066, Japan.

All the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS mith-Waterman algorithm against GenBank and GenPept release 103; EMBL release 5.0; Swissprot release 34.0; PRF-Protein release 54.0; And OWL release 29.5.

E-mail address for comments and questions: genomeOr3@nite.go.jp Restriction map, ORF organization, sequence alignment and more information are available at W.W. site of Biotechnology Center, Location/Qualifiers

I. 253505

//strain="Psycoccus horikoshii"
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NSERLEEWTLRWFGHLEKIKVLNELGFFKPENLDFTLRVIEPLMKYETKDFSIMKVVG
PRRIIDELKERGISIEGT"
298. 780
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Shizuya, H. is at the California Institute of Technology, Pasadena,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILVIDGTIGQQAYNQALAFKEATPIGSIIVTKLDSSAKGGGLSAVAATGAPIKFIGV
GERIDDLEPPDPARFYSRLIGJGDIGGLEKFRELEKBVETFEBDIDRFLKGKFTLKD
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EIINYSRIKRIARGSGTSIKDVKELLTQYNQMKKFFKSMNKRQLSRLARRFGM
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                                                                                                                                  /gene-maintain to PIR:E64312 percent identity:60.870 in 444aa: owl:AAFFH1 percent identity:50.236 in 430aa; owl:SAFFH percent identity:50.611 in 415aa. motif-AFFH percent identity:50.611 in 415aa. proteins GTP-binding site motif A (P-loop); SRP54-type proteins GTP-binding domain signature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to PIR:F64336 percent identity: 42.778 in 196aa. motif=ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="205aa long hypothetical thymidylate kinase"
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/db_xref="GI:3258125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                         /transl_table=11
/product="445aa long hypothetical signal recognition
particle protein"
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Caenorhabditis briggsae cosmid CB027J01, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoldea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 1; Length 253505; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Washington University Genome Sequencing Center.
The C. briggsae Genome Sequencing Project
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%; Score 23; DB nilarity 100.0%; Pred. No. 0.1 Conservative 0; Mismatches
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/transl_table=11
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                                                                                                                     /gene="PH1694"
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Matches 23; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
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Muzny, D. M., Adang, C., Adio-Odoola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bonton, D., Bouck, J., Banage, K., Blankeburg, K., Bonth, D., Bouck, J., Bhanage, K., Blankeburg, K., Bonth, D., Bouck, J., Bhanay, C., Britana, M., Bryant, N.P., Buhay, C., Bourth, P., Chen, C., Carcon, T.F., Caraco, J., Chen, C., Caraco, J., Chen, C., Caraco, J., Chen, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Escotto, M., Erratz, P., Garis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gall, R., Garis, A., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hamilton, K., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Hernandez, J., Howard, S., Huber, J., Hully, S., Karlsson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Mavinney, E., McLer, M., Malos, M., Mapus, P., Martindale, A., Maheshwari, M., Mapus, P., Martin, R., Maheshwari, M., Mapus, P., Martindale, A., Maheshwari, M., Mapus, P., Martin, R., Mattindale, A., Martinez, S., Scotte, M., Sparks, A., Stanley, H., Peterz, L., Peterz, L., Pickerson, E., Nuckenson, R., Nucyen, M., Norris, S., Soder, M., Rojas, A., Rojubokan, I., Roden, R., Suthon, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Thomas, S., Usana, J., Wall, P., Wall, P., Wall, D., Wall, D., Wall, L., Wall, R., Wa
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Rattus norvegicus clone CH230-1C12, *** SEQUENCING IN PROGRESS ***,
NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/organism="Caenorhabditis briggsae"
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10945 c 11417 g 18099 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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HTG; HTGS_PHASE1.
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Rattus norvegicus
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40991: contig of 1976 bp in length

39016

us-08-957-709-70.rge

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COMMENT
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Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Wolley, K., Wu, C., Ru, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. Direct Submission

AL Direct Submission

AL Gabases 1 to 102195)

RS Morley, K.C.

Direct Submission

AL Submitted (18 APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Apr 21, 2001 this sequence version replaced gi:13661904.

Center: Baylor College of Medicine

Center: Baylor College of Medicine

Center: Code: BCM

Web site: Nttp://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: broject name: TyCG

Center clone name: CH20-1012

Center clone name: CH20-1012

Center clone name: CH20-1012

Center clone name: CH20-1012

Center project name: TyCG

Consensus quality: 105840 bases at least 030

Consensus quality: 115847 bases at least 030

Consensus quality: 115847 bases at least 030

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Consensus quality: 1158487 bases at least 030

Consensus quality: 1158487 bases at least 030

Consensus quality: 105847 bases at leas TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

NOTE: Estimated insert size may differ from sequence length (see http://www hgsc.bcm.unc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

	bp in length	ngth	bp in length	length	bp in length	length	bp in length	length	bp in length	length	bp in length	length	bp in length	length	bp in length	length	bp in length	length .	bp in length	length	bp in length	length	bp in length	len	Ω	length	bp in length	ngth	bp in length	length
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preserved	-	3200	3300	5886	5986	8663	8763	11486	11586	13834	13934	16517	16617	19592	19692	22012	22112	24544	24644	26378	26478	29383	29483	32144	32244	34482	34582	36920	37020	38916
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888 48479: contig of 1197 bp in length 48579; gap of unknown length 148   52831: contig of 2768 bp in length 52831: contig of 1364 bp in length 52831: contig of 1364 bp in length 524300: gap of unknown length length 54140: contig of 1269 bp in length 5414: contig of 1269 bp in length 5418: contig of 1278 bp in length 5418: contig of 1274 bp in length 5518: gap of unknown length length 5518: gap of unknown length length 5518: gap of unknown length length 6558: contig of 1384 bp in length 6558: gap of unknown length length 6559: gap of unknown length length 6555: gap of unknown length 122 gap of unknown length 6555: gap of unknown length 122 gap of unknown length 65570: gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 122 gap of unknown length 123 gap of unknown length 123 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 124 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of unknown length 125 gap of		200			nknown	th
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                                   FEATURES
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 158813 bases at least Q40
Consensus quality: 159743 bases at least Q30
Consensus quality: 159760 bases at least Q20
Insert size: 161640; sum-of-contigs
Ouality coverage: 7.4x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-MAR-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA On May 25, 2001 this sequence version replaced gi:14190658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162041)
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HOMO sapiens chromosome 10 clone RP11-78A18, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown length
contig of 25236 bp in length
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1674: gap of unknown length
2928: contig of 11254 bp in length
3028: gap of unknown length
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             99454: contig of 1062 bp in length 99554: gap of unknown length 100912: contig of 11838 bp in length 101012: gap of unknown length 102195: contig of 1183 bp in length.
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
unknown length
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gap of
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Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12928:
                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                 Best Local Similarity
Matches 21, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                 98393
99455
99555
100913
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1675
12929
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28415
28515
53751
53851
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                                                                                         101013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
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AC025947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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AF331362 1686 bp RNA VRL 22-FEB-2001
HIV1 isolate T9C16 from the Netherlands pol polyprotein (pol) gene,
partial cds.
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1 (bases 1 to 1686)
Lukashov,V.V., Huismans,R., Jebbink,M.F., Danner,S.A., de Boer,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selection by A2T and rapid replacement in the absence of drugs of HIV type I resistant to multiple nucleoside analogs AIDS Res. Hum. Retroviruses (2001) In press 2 (bases 1 to 1686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center, University of Amsterdam, Meibergdreef 15, Amsterdam 1105
AZ, The Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:11676"
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/country="Netherlands"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (22-DEC-2000) Human Retrovirology, Academic Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Human immunodeficiency virus type 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 others
95749: gap of unknown length 162041: contig of 66292 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                 13029. .28414
/note="assembly_name:Contig25"
28515. .53750
                                                                                                                                                                                                                                                                                                                            z8515. .53750
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53851. .95649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
1.8;
                                                                                                                                                                   /clone_lib="RPCI-11"
1. 1574
/note="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig27"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       95750. .162041
/note="assembly_name:Contig28
                                                                                                                                                                                                                                      48263 a 34100 c 33559 g 45618 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.5%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 21; Conservative 0; Mismatches
                                                             1. .162041
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                                           Location/Qualifiers
                                                                                                                                                   /clone="RP11-78A18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 144239 AAAATCAGAAAAGAAATACTT 144259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF331362.1 GI:13095339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_end:T7'
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| Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1633...702) | Conquerer(1631...1129) | Conquerer(1631...1129) | Conquerer(1631...1129) | Conquerer(1631...1129) | Conquerer(1632...702) | Conquerer(1633...702) | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to hypothetical protein GB:AAF18647"

join(4584. .4631,4701. .4874,4967. .5056,6271. .6390,

Agaz. .6602. .6793,6901. .7006,7106. .7192,7393. .7806)

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(http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with cenes with experient are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by KINAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .93859
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complement(9378 . 9400)
/rpt_family="AT_rich"
complement(9490 . 9569)
/rpt_family="AT_rich"
complement(10188 . 10218)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="AT_rich"
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/rpt_family="AT_rich"
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complement(11112.
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GGGGWTYOIYOEPFRNINGKAHTNDVACHTENDYGLTARDYOYLARGI
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QAQPDQSESELVSQIIEGLIKKEKVYTAWVPAHKGIGGNEGVDKLVSAGIRKVL"

273 c 273 c 372 g 369 t
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnaliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnaliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnalida II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 93859)

E 1 (bases 1 to 93859)

E 1 (bases 1 to 93859)

Arabidopsis thaliana chromosome 1 BAC T22A15 genomic sequence on published

In yrabidopsis thaliana chromosome 1 BAC T22A15 genomic sequence or that.

E 2 (bases 1 to 93859)

E 3 (bases 1 to 93859)

E 3 (bases 1 to 93859)

E 4 (19-JAN-2000) The Institute for Genomic Research, 9712

B 7 (bases 1 to 93859)

E 3 (bases 1 to 93859)

E 4 (19-JAN-2001) The Institute for Genomic Research, 9712

B 8 (19-JAN-2001) The Institute for Genomic Research, 9712

B 9 (19-JAN-2001) The Institute for Genomic Research, 9712

B 1 (bases 1 to 93859)

E 2 (bases 1 to 93859)

E 3 (bases 1 to 93859)

E 4 (19-JAN-2001) The Institute for Genomic Research, 9712

E 5 (bases 1 to 93859)

E 6 (19-JAN-2001) The Institute for Genomic Research, 9712

E 7 (bases 1 to 93859)

E 8 (19-JAN-2001) The Institute for Genomic Research, 9712

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prediction programs including Genescan+ (Chris Burge,
http://CGR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky,
http://genemark.biology.gatech.edu/GeneMark/), Glimmerk (a variant
of Glimmerk, see Mihaela Pertea,
http://www.tigr.org/scfilab/glimmerm_htm/glimmerm.html, and
GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
mpertea@tigr.org), searches of the complete sequence against a
peptide database and the plant EST database at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC clone T22A15 is from Arabidopsis thaliana chromosome 1 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Arabidopsis thaliana chromosome 1 BAC T22A15 genomic sequence,
complete sequence.
AC021666.5 GI:12324708
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0
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4.2%; Score 20; DB 14; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels
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AUTHORS
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AC021666
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.>7806)

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Direct Submission

Submitted (11-APR-1999) Arabidopsis thaliana Genome Center,
Direct Submission

Submitted (11-APR-1999) Arabidopsis thaliana Genome Center,
Department of Bolology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

4 (bases 1 to 104806)

5 Chao, O., Brocks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C.,
Shinn, P., Altefil, H., Bebl, B., Chin, C., Choi, J., Choi, E., Conn, L.,
Conway, A., Gonzalez, A., Hanen, N., Howing, B., Koo, T., Lam, B.,
Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N.,
Thaveri, A., Parlm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A.,
Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R.,
Federspiel, N., Theologis, A. and Ecker, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Srosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 104806)
Chao, 0., Shinn, P., Dunn, P., Buehler, E., Kahn, S., Kim, C., Walker, M., Williams, S., Altafi, H., Araujo, R., Conn, L., Conway, A.B.,
Gonzalez, A., Hansen, N.F., Huizar, L., Kremenetskala, I., Lenz, C.,
Ii, J., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M.,
Vysotskala, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-DEC-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

5. (bases 1 to 104806)

Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-DEC-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Genomic sequence for Arabidopsis thaliana BAC F5J5, complete
                                                                                                                                                                                                                                                               complement(30758. .31044)
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Genomic sequence for Arabidopsis thaliana BAC F5J5
Unpublished
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AC006228.5 GI:12039051
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Ecker, J.R.
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Best Local Similarity 100.
Matches 20; Conservative
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MAYQYFINVOPTVYTDIRGHTIQSNOFSVTEHVKSSEAGOLGSLPGVFFFYDLSPIK
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complement(25198..25397)
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SELRYLLHTVWETKLIVDTSRGETLERINFDIPFPALGSILSTVDAMDISGELHLDVKH
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NSCEDVREAYRKGWGVTNPDLIDQCKREGFLQRVKDEBGGGGCNITGFLEVNKVAGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(21911. .22002,22089. .22155,22238. .2233(22416. .22469,22562. .22613,22690. .22757,22844. .23023,23276. .22368,23612. .23692,23857. .23937,24032. .24115,74092. .34252,24358. .24499))
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KFTMEVKPVPLLQSDSPTLDAALETLIASLTTMHVRLAGGEYSDVSYSVPDDVGDEDV
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PREGRELAMARPADFYHIFDTQSGFLQSQEIDLEGEIAGISFSPDTEALYVGVADRTY
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Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Tanveriah. Thaveriah. Toriuni, M., Vayaberg, M., Yu, G., Davis, R., Federspiel. M., Theologis, A. and Ecker, J. Direct Submission Cor-2000 Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA and Cont. S. Kim, C., Altafil, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Comway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Khan, S., Kim, C., Altafil, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Comway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Theoreti, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Erec, T., Theologis, A. and Ecker, J.
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All Southwick, Whiladelphia, PA 19104-6018, USA
Hamilton Walk, Philadelphia, PA 19104-6018, USA
Hamilton Walk, Philadelphia, PA 19104-6018, USA
Cation/Qualifiers
I. 104806

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LTGVSGAGGOPSAATPSDPPPPPADARY
LAGYSGAGGOPSAATPSDPPPPPADARY
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                       consists of 23 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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98715 107307: contig of 8593 bp in length
107308 107407: gap of 100 bp
107408 120788: contig of 13381 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11896: gap of 100 bp 14787: contig of 2891 bp in length 14887: gap of 100 bp 18648: contig of 3761 bp in length 18748: gap of 100 bp 23568: contig of 4820 bp in length
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contig of 10119 bp in length
                                                                                                                                                                                                                                                                                      100 bp
of 1087 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: gap of 100 bp
8250: contig of 1497 bp in length
0: gap of 100 bp
11796: contig of 3446 bp in length
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88803: contig of 8658 bp in length
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32571: contig of 3849 bp in length
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44015: contig of 6581 bp in length
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50291: contig of 6176 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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                                                                                                                        /translation="MRMIKLKRISKKKIRIMNCVWKMMRKSFRTQSFIFVGLDSVCFH
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC012124 146393 bp DNA HTG 12-MAR-2000
Homo sapiens clone RP11-3B7, WORKING DRAFT SEQUENCE, 23 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146393)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center clone name: L2707
Center clone name: 3.B.7
Center clone name: 3.B.7
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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Insert size: 14419; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 5.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                     Length 104806;
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Unpublished
                                                                                                                                                                                        4.2%; Score 20; DB 8;
100.0%; Pred. No. 6.5;
tive 0; Mismatches
/evidence=not_experimental
                                                         /protein_id="AAF18646.1"
/db_xref="G1:6598591"
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                          /product="F5J5.
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AC012124/c
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KEYWORDS
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SOURCE

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The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): C-2190612
Downstream BAC (overlapping the SP6 end): R-16B13 (AC-AL157911)
ASSEMBLY DOWNSTREAM STATISTICS
ASSEMBLY Program: Phrap: version 2.0
Quality coverage: 9.39x in Q20 bases; sum-of-contigs
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           dbSTS:STS825
Identified using the è-PCR software (G. Schuler)"
163594. 163754
Anote—"matching EMBL:R37868
RHdb:RH80977
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Identified using the e-PCR software (G. Schuler)"
136777. 136955
//note-matching EMBL:AI033968
RHdb:RH103549
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Identified using the e-PCR software (G. Schuler)"
163542. ..163659
//note-matching EMBL:G20222
RHdb:RH16711
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Identified using the e-PCR software (G. Schuler)"
a 32505 c 30834 g 52111 t
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red. No. 6.7;
Mismatches 0; Indels 0
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Identified using the e-PCR software (G. 163645. .163717
/note="matching EMBL:241154
                                                                               Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="matching EMBL:G11072
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/organism="Homo sapiens
/db_xref="taxon:9606"
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/clone_lib="RPCI-11"
122807. .122993
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Range : bases
0 :
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40 - 49
50 - 59
70 - 69
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Direct Submission

Submitted (23-MAY-2001) Genoscope - Centre National de Sequencage :

Submitted (23-MAY-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla: Primates; Catarrhin; Hominidae; Homo.

( Dases I to 164935)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Bortler,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSOlDUN 164935 bp DNA PRI 23-MAY-2001 Human chromosome 14 DNA sequence BAC R-62H20 of library RPCI-11 from chromosome 14 of Homo saplens (Human), complete sequence.
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vector_side:right,
37455. 44015
//note="assembly_fragment"
44116. 50291
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18749. .23568
/note-"assembly_fragment"
23669. .286?
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17408. .120788
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note-"assembly_fragment"
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AUTHORS
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REFERENCE AUTHORS TITLE

REFERENCE AUTHORS

ACCESSION

VERSION KEYWORDS

SOURCE

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it is available and the accession number will
This record will be updated with the finished sequence
                                                                                         p of 100 bp contig of 86 bp in length p of 100 bp in length p of 106 bp in length p of 100 bp contig of 1032 bp in length
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149080 175291: contig of 26212 bp in length
Location/Qualifiers
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95960: contig of 10370 bp in length
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138858 148979: contig of 15122 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30451: gap of 100 bp
33936: contig of 3485 bp in length
34036: gap of 100 bp
37015: contig of 2979 bp in length
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85490: contig of 7886 bp in length
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124322 133757: contig of 9436 bp in length
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30351: contig of 3083 bp in length
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23631: contig of 3269 bp in length
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27168: contig of 3437 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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3552: con
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be preserved.
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                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 175291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA HTG 14-MAR-2000
5 clone RP11-402F5 map 5, WORKING DRAFT
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Center close name: 402_5.5

Sequencing vector: M13, M77815, 100% of reads Chemistry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 150729 bases at least Q40

Consensus quality: 163124 bases at least Q30

Consensus quality: 168741 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: 16936
                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 5, clone RP11-402F5
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Insert size: 172291; sum-of-contigs
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SEQUENCE, 31 unordered pieces
                                                                                                                                                                                                                 AC024429.2 GI:7239654
HTG; HTGS_PHASE1; HTGS_DRAFT
Db 119882 TCAGAGTGGGCAGAGGCT 119863
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 175291)
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                                                                                                                     175291 bp
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JOURNAL
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COMMENT

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Human Homo sapiens

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 18479)

El (bases 1 to 187479)

El Sequencing of Human Chromosome 5

Unpublished

El (bases 1 to 187479)

El (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 172550 bases at least Q40
Consensus quality: 181778 bases at least Q30
Consensus quality: 18184 bases at least Q30
Consensus quality: 18184 bases at least Q30
Consensus quality: 18184 bases at least Q30
Estimated insert size: 195990; sum-of-contigs estimation
Estimated insert size: 18679; sum-of-contigs estimation
Quality coverage: 10.98 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1053
1152: gap of unknown length
1053
1300: contig of 2048 bp in length
1301: 6058: contig of 2048 bp in length
1301: 6058: contig of 2758 bp in length
1559: 9504: contig of 2758 bp in length
1559: 9504: contig of 1346 bp in length
15605: 16802: contig of 1346 bp in length
15707: 22096: contig of 1798 bp in length
15707: 22196: gap of unknown length
15707: contig of 1058 bp in length
1525: 44124: contig of 10580 bp in length
1525: 60616: contig of 10532 bp in length
1525: contig of 16392 bp in length
1526: contig of 16392 bp in length
1526: gap of unknown length
1526: gap of unknown length
1526: gap of unknown length
1527: ll1269: gap of unknown length
1528: gap of unknown length
1529: gap of unknown length
1529: gap of unknown length
1528: gap of unknown length
1529: gap of unknown length
1528: gap of unknown length
1529: gap of unknown length
1529: gap of unknown length
1529: gap of unknown length
                             AC093250.1 GI:15193424
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
human.
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Center Project Name: 424694
Center clone name: RPCI-11_47L17
unordered pieces.
                             ACCESSION
VERSION
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SOURCE
ORGANISM
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AUTHORS
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Best Local Similarity 100.0%; Pred. No. 6.7,
Matches 20; Conservative 0; Mismatches 0; Indels 0
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77605. 85490
77606. assembly_fragment"
85591. 95960
/note-assembly_fragment"
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7116. 42151
700te—"assembly_fragment"
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|note="assembly_fragment"
|04179, .114515
|note="assembly_fragment"
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1351. .71393
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/note="assembly_fragment"
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note-"assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
                             172. 1257
note-"assembly_fragment
                                                                                                                                              ector_side:right"
                                                                                                                      clone_end:T7
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1. .187479
//organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-47L17" source

111370 144755 144855

FEATURES

RESULT 11
AC093290/c
LOCUS
AC0932290 187479 bp DNA
DEFINITION HOMO Sapiens chromosome 5 clone RP11-47L17, WORKING DRAFT SEQUENCE,

DD 87053 AAFACTTATAGAGCCATTT 87034 33 AATACTTATAGAGCCATTTT 52

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Quality coverage: 7.0 in Q20 bases; sum-of-contigs
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/clone_lib="RPCI-11 Human Male BAC"
1. 58818
/note="assembly_fragment
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'note="assembly_fragment"
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/chromosome="4"
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AC087841.1 GI:12621392
HTG; HTGS_PHASE1; HTGS_DRAFT.
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vector_side:left"
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Matches 20; Conservative
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG 04-OCT-2000

HOMO Sapiens chromosome 4 clone RP11-570L13 map 4, WORKING DRAFT SEQUENCE, 7 unordered pieces.
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                                                                                                                                           Length 187479;
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Center clone name: 570_L_13

Center clone name: 570_L_13

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 185540 bases at least Q40

Consensus quality: 188787 bases at least Q20

Consensus quality: 188645 bases at least Q20
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Contact: sequence_submissions@genome.wi.mit.edu
/clone_lib="RPCI human BAC library 11"
57600 a 35701 c 35441 g 57486 t 1251 others
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                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-570L13 Unpublished
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Insert size: 189574; sum-of-contigs
                                                                                                                                           DB 2;
6.7;
                                                                                                                                           Score 20; DB 2
Pred. No. 6.7;
0; Mismatches
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                                                                                                                                              100.08; Pr
                                                                                                                                                                                                                                                                                      AC022739.3 GI:10567959
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                                                                                                                                                                                                                                                      33 AATACTTATAGAGCCATTTT 52
                                                                                                                                                                                             20; Conservative
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Direct Submission
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                                                                                                                                           Query Match
Best Local Similarity
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ORGANISM
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REFERENCE
AUTHORS
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AC022739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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Gaps
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                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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.00.0%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610 others
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62639 62738: gap of 100 bp
62739 73191: contig of 10453 bp in length
73192 73291: gap of 100 bp
73292 90983: contig of 17692 bp in length
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91084 145445: contig of 54362 bp in length
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145546 190174: contig of 44629 bp in length
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REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Gaps
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Pred. No. 6.7;
0; Mismatches 0; Indels 0
   5286 86139: contig of 10854 bp in length 6440 98729: gap of unknown length 9373 99472: gap of unknown length 9473 17995: contig of 13133 bp in length 9473 17995: contig of 18523 bp in length 18095: contig of 18523 bp in length 18096: 336106: contig of 18011 bp in length 6107 162352: contig of 26146 bp in length 2353 162452: gap of unknown length 2353 162452: gap of unknown length 2453 192725: contig of 30273 bp in length 1803725: contig of 30273 bp in length 192725: contig of 30273 bp in length 192725: contig of 30273 bp in length 192725:
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43032 c 43919 g 51808 t
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30483. 38702
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38803. 46799
/note="assembly_fragment"
46900. 56572
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/note="assembly_fragment
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136207, .162352
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Dases 1 to 192725)

Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dletrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karllins, E., Lee-Lin, S.-Q., Mastrian, S.-D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Welherby, K.D., Zhang, L.H. and Green, E.D.

MISC Comparative Sequencing Initiative

Green, E.D.

Green, E.D.

Green, E.D.
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Submitted (31-JAN-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
Grovemont Circle, Gaithersburg, MD 20877, USA
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@hipgi.nih.gov
Contact: nisc_mouse@hipgi.nih.gov
Center project name: 40
Center project name: 40
Center project name: 41519
Center project name: 41519
Sequencing vector: plasmid: n/a; 100% of reads
Center project name: 41519
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contig of 2023 bp in length
gap of unknown length
contig of 2848 bp in length
contig of 2848 bp in length
gap of unknown length
contig of 3848 bp in length
gap of unknown length
contig of 3768 bp in length
gap of unknown length
gap of unknown length
contig of 3873 bp in length
gap of unknown length
contig of 4667 bp in length
gap of unknown length
gap of unknown length
contig of 7051 bp in length
gap of unknown length
contig of 8220 bp in length
gap of unknown length
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contig of 8230 bp in length
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Search completed: January 31, 2002, 12:14:33 Job time: 1506 sec
                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                          FEATURES
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ICTEMEREGKVSKVGPENPYNTPVFAIKKKDSTKWRKIVDFRELNKKTQDFWEVQLGI
PHPAGLKKKKSVTVLDVGDAYFSVP"
54 c 74 g 95 t
                 HIVUG9075 380 bp DNA VRL 16-SEP-1996
HIV-1 patient D clone L5 from USA reverse transcriptase (pol) gene,
partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by codons 1-118 of the reverse transcriptase as represented in HIV-1 LAI GenBank Accession Number K02013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 418)
Gregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E. Direct Submission
Submitted (18-NOV-1998) The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSPE48B07 418 bp DNA STS 18-NOV-1998
H.sapiens flow-sorted chromosome 1 HindIII fragment, SClpE48B07,
                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-SEP-1996) Department of Medicine, University of
California School of Medicine, 9500 Gilman Drive, La Jolla, CA
92093-0679, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marker stSG33217FS (Primer A : AGAAAGAAATGAAGGCATCA; Primer B CCTGCAACTTCACTGAATTCA; amplimer size : 139 bp) was mapped to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                             Human immunodeficiency virus type 1.

Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
1 (bases 1 to 380)
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Human immunodeficiency virus type 1"
/isolate="patient D"
/db_xref="taxon:11676"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="reverse transcriptase"
/protein_id="AAB08364.1"
/db_xref="GI:1546648"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //tissue_type="lymph node"
/clone="L5"
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                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AL033810
AL033810.1 GI:3893549
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<1. .>380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 TGGAAAGGAAGGAAAGT 164
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                                                                                                       U69075.1 GI:1546647
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                       Wong, J.K.
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HSPE48B07
                                        DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
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ð a

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Gaps
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                                                                                                      /dev_stage="adult"
/tissue_type="EBV lymphoblastoid cell line"
/clone_lib="SC1pE"
/clone="SC1pE48807"
78 c 82 9 102 t
                                                                                                                                                                                                                  Length 418;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                  Score 19; DB 11;
Pred. No. 18;
0; Mismatches 0
chromosome 1 using Radiation Hybrid panel Genebridge 4 (GB4).
Location/Qualifiers
                                    1. 418
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                        4.0%; Scor.
100.0%; Pre
0;
                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                        237 GAGCAGTTTAGCAAGAGA 255
                                                                                                                                                                                                                                                                                      91 GAGCAGTTTAGCAAGAGAA 109
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT: HOGREFE, Holly TITLE OF INVENTION: Polymerse Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same
70.50 132.84 1.45
70.00 123.64 2.38
70.00 123.64 2.38
+ 69.00 129.36 2.26
+ 69.00 129.36 2.26
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David J. Kullk, Evenson, McKeown, Edwards & ADDRESSEE: Lenahan, P.L.L.C. STREET: 1200 G Street, N.W. Suite 700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 CCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 GGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAGCTT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SerSerLysGlyIleArgLeuAsnProAsnProArgGluAspLysValAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 TCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 105
Gaps: 0
Percent Identity: 98.095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seq 1/1 to: US-08-822-774-45 from: 1 to: 246
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                       /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-483-2 + 
/qgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-483-5 + 
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-599-171A-25 
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-646-590B-25 
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      /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-149-223A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KULIK, David J.
REGISTATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               Sequence 45, Application US/08822774 Patent No. 6183997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-957-709-70 x US-08-822-774-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     558.00
5.417
98.095
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YES
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                            -WODEL-frame+_n2p.model -DEV=x1h
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0.3029 65
0.3029 65
1.42 0.3029
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5 0.0310
0.0571
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160.58 0.0149
171.05 0.0310
166.13 0.0571
164.20 0.0757
0 164.20 0.0757
0 186.85 0.0420
141.42 0.3029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 26 3
993.90 78 6
369.20 78 6
290.21 289.78 278.51 248.74 242.03 26 .96
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70.50 132.84
70.50 132.84
70.50 132.84
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                                                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.50
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533.00
1436.00
124.00
114.00
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112.00
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79.50
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                                                                                                                                                                                                                                                                                                                                                                   -USER-US08957709_@CGN1_1_0 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_IIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + 76
74.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptodata/2/iaa/6B_COMB.pep:US-08-822-774-54 +
ptodata/2/iaa/5A_COMB.pep:US-08-258-639a-4 +
ptodata/2/iaa/5B_COMB.pep:US-08-900-951-4 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pep:US-08-862-903-8
pep:US-08-824-405-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-458-731-8
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ptodata/2/iaa/5A_COMB.pep:US-08-453-4/

ptodata/2/iaa/5A_COMB.pep:US-08-038-9/

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ptodata/2/iaa/5A_COMB.pep:US-08-453-9/

ptodata/2/iaa/5A_COMB.pep:US-08-862-9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ptodata/2/iaa/5B_COMB.|
ptodata/2/iaa/5B_COMB.|
ptodata/2/iaa/5A_COMB.|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: Issued_Patents_AA:*
Database sequences: 212252
Database Iength: 22503292
Search time (sec): 26.380000
                                        Date: Jan 31, 2002 12:58 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : US-08-957-709-70
length: 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query:
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seq_documentation_block:
    Sequence 43, Application US/08822774
    Sequence 43, Application:
    ApplicATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION:
    TITLE OF INVENTION:
    AURESPONDENCE ADDRESS:
    ADDRESSE:
    CORRESPONDENCE ADDRESS:
    ADDRESSE:
    ADDRESSE:
    Lenahan, P.L.L.C.
    STREET:
    ADDRESSE:
    Lenahan, P.L.L.C.
    STREET:
    ADDRESSE:
    COMPUTER READABLE FORM:
    MEDIUM TYPE:
    COMPUTER READABLE FORM:
    COMPUTER:
    MEDIUM TYPE:
    COMPUTER:
    SOFTWARE:
    SEQUENCE:
    COMPUTER:
    SEQUENCE:
    COMPUTER:
    SEQUENCE:
    SOFTWARE:
    SEQUENCE:
    COMPUTER:
    COMPUTER:
    SEQUENCE:
    COMPUTER:
    COMPUTER:

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                                                                                                                 257 GGGTTATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTA 306
                                                                                                                                                                                                                                         307 ACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGG 356
                                                                                                                                                                                                                                                                                                                                                              357 AGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 ACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAG 456
                               seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-43
                                                                                                                                                                                                                                                                         104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEFAN: (202) 628-884
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 246 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality: 436.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 AGAAAGAAACTC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FRAGMENT TYPE:
US-08-822-774-43
                                                                                                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:

Sequence 44, Application US/08822774

Patent No. 6183997

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61

ADDRESSEE: Landan, P.L.L.C.

ADDRESSEE: Landan, P.L.L.C.

STREET: 1200 G Street, N.W. Suite 700

STATE: D.C.

ZIF: 20005
                                                                                 seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 43 6
ATTORNEY/AGENT INPORMATION:
NAME: KULIK, DAVId J.
REGISTRATION: UMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INDERS: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 104
Gaps: 0
Percent Identity: 98.077
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US-08-957-709-70 x US-08-822-774-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 amino acids
amino acid
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Ratio: 5.125
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 246 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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PEF Proteins, Same amino acid

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Polymerase Enhancing Factor (PEF)
Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAA 407
                                                                                                                                                                                            158 CICCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCC 207
                                                                                                                                                                                                                                                                                        GACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGG 257
                                                                                                                                                                                                                                                                                                                                                                                        GGTTATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                 67 uArgAspLeuCysArgSerHisLeu***Gly***ArgValArgGlnGluT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evenson, McKeown, Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-41
                         Percent Identity: 88.462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
                                                                                                                                              from: 1 to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, MCK
ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
2 IP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: IDM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
    Sequence 41, Application US/08822774
    TITLE OF INVENTION: Polymerase Enhance of INVENTION: Extracts, PEF 17 TITLE OF INVENTION: and Methods for UNMBER OF SEQUENCES: 61
                                                                                                                                            to: US-08-822-774-43
                                                                      alignment_block:
US-08-957-709-70 x US-08-822-774-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 436
ATTORNEY/ACENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
4.739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 GAAAGAAACTCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GluArgAsnSer 104
  Ratio:
                         Percent Similarity:
                                                                                                                                            Align seg 1/1
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                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                        258
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APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 MetLeuLeuProAspTrpLysileArgLysGluIleLeuIleGluProPh 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards
ADDRESSEE: Lenahan, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 TTCTGAAGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eSerGluGluTrpLeuGlnProAlaGlyTyrAspLeuArgValGly 42
                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 96.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                to: 42
                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1200 G Street, N.W. Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
    Sequence 37, Application US/08822774
    Patent No. 6183997
                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-822-774-41
                                                                                                                                                                                                                                                                                            alignment_block:
US-08-957-709-70 x US-08-822-774-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING CVCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INPERMATION FOR SEC ID NO: 37
SEQUENCE CHARACTERISTICS:
                                                                                       N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 amino acids
                                                                                                                                                                                                160.00
5.161
96.875
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           MOLECULE TYPE: peptide HYPOTHEICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: YES
  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HOGREFI
                                          HYPOTHETICAL: N
ANTI-SENSE: NO
FRAGMENT TYPE:
US-08-822-774-41
                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FRAGMENT TYPE:
US-08-822-774-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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CAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAA 136
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US-08-822-774-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:

Sequence 39, Application US/08822774

Patent No. 6183997

GENERAL INFORMATION:

TILLE OF INVENTION: Polymerase Enhancing Factor (PEF)

TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61

NUMBER OF SEQUENCES: 61

ADDRESSEE: Lenhan, P.L.C.

STREET: 1200 G Street, N.W. Suite 700

STATE: D.C.

21P: 20005
                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21P: 2005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBE: US/08/822,774
FILING DATE: 21 WAR-1997
CLASSIFICATION NUMBER: 35,576
ATTORNEY/AGENT INPORMATION:
NAME: KUILK, David J.
REGISTRATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
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TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8800
                           Length: 27
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 28
Gaps: 0
Percent Identity: 85.714
                                                                                                                                                                                                                        Align seg 1/1 to: US-08-822-774-37 from: 1 to: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-822-774-39 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-957-709-70 x US-08-822-774-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-957-709-70 x US-08-822-774-39
                    124.00
5.167
88.889
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Quality: 124.00
Ratio: 4.960
Percent Similarity: 89.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-822-774-39
                    Quality:
Ratio:
Percent Similarity:
alignment_scores:
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seq_documentation_block:
Sequence 38, Application US/08822774
Sequence 38, Application US/08822774
Sequence 38, Application US/08822774
Sequence 38, Application US/08822774
Sequence 38, Application US/08822774
Sequence 38, Application US/0882177
Sequence 38, US/08821000
SEQUENCES 401, APPLICATION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBERS OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
STATE: D.C.
21P: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 AGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAA 137
1 GlnSerGlyGlnArgGly***Cys***GlyGlulleAsnArgSerGlyLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgValGlyArgGluAla***ValLysGlyLysLeuIleGluValGluLy 17
                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-822-774-38
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION ON #36
ATTORNEY/AGBNT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 38:
FELEPHONE: (202) 628-8800
TELEPHONE: (202) 628-8806
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acids
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Ratio: 4.760 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-822-774-38 from: 1 to: 27
                                                                                             138 GGAAGGAAAGTCGTTATTCCTCCAAGGGAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 sGluGlyLysVal***IleProProArgGlu 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-957-709-70 x US-08-822-774-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-824-405-11

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CCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 GAAGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 TTTTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAAGGAAAAGTCGTTA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 TICCICCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 .....IleMetI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 leProValSerAspThrLysIleIleProThrAspValLysIleGlnVal 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GluLysArgAspGluAspAlaGlyPheAspLeuCysValProTyrAsp.. 29
                                                   APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Lynch, Frank
APPLICANT: Lynch, Frank
APPLICANT: Lynch, Frank
TITLE OF INVENTION: dUTPase, its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 22.764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-824-405-11 from: 1 to: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO FOR WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERNCE/DOCKET NUMBER: 350163-101
TELECOMMUNICATION:
TELEPHONE: 609/520-3214
seq_documentation_block:
    Sequence 11, Application US/08824405
    Patent No. 5962246
    GENERAL INFORMATION:
    APPLICANT: Ladner, Robert D.
    APPLICANT: Lynch, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-957-709-70 x US-08-824-405-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 138 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
US-08-824-405-11
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114.50
1.568
59.350
                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
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255 AGGGGTTATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACT 304
                                                                                        305 TAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATAT 354
                                                                                                                                                                                  355 GGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGTCCGGCAAG 404
                            82 leGlnValileCysThrAsnileGlyLysSerAsnileLysLeuileGlu 98
                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-824-405-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
    sequence 2, Application US/08824405
    Patent No. 5962246
    Septence Information
    Sequence 2, Application US/08824405
    Sequence 2, Application US/08824405
    Septence No. 5962246
    APPLICANT: Ladner, Robert D. APPLICANT: Lynch, Frank
    APPLICANT: Caradonna, Salvatore J. TITLE OF INVENTION: durpase, Its Isoforms, and TITLE OF INVENTION: Diagnostic and Other Uses
    NUMBER OF SEQUENCES: 20
    CORRESPONDRESCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 29.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 350163-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-957-709-70 x US-08-824-405-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                             405 AAACCCTTACAGAGGAAAC 423
                                                                                                                                                                                                                                                                                                       |:::|||:::
|115 gGlnProTrpAspGluAsn 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112.50
1.607
53.030
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4000 Bell A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103-2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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us-08-957-709-70.rai

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127 AspArglleAlaGlnLeulleCysGluArgllePheTyrProGlu.lleG 143
                                                                                                                                        111 TAAGGGGAAATTAATCGACGTGGAAAGGAAGGAAAAGTCGTTATTCCTC 160
                                                                                                                                                                                                                                          161 CAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGAC 210
                                                                                                                                                                                                                                                                                                                                      211 GATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 eileAspValGlyAlaGlyValileAspGluAspTyrArgGlyAsnValG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGAGATTTGTGCAGATCGCATTTATAAGGCTA......GAGGGTCC 398
                                               61 TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGGCTTTTGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                  :::|||||||
09 Goran TyrThrIleProP
                                                                                                                                                                                                                                                                            || ||| |||| ||||:::::: ||| |||||||:::
60 roMetGluLysAlaValValLysThrAspIleGlnIleAlaLeuProSer 76
                                                                           seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-824-405-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: USA
2IP: 19103-2793
  to: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ladner, Robert D.
APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: durpase, Its Isoforms, and
TITLE OF INVENTION: Disgnostic and Other Uses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DAY
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/824,405
FILING DATE: 26-MAR-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
to: US-08-824-405-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eg_documentation_block:
Sequence 4, Application US/08824405
Patent No. 5962246
GENERAL INFORMATION:
APPLICANT: Ladner, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 35(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
Align seg 1/1
                                                                                                                                                                                        26
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61 TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 CAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGAC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 roMetGluLysAlaValValLysThrAspIleGlnIleAlaLeuProSer 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 GATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 TATTGGTTCTTTTGCTTGGGTT. . . GACCCAGGATGGAAACTTAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 elleAspValGlyAlaGlyVallleAspGluAspTyrArgGlyAsnValG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 lyvalvalLeuPheAsnPheGlyLysGluLysPheGluValLysLysGly 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 GAGAGATTIGTGCAGATCGCATTTATAAGGCTA.....GAGGGTCC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AspargileAlaGlnLeuIleCysGluArgilePheTyrProGlu.ileG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-824-405-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 TAAGGGGAAATTAATCGACGTGGAAAAGGAAGGAAAAGTCGTTATTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 GGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CTTY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2793
CMMPUTER READABLE FORM:
MEDIUM TYPE: 18M COMPUTER: 18M C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 132
Gaps: 4
Percent Identity: 29.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 252
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APPLICANT: Ladger, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: Diagnostic and Other US
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price 6 Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-824-405-4 from: 1
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    sequence 10, Application US/08824405
    patent No. 5962246
        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-957-709-70 x US-08-824-405-4
INFORMATION FOR SEQ ID NO: 'SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112.50
1.607
53.030
                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Outlity:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-824-405-4
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us-08-957-709-70.rai

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155 ITCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTG 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 GlyArgLysPheAlaGlnLeuIleLeuMetProLeuIleHisGluGluLe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GAAGAATCGCTCCAACCAGCATTATGACCTCAGAGTGGGCAGAGAGGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 AGGGGTTATTGGTTCTTTGGGTTGGGTTGACCCAGGATGGGATGGAAACT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::||||||::: ::: ::: :::||| | |||::::|||:::: 65 sGlyValPheValGlnGlyGlyIleIleAspSerGlyTyrGlnGlyThrI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GlnLysArgAlaGluAspAlaGlyTyrAspLeuIleCysProGlnGlu. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 LysLysAspGlnTrpAlaMetIleGlyThrLysSerSerPheAlaAsnLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 AAACCCTTAC.....AGAGGAAACTATCAGGGGAGCACAAGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||| :::||||:::||| 32 leProAlaGlyGlnValLysArgIleAlaIleAspLeuLysIleAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-238-303-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 26.316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-824-405-10 from: 1 to: 138
                         SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26 MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 350163-101
TELEPHONE: 609/520-3214
TELEPRAX: 609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/09238303B
; Patent No. 6284253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-957-709-70 x US-08-824-405-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112.00
1.534
54.887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single; TOPOLOGY: linear
US-08-824-405-10
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
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APPLICANT: Barr, Margaret C.
TITLE OF INVENTION: No. 6284253el Feline Immunodeficiency Virus Nucleotide Sequenc FILE REFERENCE: 18617.0059
CURRENT APPLICATION NUMBER: US/09/238,303B
CURRENT PILING DATE: 1999-01-28
EARLIER APPLICATION NUMBER: US 60/072,927
EARLIER PILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                  cat felin
                                                                                                                                                                                                                                                                                                          protein encoded by the pol gene of a recombinant viral clone constructed from the genomic DNA of a Pallas's cimmunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 CAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGGCTTTTGTTAAGGG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   768 luValArgIleValProThrGlyValArgLeuMetLeuProLysGlyHis 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 TATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 TAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816 alileMetileAsnLeuGlnLysArgSerileThrLeuLysGluLysGln 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-824-405-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 GAAATTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCCAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AATACGCCTTAATCCTAACCCTCGAGGGATAAAGTTGCCCGACGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 ATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGG.....GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 108
Gaps: 3
Percent Identity: 24.074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ladner, Robert D.
APPLICANT: Ladner, Rrank
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPase, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
ADDRESSEE: Dechert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08824405
Patent No. 5962246
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AGATTTGTGCAGATCGCATTTATA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-238-303-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-957-709-70 x US-09-238-303-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.50
1.535
52.778
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                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
COTHER INFORMATION:
US-09-238-303-9
                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                 1150
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                                                                                                                                                                                                                                                                                    FEATURE:
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251 GAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 GTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 ATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-824-405-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 84
Gaps: 0
Percent Identity: 27.381
                                                                                              COUNTER READALE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: DISKETTE
APPLICATION NUMBER: DISKETTE
COMPUTER: DISKETTE
ATORIAN ALLE
REFERENCE/DOCKET NUMBER: 350163-101
TELEPHONE: 609/520-3259
FILISKETE
FILISKETTE
COMPUTER: DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-957-709-70 x US-08-824-405-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEO ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 147 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.00
1.673
61.905
    Philadelphia
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
US-08-824-405-12
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CITY: Ph
STATE: P
COUNTRY:
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seq_documentation_block:
; Sequence 13, Application US/08824405
; Sequence 10, Sp62246
; GENERAL INFORMATION:

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251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 TTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 AGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCCAGGATGGGATGGAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 ACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 ThrangGlnSerProTyraladlaGlyTyrAspLeuTyrSerAlaTyrAs 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 p.....TyrT 38
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||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: 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38 hrllePheProGlyGluArgGlnLeuIleLysThrAspIleSerMetSer
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                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 1
Percent Identity: 24:138
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APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPase, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Declert, Price & Rhoads
ADDRESSE: Declert, Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2793
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNDERS: US/08/824,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-MAR-1997
CLASSIFCATION NUMBER: 95-MAR-1997
CLASSIFCATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY.AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 29,135
TELECOMMUNICATION:
TELEPHONE: 609/520-3214
TELEFAX: 609/520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-957-709-70 x US-08-824-405-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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US-08-824-405-13
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101	IOI CAAGGGAAIACGCCIIAAICCIAACCCICGAGAGGAIAAAGIIGCCCGAC ZIU	770
43	laMetGlyGln	59
211		257
09	60 GlyThrTyrGlyArgIleAlaProArgSerGlyLeuAlaValLysAsnGl	97
258	258 GGTTATTGGTTTTTGCTTGGGTTGACCCAGGATGGGATG	307
16	76 yıleGlnThrGlyAlaGlyValValAspArgAspTyrThrGlyGluValL	93
308	308 CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357	357
93	ysvalvalvalpheAsnHisSerGlnArgAspPheAlaIleLysLy	109
358	GAGAGATTTGTGCAGATCGCATTTATAAGG	387
110		126
388	CTAGAGGGTCCGGCAAGAAACCCTTAC	421
126	126 eValValValAspSerLeuGluGluSerAlaArgGlyArgGlyG 141	141
422	422 ACTATCAGGGGAGCACA 438	
141	:::::	

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polymerase enhancing factor (EFF) of pyrococcus furiosus DSM 3638.

The sequence is predicted from a DNA sequence (see AAV63860) obtained from genomic DNA by PCR. P45 and P50 (see AAV6386) obtained from genomic DNA by PCR. P45 and P50 (see AAV6386) obtained from genomic DNA by PCR. P45 and P50 (see AAV6386) obtained from genomic DNA by PCR. P50 (see AAV6386) obtained the activity of predominant components of PEE, which acts to enhance the activity of P. furiosus DNA polymerase. P45 functions as a dUTPase, and can be used to enhance uncleic acid replication, polymerisation or PCR complexes that improve the polymerisation activity of nucleic acid polymerases, as well as DNA constructs and antibodies. Also included are methods for identifying compositions with PEF activity. For purifying and using these compositions, and specific extracts, proteins and complexes that function to enhance polymerase activity. Composition having polymerase enhancing activity. Rits are provided for replicating nucleic acid sequencing or site-directed mutagenesis, for nucleic acid sequencing or amplification (preferably PCR or RT-PCR).
   4.18
1.83
1.94
1.94
2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
122.71
151.32
149.62
149.54
148.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enhancing factor; PEF; dUTPase; DNA polymerase; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-terminal peptide used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of the P45 component of the
74.00
73.50
73.50
73.50
                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:AAW72847
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymerase enhancing factor P45 (dUTPase) component.
/SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAV41139
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAG55137
SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAG55530
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAG55136
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAG55136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplification; sequencing; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus strain DSM 3638.
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                                                                                                                                                                                                                                                                              AAW72847 standard; Protein; 156
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Query length: 471
Database: A_Geneseq_1101:*
Database sequences: 522463
Database length: 74073290
Search time (sec): 47.930000
                                                               Date: Jan 31, 2002 12:57 PM
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A sequence encoding a thermostable DNA ligase was cloned into the plasmid ppam-13. The DNA ligase is AFP dependent and is useful for detecting nucleic acids by hybridising two oligonuclectides with adjacent sequences of the target nucleic acid, ligating the two oligonuclectides (using the ligase) and detecting the ligation product. Analysis of the fragment revealed three other open reading frames (ORF's). This is a polypeptide encoded by ORF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|||||| | |||:::::
100 heAlaArgLeuGlyLeuPheValProProThrIleValAspAlaGlyPhe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 GATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 ATTAAGATATGGAGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 GTCCGGCAAGAACCCTTACAGAGGAACTATCAGGGGAGCACAAGGTTA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAG92886
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GluPheIleIleTyrProAsnGluHisValLeuLeuValThrGluGluTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 TAGCAAGAGAAGGGGTTATTGGTTGTTTGGTTGGGTTGACCCAGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 ATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 GATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 156
Gaps: 3
Percent Identity: 35.897
                        Kletzin A,
                                                                                                                    Thermostable ligase from archaebacteria - and useful for nucleic acid detection
                                                                                                                                                                            Example 3; Figure 1; 26pp; German.
                        Kessler C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                242.00
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US-08-957-709-70.x AAR51078
                        Jarsch M, Kaletta C,
                                                          WPI; 1993-378402/48.
N-PSDB; AAQ62300.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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        Ligase, thermostable; thermostability; Desulfurolobus ambivalens; archaebacteria; detection; ligation; ATP; adenosine triphosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 TTCTGAAGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAG 100
                                                                                                                                                                                                                                                                                                                                GTTATICCICCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 ATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATT 50
                                                                                                                                                                                                eSerGluGluSerLeuGlnProAlaGlyTyrAspLeuArgValGlyArgG 34
                                                                                                                                                                                                                                                                                                                                                     ValileProProArgGluTyrAlaLeulleLeuThrLeuGluArgIleLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT:AAR51078
    Length: 156
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BOEF ) BOEHRINGER MANNHEIM GMBH.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide encoded by pDam-L3 plasmid fragment.
                                                                                                                                      Align seg 1/1 to: AAW72847 from: 1 to: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID AAR51078 standard; Protein; 173 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAAAGAGAAAGAACTC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Quality: 806.00
Ratio: 5.167
Percent Similarity: 100.000
                                                                            alignment_block:
US-08-957-709-70 x AAW72847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1992;
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117

401

451

106

144

99

294

244

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Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; vitamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum MP protein sequence SEQ ID NO:1012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carbohydrate; aromatic compound; cofactor; polyketide; enzyme
                                                                                                                                                                                                                                                   ::!!! |||:::||||
134 laAsnLeuProlleThrLeuTrpProGlyMetLysValGlyGlnLeuAla 150
                                                                                                                                                                AAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
                                                                                                                                                                                                                                CCCTCGAGGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGATA 234
                                                                                                                                                                                                                                                                                                                                                                   279 GGTTGACCCAGGATGGATGGAACTTAACACTAATGCTCTACAATGCCT 328
                                                                                                                                                                                                                                                                                                                                                                                      CAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 ITTATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 LeuPheGlnMetSerSerProAlaGluThrProTyrGlySerGlyLysLe 167
17 uGlyIleGluProPheAspAlaGluLeuIleGlnProSerSerValAspV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB80139
                                                                                                                   235 AGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GGTTCTTTTGCTTG
                                                               34 alArgMetAspArgTyrPheArgValPheAsnAsnSerLysTyrThrHis
                                                                                                121 .....TTAATCGACGTGGA
                               86 TCAGAGTGGGCAGA.....GAGGCTTTTGTTAAGGGGGAAA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB80139 standard; Protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DE-1031415.
99DE-1031418.
99DE-1031419.
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99DE-1031424.
99DE-1031428.
99DE-1031434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 uGlySer 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40200100843-A2
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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08-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                   329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokoi H;
                                                                                                                                                              Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; SEQ ID NO: 6640; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGCTACTTCCAGACTGGAAAATCAGAAAA......GAAAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLeuLeuSerAspArgAspIleArgLysSerIleAspAlaGlyAspLe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 33.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                 C glutamicum protein fragment SEQ ID NO: 6640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAG92886 from: 1 to: 189
                               AAG92886 standard; Protein; 189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                  99JP-0377484.
                                                                                                                                                                                                                                                                                                                                                                07-APR-2000; 2000JP-0159162.
                                                                                                                                                                                                                                                                                                                 18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                Corynebacterium glutamicum
                                                                                              (first entry)
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2.057
62.722
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US-08-957-709-70 x AAG92886
                                                                                                                                                                                 organic acid synthesis.
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        WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
Percent Similarity:
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alignment_scores

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                                                                                                                   99DE-1042095.
99DE-1042124.
99DE-1042129.
2000US-0187970.
                                                                        990S-01
99DE-10
99DE-10
99DE-10
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99DE-1(
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                             99DE-1
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                                                                                                                                          WPI; 2001-137957/14.
N-PSDB; AAF72258.
                                                                                                                                AG.
                                                                                                                                (BADI ) BASF
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Haberhauer

Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purline and pyrimidine bases.

Claim 20; Page 1554; 1737pp; English.

AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB0221. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, unoproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.

160 AA; Sequence

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Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 CAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCA 378
                                                                                                                                                                                                                                                             86 TCAGAGTGGGCAGA.....GAGGCTTTTGTTAAGGGGAAA......120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 hrLeuGluLysPheThrLeuProAlaHisLeuAlaGlyArgLeuGluGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::111 | 111::: | 11
134 laAsnLeuProIleThrLeuTrpProGlyMetLysValGlyGlnLeuAla 150
                                                                                                                                                                                                                                                                                                                         .....TTAATCGACGTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                      135 AAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGATA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AGGAGCAGITTAGCAAGAAAGGGGTTATT.....GGTTCTTTTGCTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 GGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTCTACAATGCCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 elleAspProGlyPheSerGlyTyrIleThrLeuGluLeuSerAsnValA 134
                                                                                                                                                                                                                     ::||||::: |||| :::::||| :::::|||| 34 alargMetAspArgTyrPheArgValPheAsnAsnSerLysTyrThrHis 50
                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                       67
                                                                                                                                                                                                   36 ACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAW89818
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 4
Percent Identity: 32.911
Length:
                                                                                                         to: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAW89818 standard; Protein; 188 AA.
                                                                                                         from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 TTTATAAGGCTAGAGGGTCCGGCA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US08487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
196.00
2.000
62.025
                                                                                                         Align seg 1/1 to: AAB80139
                                                          alignment_block:
US-08-957-709-70 x AAB80139
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Quality:
Ratio:
                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   67
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The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immuno response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, sallaw etc., they previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in waccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                 New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 aAsnAlaPheAlaLeuAlaHisThrIleGluTyrPheLysMetProLysA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleValAsnValThrProPheGluProGluPheGluGlyTyrIleThrIl 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ::: |||::::||| |||:::::::
eGlulleSerAsnThrThrAsnLeuProAlaLysValTyrAlaAsnGluG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TTAATCGACGTGGAAAAGGAAAGGAAAGTCGTTATTCCTCC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGGAATACGCCTTAATCCTAACCCTCGAGGGATAAAGTTGCCCGACG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spThrLeuAlalleCysLeuGlyLysSerThrTyrAlaArgCysGlyIle 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 AATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euPheAspAsnLysAsnAlaLeuIleAspProLysAsnPheAspProAsn 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 rGlyLeuSerSerTyrGlyTyrAspIleArgValGlySerGluPheMetL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTATAGAGCCATTTTCTGAAGAA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 4
Percent Identity: 27.976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 .TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                       peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 188
                                                                                                                                                                                                                                   Claim 15; Page 104-105; 402pp; English.
                                                                                 Lim MY, McAtee CP;
                                                (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: AAW89818 from: 1
                                                                                                                                                                                                  long-lasting immune response
97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.792
60.119
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US-08-957-709-70 x AAW89818
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                                                                                                                WPI; 1999-009433/01.
                                                                               Chow TP, Fry KE,
                                                                                                                                  N-PSDB; AAV90555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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14-OCT-1997;
25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immuno response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, sallva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenic cluster family; vaccine; gastritis; diagnosis;
362 GATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCT 411
                                                 151 lyIleAlaGlnValValPheLeuGlnGlyAspGluMetCysGluGlnSer 167
                                                                                                                                        seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAW89897
                                                                                                           TACAGA.......GGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptic ulcer; gastric adenocarcinoma; gastric lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaps: 4
Percent Identity: 27.976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 236-237; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAW89897 standard; Protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US08487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0061958.
97US-0045107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen 3 from cluster 28c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.792 60.119
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US-08-957-709-70 x AAW89897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori
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                                                                                                           412
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to: 190

from: 1

Align seg 1/1 to: AAW89897

(GEST ) GENSET

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us-08-957-709-70.rag

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Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perhhepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein involved in intermediate metabolism of nucleic acids
                                                                                                                                                                                                                                                                                                              : ::: ||||:::::||| |||:::::::: :::|||
136 eGluIleSerAsnThrThrAsnLeuProAlaLysValTyrAlaAsnGluG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 lylleAlaGlnValValPheLeuGlnGlyAspGluMetCysGluGlnSer 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 TACAGA......GGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTC 452
                                                                                                                                                                                                                                                                                                                                                          ATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                 262 ATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 AATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY37187
                                                                                             :::|||:::
36 rGlyLeuSerSerTyrGlyTyrAspIleArgValGlySerGluPheMetL
                     :::|||:::||||||
MetIleSerProPheCysGluLysGlnValGlyLysAsnValIleSerTy
                                                                                                                                                                            euPheAspAsnLysAsnAlaLeuIleAspProLysAsnPheAspProAsn
                                                                                                                                                                                                                .....TTAATCGACGTGGAAAAGGAAAAGGTCGTTATTCCTCC
                                                                                                                                                                                                                                                                                    162 AAGGGAATACGCCTTAATCCTAACCCTCGAGGGATAAAGTTGCCCGACG
                                                                      .TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG.....
CTTATAGAGCCATTTTCTGAAGAA............
                                                                                                                                          ......GCTTTTGTTAAGGGGAAA......
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37
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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis. (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, nonendemic trachoma, nonendemic trachoma, nonendemic trachoma, nonendemic paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitts, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 TAAGGGGAAATTAATCGACGTGGAAAAGGAAAAGTCGTTATTCCTC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 GATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::|||:::
105 AsnValLeuThrValCysIleGlyLysSerThrTyrAlaArgCysGlyLe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAACTTAACAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 leGluIleSerAsnThrThrProLeuProAlaLysValTyrAlaAsnGlu 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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erTyrGlyLeuSerSerTyrGlyTyrAspLeuArgIleSerArgGluPhe
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LysValPheThrAsnValTyrAsnSerLeuValAspProLysCysPheTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 CAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GACTGGAAAATCAGAAAA......GAAATACTTATAGAGCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eAlaAspSerGlnValLysLeuHisProGluThrGlyGluLysLeuIleS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Length: 176
Gaps: 6
Percent Identity: 26.136
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                                                                                                             Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGAAGAA.....
                                                                                                                                                   Disclosure; Page 961; 1755pp; English.
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1.526
55.682
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US-08-957-709-70 x AAY37187
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                                                                        WPI; 1999-371125/31.
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Ratio:
Percent Similarity:
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                                   Griffais R;
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34 yGluLysLeuIleSerTyrGlyLeuSerSerTyrGlyTyrAspLeuArgL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rahme LG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae mucleotides sequences an also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                             / disease; pneumonia; bronchitis; heart disease; sarcoidosis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                               Protein involved in intermediate metabolism of nucleotides
155 GlyIleAlaGlnValLeuPhePheGluGlyAspAlaAlaCysAspValSe 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
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                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY34994
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MetIleHisProPheValAsnGlyGlnValAsnValAsnGluGluThrGl
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Percent Identity: 24.390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia pneumoniae
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                                                                       411 TTAC.....AGAGGAAACTATCAG 429
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                                                                                                                                                                                  seq_documentation_block:
ID AAX34994 standard; Protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; neutralising epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-IB01890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                  (first entry)
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US-08-957-709-70 x AAY34994
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                                                                                                                                                                                                                                                                                                                                                                                               Respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409927105-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                       sinusitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                       AAY34994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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The present sequence represents a Pseudomonas aeruginosa polypeptide sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahajan-Miklos S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a virulence factor encoded by ORF19027c.
                                      83 lCyslleValProProAsnSerPheAlaLeuAlaArgSerValGluTyrP 100
                                                                                                                                                                                                       TAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTA 246
                                                                                                                                                                                                                                               100 heArgIleProArgAsnValLeuThrMetCysIleGlyLysSerThrTyr 116
                                                                                                                                                                                                                                                                                        247 GCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGA 296
                                                                                                                                                                                                                                                                                                             TGGAAACTTAACACTAAATGCTCTACAATGCCTCAAATGAACCTGTCGAAT 346
                                                                                                                                                                                                                                                                                                                                                                                                            133 uGlyHisValThrIleGluIleSerAsnThrThrProLeuProAlaLysI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 TAAGATATGGAGAGAGTTTGTGCAGATCGCATTTATAAGGCTAGAGGGT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 leTyrAlaAsnGluGlyIleAlaGlnValLeuPhePheGluSerSerThr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY29169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pathogen; virulence polypèptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
euSerArgGluPheLysValPheThrAsnValTyrAsnSerValValAsp
                                                                          ProLysCysPheThrGluAspIlePheIleSerIle...ThrAspAspVa
                                                                                                                       AGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ThrCysGluValSerTyrAlaAspArgLysGlyLysTyrGln 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 CCGCCAAGAACCCTTAC.....AGAGGAAACTATCAG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodman HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAY29169 standard; Protein; 177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drenkard E,
Tsongalis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drenkard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US25247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97us-0066517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-357851/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cao H,
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can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection note: a a caruginosa infection in the specification were poorly legible, and in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is not entirely correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......AGAGAGGCTTTTGTTAAG......GGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AAATTAATCGACGTGGAAAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 ATACGCCTTAATCCTAACCCTCGAGGATAAAGTTGCCCGACGATGTTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGAGTTTG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 TGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 TGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 GluValValLeuAlaAspProAspAspCysPheValMetGluProGlyLy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTC.....66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 ValArgAspGlyLysLeuileLysHisLeuAlaHisArgGluLeuThrTh 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 rProGluGlyValGlyPheAspLeuArgLeuAlaGlyLeuSerArgLeuT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111111::
45 hrValGlyGlyGlySerLeuArgGluSerThrArgArgThrProAlaSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB35755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 ....CAACCAGCAGGTTATGACCTCAGAGTGGGC.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTTTGCTTGGGTTGACCCAGGATGGGAAACTTAACACTAATGCT
                                                                                                                                                                                                                                                                                 Length: 155
Gaps: 4
Percent Identity: 26.452
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                                                                                                                                                                                                                                                                                                                                                                                                                     to: 177
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                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAY29169 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAB35755 standard; Protein; 1143
                                                                                                                                                                                                                                                                                 134.50
1.478
58.710
                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-957-709-70 x AAY29169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAACTATCAGGGG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 GlyGlnTrpGlnGly 165
                                                                                                                                                                                                 177 AA;
                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318
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    88888888888
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This invention relates to a full length provirus genomic DNA sequence AAC66281 of equine infectious anemia virus (EIAV) from the donkey tat. and 52 genes sequences AAC66314 - AAC66319 and their encoded proteins AAB35754 - AAB35759. The invention also relates to PCR primers AAC66282 - AAC66289 which are used to isolate the EIAV DNA sequences. Other primers represented in AAC66289 - AAC66313 are also used in the sequences identified in the invention. The genes and proteins can be used for preparing gene mutation and deletion vaccines, DNA vaccines and also because of in producing an equine infectious anemia virus gene transfer system for gene therapy. The proteins and polynucleotides may also be used in the study of HIV.
           Equine infectious anemia virus; EIAV; donkey leukocyte strain; vaccine; gene therapy; human immunodeficiency virus; pol; HIV.
                                                                                                                                                                                                                                                                                                                                                                                    Full-length DNA sequence of provirus genomes, sequences of various functional genes and protein of donkey leukocyte strain of equine infectious anemia virus, used for preparing vaccines and studying HIV
                                                                                                                                                                                                                                                                                      F)
                                                                                                                                                                                                                                                                                          xne
                                                                                                                                                                                                                                                                                        Feng Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 TTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAGGAAAAGTCGTTATT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProvalSerGluThrLysVallleProThrAspValLysIleGlnValPr 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......IleMetile 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AAAATCAGAAAAGAAATACTTATA......GAGCCATTTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 CCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 127
Gaps: 2
Percent Identity: 24.409
                                                                                                                                                                                                                                                                                  Yu K, Pan P, Jia B,
Zhao L;
                                                                                                                                                                                                                                    (NAAI-) NAT CENT AIDS PREVENTION & CONTROL. (HARB-) HARBIN VETERINARY RES INST CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 16-17; 26pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                             Equine infectious anemia virus.
                                                                                                                                                                   21-APR-2000; 2000WO-CN00096
                                                                                                                                                                                                    99CN-0105852
                                                                                                                                                                                                                                                                                    Shen R, Chen G,
Fan X, Lue X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119.50
1.637
57.480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAB35755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-957-709-70 x AAB35755
                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672738/65.
N-PSDB; AAC66315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                 WO200063387-A1.
                                                                                                                                                                                                  21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                    Shao Y, Xiang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pure native human deoxyuridine tri:phosphate nucleotido:hydrolase - used to identify inhibitors, potentially useful as antimicrobial and anticancer agents
CGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAG 256
                               257 GGGTTATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAACTTA 306
                                                                                                                                       307 ACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGG 356
                                                                                                                                                                                                                                                   818 GlnValIleCysThrAsnIleGlyLysSerAsnMetLysLeuArgGluGl 834
                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR70144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deoxyuridine-triphosphate-nucleotidohydrolase; dUTPase; antimicrobial; anticancer; cytostatic; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 132
Gaps: 4
Percent Identity: 29.545
                                                                                                                                                                                                                                                                                                                         357 AGAGAGATTTGTGCAGATCGCATTTATAAGG 387
                                                                                                                                                                                                                                                                                                                                                                               834 yGlnLysPheAlaGlnLeuIleIleLeuGln 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALLX ) ALLELIX BIOPHARMACEUTICALS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAR70144 standard; Protein; 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig.1; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94CA-2126001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0097220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Climie S, Vandenberg E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human dUTPase protomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-115928/16.
N-PSDB; AAQ83219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA2126001-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR70144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
207
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61 TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGGGCTTTTGT 110

to: AAR70144 from: 1 to: 141

Align seg 1/1

1.607 53.030

Percent Similarity:

alignment_block: US-08-957-709-70 x AAR70144

112.50

Quality:

Ratio:

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dUTPase; DUT-N; human; cell proliferation; inhibitor; cytostatic;
antiviral; antibacterial; antifungal; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding two isoform(s) of human dUTPase - used in assays for assessing status of cell proliferation, effect of anticancer agents and progress of treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-terminal peptide unique to DUT-N"
                                                                                                                     260
                                                                                                                                                                                                                                                                          103
TAAGGGGAAATTAATCGACGTGGAAAGGAAGGAAAGTCGTTATTCCTC 160
                                                         161 CAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGAC 210
                                                                                                                                                                                                                                            308 CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357
                                                                                                                                                                                                                                                                                                        GAGAGATTTGTGCAGATCGCATTTATAAGGCTA......GAGGGTCC 398
                                                                                                                                                                                                                                                                                                                                   104 AspArgIleAlaGlnLeuIleCysGluArgIlePheTyrProGlu.IleG 120
                                                                                                                                                                                ||| ||| ||| ||| ||| elleAspValGlyAsnValGlyAlaGlyValIleAspCluAspTyrArgGlyAsnValG 87
                          .....TyrThrileProp 37
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW30280
                                                                                                                                                                                                                                                                 211 GATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGT
                                                                                                                                      GlyCysTyrGlyArgValAlaProArgSerGlyLeuAlaAlaLysHisPh
                                                                                       roMetGluLysAlaValValLysThrAspIleGlnIleAlaLeuProSer
                                                                                                                                                                                                                                                                                                                                                                     442
                                                                                                                                                                                                                                                                                                                                                                                                120 luGluValGlnAlaLeuAspAspThrGluArgGlySerGlyGly 134
                                                                                                                                                                                                                                                                                                                                                                     GCCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "O-phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAW30280 standard; Protein; 164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lynch F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human dUTPase (nuclear form).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US04886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0824405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ladner RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNE-) UNIV NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-503040/46.
N-PSDB; AAT90987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caradonna SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9736916-A1
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29-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                        37
                                                                                                                                                                                                                                                                                                        358
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dUTPase; DUT-M; human; cell proliferation; inhibitor; cytostatic; antiviral; antibacterial; antifungal; antibiotic.

Homo sapiens

Key Peptide

 $\overset{\alpha}{\times}\overset{\times}{\times}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}{\cup}\overset{\circ}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

WO9736916-A1

39-0CT-1997

26-MAR-1997; 26-MAR-1997; 29-MAR-1996;

Human dUTPase (mitochondrial form).

14-APR-1998 (first entry)

4AW30281

common Glu

Location/Qualifiers 70..93 /note= "DUT-M unique sequence 5' to residue of DUT-M and DUT-N"

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This polypeptide comprises the nuclear form, designated DUT-N, of muman decaywridine triphosphate nuclectidohydrolase (durpase). Its amino acid sequence was deduced from a T-cell cDNA clone (see AAT90987). A single gene codes for 2 isoforms of human durpase, the nuclear form (DUT-N, see AAT90281) which is targeted to the mitochondria. The isoforms arise by the which is targeted to the mitochondria. The isoforms arise by the cuse of alternative 5 exons which then join in a common sequence. The DUT-N isoform is produced at low or undetectable levels during non-proliferative periods of the cell cycle, and can be used as a marker for cellular proliferation. It is phosphorylated by placed: at a Ser residue within the consensus sequence for cyclin-dependent can be used to determine its proliferative farts or cellular proliferation. It is phosphorylated by placed: at a Ser residue within the consensus sequence for cyclin-dependent can be used to determine its proliferative farts or cellular proliferations. It is phosphorylated by placed in a cell can be used to determine its proliferative fact of calmed). This method can be used for determining the effect of calmed). Agents that inhibit durpase are potential

(claimed). Agents that inhibit durpase are potential

can throadpastic, antiviral, antibacterial and antifungal agents.

The durpase can also be used to raise antibodies for assaying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 elleAspValGlyAlaGlyVallleAspGluAspTyrArgGlyAsnValG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCGCTCCAACCAGCTTATGACCTCAGAGTGGGCAGAGGCTTTTGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 TAAGGGGAAATTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 CAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGAC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 TATTGGTTCTTTGCCTTGGGTT...GACCCAGGATGGAAACTTAA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 .....TyrThrlleProP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW30281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 luGluValGlnAlaLeuAspAspThrGluArgGlySerGlyGly 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132
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Percent Identity: 29.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAW30280 from: 1 to: 164
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ID AAW30281 standard; Protein; 252 AA.
Claim 6; Fig 1A-B; 89pp; English
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1.607
53.030
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US-08-957-709-70 x AAW30280
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   Ratio:
   Percent Similarity:
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Nucleic acid encoding two isoform(s) of human durPase - used in assays for assessing status of cell proliferation, effect of anticancer agents and progress of treatment

Lynch F;

Caradonna SJ, Ladner RD,

WPI; 1997-503040/46. N-PSDB; AAT90989.

(UYNE-) UNIV NEW JERSEY

97US-0824405. 96US-0014748. 97WO-US04886.

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This polypeptide comprises the mitochrondrial form, designated DUT-W, of human decoyuridine triphosphate nucleotidohydrolase (dUTPase). Its amino acid sequence was deduced from a fibroblast (dUTPase). Its amino acid sequence was deduced from a fibroblast considers, the nuclear form (DUT-W), see AAW30280 and the cytoplasmic form (DUT-M) which is targeted to the mitochondria. The isoforms arise by the use of alternative 5' exons which then join in a common sequence. The DUT-W isoform is detectable in proliferating and non-proliferating cells, but is produced in tumours. Unlike DUT-W, it is not phosphorylated in vivo. Weasuring the amount of dUTPase in a cell can be used to determine its proliferative status (or changes in this status), particularly in nutrient-deprived or neoplastic cells (claimed). This method cells, or monitoring the effect of (A) (claimed). Agents that an election the diffect of anticancer agents (A) on cells, or monitoring the effect of (A) (claimed). Agents that antihothed be used for assaying the enzyme and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGT 110
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Percent Identity: 29,545
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Claim 6; Fig 2A-B; 89pp; English.
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1.607
53.030
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US-08-957-709-70 x AAW30281
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Ratio:
Percent Similarity:
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is a P. aeruginosa infection.

note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is not entirely correct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 GAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 laValSerAspIleAlaGlnLeuTyrLeuValLysCysSerThrSerAla 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 AGAAACCCTTACAGAGGAAACTAT......CAGGGGAGCAC 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuValAlaGlnCysAlaIleCysGluLysThrLeuPheAspGluPheSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CTACTICCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTC
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                                                                                                                                                                                                                           Length: 173
Gaps: 5
Percent Identity: 24.855
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ID AAP71667 standard; Protein; 1105
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1.217
53.179
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US-08-957-709-70 x AAY29165
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                                                                                                                                         181 AA;
                                                                                                                                                                                                                                  Quality:
Ratio:
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                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                           Sequence
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  888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of, virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a Pseudomonas aeruginosa polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a virulence factor encoded by ORF17793c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahajan-Miklos
  SerAlaArgAlaAlaGlyTyrAspLeuTyrSerAlaTyrAsp..... 143
                                             111 TAAGGGGAAATTAATCGACGTGGAAAAGGAAGGAAAAGTCGTTATTCCTC 160
                                                                                         ....TyrThrIleProP 148
                                                                                                                                       CAAGGGAATACGCCTTAATCCTAACCCTCGAGGGATAAAGTTGCCCGAC 210
                                                                                                                                                                                  roMetGluLysAlaValValLysThrAspIleGlnIleAlaLeuProSer 164
                                                                                                                                                                                                                                                          elleAspValGlyAlaGlyValIleAspGluAspTyrArgGlyAsnValG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                               358 GAGAGATTTGTGCAGATCGCATTTATAAGGCTA......GAGGGTCC 398
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| AspArgIleAlaGlnLeuIleCysGluArgIlePheTyrProGlu.IleG 231
                                                                                                                                                                                                                                                                                                                         308 CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY29165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                                                                                                                                                  GATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 luGluValGlnAlaLeuAspAspThrGluArgGlySerGlyGly 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAY29165 standard; Protein; 181
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Tsongalis
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Rahme LG,
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VISNA; vaccine; reverse transcriptase; Ovis aries; lentivirus; meningoencephalitis of sheep.
                                                                                                                                                                                                                                                                                                                                                                                                                              New envelope protein of Visna virus, its fragments - and DNA coding sequences, useful in diagnosis and for making vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   719 leProAlaGlyGlnValLySArgIleAlaIleAspLeuLysIleAsnLeu 735
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769 leglnValValIlleTyrAsnSerAsnAsnLysGluValValIleProGln 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 GGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAG 404
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786 GlyArgLysPheAlaGlnLeuIleLeuMetProLeuIleHisGluGluLe 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 TAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 AAACCCTTAC.....AGAGGAAACTATCAGGGGAGCACAAGGT 442
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Percent Identity: 26.316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 1-6; 27pp; French
                                                                                                                                                                                            85FR-0512543.
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Quality: 112.00
Quality: 1.534
Percent Similarity: 54.887
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US-08-957-709-70 x AAP71667
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N-PSDB; AAN70608.
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                                                            visna lentivirus.
                                                                                                                                                                                         20-AUG-1985;
                                                                                                                                                                                                                                    20-AUG-1985;
                                                                                                       FR2586427-A.
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233 TAAGGAGCAGTTTAGCAAGAGAAGGGGTT...ATTGGTTCTTTTGCTTGG 279
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US-08-957-709-70 x Q9KFV3
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                                           sp_organelle:Q9G4C0
sp_virus:Q66933
sp_virus:P90246
                                                                                                                                                                             sp_bacteria:09A253
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             sp_virus:09JFF1
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Q9KFV3;
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170 10994/13 agrotis segetum granulos 1138 1094/13 agrotis segetum granulos 1146 1089468 equine infectious anemil 146 1089478 equine infectious anemil 148 109ep46 equine infectious anemil 148 109ep46 equine infectious anemil 199 10921/6 equine infectious anemil 199 10921/6 equine infectious anemil 199 10921/6 equine infectious anemil 198 10992/6 equine infectious anemil 198 10992/6 equine infectious anemil 198 10992/8 equine infectious anemil 198 10992/8 equine infectious anemil 198 10992/8 equine infectious anemil 198 10992/8 equine infectious anemil 197 10968/8 equine infectious anemil 197 1092/8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09jj44 mus musculus (mouse). 60
09cq43 mus musculus (mouse). 50
09cu90 mus musculus (mouse), 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P87630. cowpox virus (cpv). 41kt
091545 fowlpox virus. orf fpv03
091880 spodoptera exigua nuclec
096889 myxoma virus (strain lau
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072165 orf virus. dutpase homo.
Q9wmy7 dioscorea alata bacilli
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                                                                                                                                                                                                                                                                                                                        About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
             out_format : pfs
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Query length: 471
Database: SPREMBL_17:*
Database sequences: 473505
Database length: 146272329
Search time (sec): 66.180000
                                                                                      Date: Jan 31, 2002 1:05 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
                                                                                                                                                                                                                                                                                                   Command line parameters:
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sp_archea:09YG32
sp_bacteria:09JRE8
sp_archea:027642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_bacteria:09KFV3
sp_virus:071028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_bacteria:P74073
sp_virus:Q9E6G1
sp_archea:029157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_bacteria:09CB17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_bacteria:09PN07
sp_archea:09HSG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_bacteria:09HYC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_archea:09HMF3
sp_bacteria:09A1K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:09JJ44
sp_rodent:09C043
sp_rodent:09CU90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea: Q58502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:0992K2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:Q9DKV8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_virus:09WMY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_virus:084809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_plant:09STG6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_virus:072165
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Ogjffl vaccinia virus (strai
Ogg4c0 thraustochytrium aure
(OG6933 feline immunodeficie
P90246 feline immunodeficie
                                                                                      ! Q9a253 caulobacter crescentu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001508: BAB04087.1; -
InterPro; IPR001232; dCTP-deaminse.

InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .13 AGGGGAAATTAATCGACGTGGAAAAG......138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 LysGluLeuGluIleThrProLeuThrGluGlnIleGlnProAlaSe 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :::|||::: |||:::
47 ysGlualaValIleSerPheGluArgProIleArgTyrArgGluTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 ThrSerAspGluThrIleValLeuProProHisThrPheLeuLeuAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 AAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....GAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 177 Aa; 19897 MW; D15AE75387847E2B CRC64;
                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 156
Gaps: 6
Percent Identity: 37.179
  147
321
1123
1150
                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                 177 AA
                      13.10.
14.84
14.85
15.74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q9KFV3 from: 1 to: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 TTATGACCTCAGAGTGGGCAGAGGCCTTTTGTT
                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-UTN-2001 (TrEMBLrel. 17, Last ann
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed=11058132;
140.97
132.43
121.70
121.51
89.50
88.00
87.50
87.50
                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242.50
2.310
67.308
                                                                                                                               seq_name: sp_bacteria:Q9KFV3
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186 CCTCGAGAGAGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAA 235

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REGUENCE FROM N.A.

SEQUENCE FROM N.A.

REDLINE-98165772; PubMed-9497317;

Replication of the duTpeselmann C.,

A. Holz I., zillig W.;

"Blochemical and phylogenetic characterization of the duTpese from the rarchean Virus STRV.";

"Blochemical and phylogenetic characterization of the duTpese from the rarchean Virus STRV.";

"Blochemical and phylogenetic characterization of the duTpese from the rarchean Virus STRV.";

"Blochemical STRV.";

"I blochemical PROJ221; AAC1893."

"InterPro: IPRO01428; dUTpese."

"InterPro: IPRO01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
PYROPHOSPHATASE) (DEOXYURIDINE-
330 AAATGAACCTGTCGAATTAAGATATGGAGAGAGTTTGTGCAGATCGCAT 379
                                                                                                                                                                                                                                         380 TTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAACTAT... 426
                                                                                                                                                                                                                                                                               86 TCAGAGTGGGCAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 AAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGCTACTTCCAGACTGGAAAATCAGA.....AAAGAAAT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 ACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ValGlyAspGluPheileIleTyrProAsnGluHisValLeuLeuThrTh 67
                                                                                                                                                         nargleuProlleGluLeuProlleGlyArgArgleCysGlnLeuValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:

Quality: 237.00 Length: 157
Ratio: 2.155 Gaps: 2
Percent Similarity: 70.064 Percent Identity: 34.395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: 071028 from: 1 to: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaeal virus SIRV.
Viruses; unclassified viruses.
NCBI_TaxID=66287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-AUN-2001 (TrEMBLrel. 17, DUTPAGE (EC 3.6.1.23) (DUTP TRIPHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                               .....CAGGGGAGCACA 438
                                                                                                                                                                                                                                                                                                                                                                                              :::|||:::|||
163 PheGlnLysGlyAlaThr 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-957-709-70 x 071028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: sp_virus:071028
                                                                                                                                                                                                                                                                                                                                                            427
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STRAIN-TN;
STRAIN-TN;
STRAIN-TN;
STRAIN-TN;
STRAIN-TN;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Cole S.T., Eiglmeier K., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Whorall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murph L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simnon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                         236 GGAGCAGTTTAGCAAGAGAGAGTTATTGGTTCTTTTGCTTGGGTTGAC 285
                                                                                                 286 CCAGGATGGGATGGAAACTTAACACTAAATGCTCTACAATGCCTCAAATGA 335
                                                                                                                                                                                                                                                                                       336 ACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCATTTATAA 385
                                                                                                                                                                                                                                                                                                                        1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTT......39
67 rLysGluTyrIleLysLeuSerAsnAspIleIleAlaPheCysAsnLeuA
                                                                                                                                                                                                                                                                                                                                                                                                  386 GGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Massive gone decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).

Matter 409:1007-1011(2001).

InterPro; IPR001213; dCTP_deaminse.

InterPro; IPR001428; dUTPase.

Promom; PD004900; dUTPase; 1.

Promom; PD004900; dCTP_deaminse; 1.

SEQUENCE 190 AA; 20820 MW; ICA936700500B6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CB17;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 ACAAGGTTAGCGTTTTCAAAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 LysGlyValThrLeuAlaLys 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: sp_bacteria:09CB17
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US-08-957-709-70 x Q9CB17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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20699 MW; 68DC660FB28FD33C CRC64;

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186 AA;
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                                               alignment_scores
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HSG3;
 ÖS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:665-668(2000).
EMBL, AL199078, CABR73119.1;.
InterPro; IPR003232; dCTP_deaminse.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-0IN-2001 (TrEMBLrel. 17, Last annotation update)
POSSIBLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
                                                                                                                                                                                                                                                                                                                      235 AGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GGTTCTTTTGCTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 CAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTCGAGAGGATAAAGTTGCCCCGACGATGTTATGGGGGGATATGAAGATA 234
                                                                                                                                                                                                                                                                                                                                                                                   279 GGTTGACCCAGGATGGATGGAACTTAACACTAATGCTCTACAATGCCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 TTTATAAGGCTAGAGGTCCGGCAAGAACCCTTAC......414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 ......GGCAGAGAGCTTTTGTTAAGGGGAAATTAATCGACGTGGA 134
                                                                                                                                                                                                                                       135 AAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
                                              ....ATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                           86 TCAGAGTG.....93
 eSerIleaspProPheAspAspThrLeuValGlnProSerSerIleAspV 34
                                                                                                                                            34 alArgLeuAspCysMetPheArgValPheAsnAsnThrArgTyrThrHis 50
                                                                                                                                                                                            ||||::::::|||
67 lAspGlyGluProPheValLeuHisProGlyGlyGlyPheValLeuGlySerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 .AGAGGAAACTATCAGGGG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID Q9PN07 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_bacteria:Q9PN07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campylobacter.
NCBI_TaxID=197;
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416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 LeuPheLeuGlnGlyAspGluLysCysAspThrThrTyrLysAspLysLy 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 ......GCTTTTGTTAAGGGGAAATTAATCGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 CGTGGAAAAGGAAAGGAAAGTC...GTTATTCCTCCAAGGGAATACGCCT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 TAATCCTAACCCTCGAGGGATAAAGTTGCCCGACGATGTTATGGGGGAT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 hrThrProLeuProAlaLysIleTyrAlaAsnGluGlyIleAlaGlnVal 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                          ...CTCCAACCAG 73
                                                                                                                                                                                                                                                                                                                                   22 eCysGluAlaAsnIleGlyLysGlyValValSerTyrGlyLeuSerSerT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                            72 pPhe......GluGlyAspValCysIleValProAlaAsnSerPheAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 CysLeuGlyLysSerThrTyrAlaArgCysGlyIleIleValAsnValTh
                                                                                                                                                                                                     13 GACTGGAAAATCAGAAAAGAAATACTT.....ATAGAGCCATT
                                                                                                                                                                                                                                                                                                                                                                                 56 AsnSerThrValValAspProLysAsnPheValGluGluAsnValValAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 ATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGGTTATTGGTTCTTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 CCTCAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 GCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTAC.....AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXXCYTIDINE TRIPHOSPHATE DEAMINASE.
DTD OR VNG0245G.
                                                Percent Identity: 29.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 AGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAG
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Length:
                             Gaps:
                                                                                                                                                         to: 186
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                                                                                                                                                           Align seg 1/1 to: Q9PN07 from: 1
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ID Q9HSG3 PRELIMINARY;
                      1.788
58.889
    189.50
                                                                                                                                                                                                                                                                                          51 TTCTGAAGAATCG.....
                                                                                           alignment_block:
US-08-957-709-70 x Q9PN07
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    Quality:
                                           Percent Similarity:
                           Ratio:
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seq_name: sp_bacteria:Q9HYC9

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MEDLINE-20504483; PubMed-11016950;

My W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Welr D., Hall J., Danson M.J., Hough D.W.,

Leithbauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Rebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

Proc. Natl. Acad. Sci. US.S. 97:12176-12181(2000).

R EMBL, Ac004988; AAG18843.1; ---

R InterPro: IPR001428; dUTPase.

Pfam: PF00692; dUTPase.

R Pfam: PF00692; dUTPase.

R Pfam: PF00690; dCTP-deaminse; 1.

R ProDom; PD004900; dCTP-deaminse; 1.

R SEQUENCE 195 AA; 21542 MW; 86CCDAA4D48BCOC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 GATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATT......GG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 ATGACCTCAGAGTGGGCAGAGGG.....GCTTTTGTTAAGGGGAAATTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......GTGGAAAAGGAAAGTCGTTATTCCTCCAAGGGAATACG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 CCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 ITCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ......129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 euSerAsnLeuGlyLysValProValAlaLeuThrProGluMetArgile 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 GTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::|||
51 ProCyslleHisProAsnArgGluAspGluValAspGluTyrValThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 uThrValValGluAspGlyAspGluPheIleLeuHisProGlyAspPheV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 ACTTATAGAGCCATTTTCTGAAGAATCGCTC.....CAACCAGCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 184.50 Length: 173
Ratio: 1.724 Gaps: 7
Percent Similarity: 61.850 Percent Identity: 31.214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9HSG3 from: 1 to: 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 AGGAAACTATCAGGGGAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-957-709-70 x Q9HSG3
                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-RADOI:

MEDLINB-20437337; PubbMed=10984043;

Stover C.K., Pham X.-G.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Radore C.K., Pham X.-G.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Radore R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

Radore R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

Radore R.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer Genome Sequence of Pseudomonas aeruginosa PAOI, an

Opportunistic pathogen.";

Ruture 406:959-964(200).

Ruture 406:959-964(200).

Ruture 406:959-964(200).

Ruture 406:959-964(200).

Reizer D. PRO041283 dUTPase.

Reizer D. PRO041283 dUTPase.

Reizer D. Reizer B. Agologic GTP_deaminse.

Reizer Probom: PubO4900 dCTP_deaminse; 1.

Reizer Probom: Po004900 dCTP_deaminse; 1.

Reizer Probom: Po004000 dCTP_deaminse; 1.
                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 TGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 GAAGGGGTTATTGGTTCTTTGGGTTGACCCAGGATGGAAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 laGluPheLysValPheThrAsnIleHisSerAlaValValAspProLys 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ......GGTTATGACCTCAGAGTGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AsnPheAspGluLysSerPheValAspIleAsnSerAsp...ValCysIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 TATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 CTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCA.......
                                           09HYC9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 171
Gaps: 4
Percent Identity: 26.316
                             188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9HYC9 from: 1 to: 188
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 GAGAG.....
seq_documentation_block:
Th O9HYC9 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 172.00
Ratio: 1.737
Percent Similarity: 57.895
                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-957-709-70 x Q9HYC9
                                                                                                                                                                                                                      NCBI_TaxID=287;
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Percent Identity: 30.496
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                                                                                                                                                                                                                                                         76 GGTTATGACCTCAGAGTGGGCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 ..GGAAACTATCAGGGGAGCACA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 snGlyLysTyrGlnGlyGlnThr 184
                                                                                                                                                                                           from: 1
                                    61.702
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ID 09YG32 PRELIMINARY;
      Ratio: 1.891
                                                                                                                                                                                           Align seg 1/1 to: Q9PFB6
                                                                                               alignment_block:
US-08-957-709-70 x Q9PFB6
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NCBI_TaxID=56636;
                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APE0069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA BLOING-LOUSD', Fubmace LOUSD', Arruda P., Abreu F.A., Acencio M., RA Blangson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Baptista C.S., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Buenco M.R.P., Camarogo A.A., Camarogo L.E.A., Carraro D.M., Carrer H., RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., RA Coutinho L.L., Cristofeni M., Dias-Neto E., Docena C., El-Dorry H., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Franca E.C., Laugret F., Lambais M.R., Leite L.C.C., RA Garnier M., Goldman G.H., Madeira M.L., Kemper E.L., Kitajima J.P., RA Camos B.G.M., Lamos B.E., Laigret F., Lambais M.R., Leite L.C.C., Anderica D.M., Martins E.M.F., Martino C.L., Mardeira A.M.B.N., Madeira H.M.F., Marino C.L., Mardeira A.M.B.N., Madeira H.M.F., Marino C.L., Mardeira B.M.F., Martino C.L., Mardeira M.A., Nascimento A.L.T.O., Netto L.E.S., Manna A.J. T., Nobrega F.G., Nunes L.R., Oliveira M.A., Reiderto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., A Salveira J.F., Silvestri M.L.Z., Siqueira W.J., Tsuhako M.H., Rago M.A., Terenzi M.F., Truffi D., Tsai S.N., Tsuhako M.H., Rago M.A., Zatz M., Meidanis J., Setubal J.C.; Savettore A.L., Rago M.A., Zatz M., Meidanis J., Setubal J.C.; Nature R. Radiosa M.A., The Genome sequence of the plant pathogen Xylella fastidiosa."; Rr Waller Rubi. Red03317: AAF83721.: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                  117 CysGlyIleIleValAsnValThrProLeuGluProGluTrpGluGlyHi 133
                                                                                                  353 ATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCA 402
                                                                                                                                                                                                                                                                                                                       403 AGAAACCCTTACAGA......GGAAACTATCAGGGGAGCACAAGGTT 443
                                                              303 CTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AA; 21531 MW; D7B23653F94B3649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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InterPro; IPR003232; dCTP_deaminse.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block: Q9PFB6 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_bacteria:Q9PFB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 164.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 AGCGTTTTCAAAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 lThrLeuProLys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-9A5C
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11D
DT-1DD
**09PFB6**;

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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Naqai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aeropyrum pernix.
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
163AA LONG HYPOTHETICAL DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
                                                                                                                                                                                                                                                                                                                     103 ......GCTTTTGTTAAGGGGAAATTAATCGACG 130
                                                                                                                                                                                                           131 TGGAAAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATC 180
                                                                                                                                                                                                                                                                                           181 CTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAA 230
                                                                                                                                                                                                                                                                                                                                                                                                     281 TTGACCCAGGATGGGATGGAACTTAACACTAATGCTCTACAATGCCTCA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 AATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCGAGATCGCATT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 TATAAGGCTA.....GAGGGTCCGGCAAGAAACCCTTACAGA.....417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 eLeuGlnAlaAspProAspAspValCysGlnThrSerTyrArgAspArgA 177
                                                                                                                                                                  61 nSerThrIleValAspProLysGlnPheAspAsnGlySerPheileAspV 78
                                                                                                                                                                                                                                                  78 alGluSerAsp...ValCysIleIleProProAsnSerPheAlaLeuAla 93
                                                                   231 GATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 AA.
to: 191
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DNA Res. 6:83-101(1999).
EMBL; AP000058; BAA78978.1; -
InterPro; IPR003232; dCTP_deaminse.
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Olocar-2000 (TrEMBLrel. 15, Created)
Olocar-2000 (TrEMBLrel. 15, Last sequence update)
Olocar-2000 (TrEMBLrel. 15, Last sequence update)
Olocar-2011 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN NMA1060 (DECOXYCYTIDINE TRIPHOSPHATE DEAMINASE, NMA1060 OR NMB0849.
Neisseria meningitidis (serogroup A), and
Meisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseri
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SEQUENCE FROM N.A.
SEROTYPE 4A;
MEDLINE=20222556; PubMed-10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TyrThrGlyArgGlyGlnAlaMetLeuLeuValAlaAsnProHisGlyLe 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 AAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 GATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGGATAAGGAGCAGTT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 TAGCAAGAGAAGGG...GTTATTGGTTCTTTTGCTTGGGTTGACCCAGGA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ValCysGluLeuGluProGlyAlaTyrArgLeuArgPheAsn...GluVa 81
                                                                                                                                                                                                                                                                                                                                 | ||||||:::
33 uSerValGlyGluIleGluSerLeuAlaAspAlaGlyPheLeuGlyGluG
                                                                                                                                                                                                                                                                                                              37 CTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 lValSerIleProProGlyHisValGlyPheCysPheProArgSerSerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 TGGGATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 CGAATTAAGATATGGAGAGAGTTTGTGCAGATCGCATTTATAAGGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 luAspLysIleMetProLysGlyAspArgIleGlnCysGlu...TyrGly
InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
Complete Proteome.
SEQUENCE 163 AA; 17384 MW; 4AA22FB0D8802F49 CRC64;
                                                                                                                           392 AGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 188 AA.
                                                                                                                                                                                                                                                                          Align seg 1/1 to: Q9YG32 from: 1 to: 163
                                                                                                                                                                                                                                                                                                                                                                                  87 CAGAGTGGGCAGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:

D 090REB PRELIMINARY;

AC 09JREB;
DT 01-OCT-2000 (TrEMBLrel. 15, DT 01-JUN-2001 (TrEMBLrel. 15, DT 01-JUN-2001 (TrEMBLrel. 15, DT 01-JUN-2001 (TrEMBLrel. 17, DE PYTATIVE)

B PROTHETICAL PROTEIN NMA106

C NMA1060 OR NME0849.

C NMA1060 OR NME0849.

C NMA1060 OR NME0849.

NMA1060 OR NMEDIALIS (Ser OC Bacteria; Protecobacteria; Secr OC Bacteria; Protecobacteria; DO N NMELTAXID=65699, 491;

RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

PREATMIN-22491 / SEROGROUP A

RX MEDLINE-2052556; PRUM-304

RA PARKHILL J., Achtman M., Ja
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                                                                                                                                                                                                                     alignment_block:
US-08-957-709-70 x Q9YG32
    SKW
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

THEATINH MCS8 / SENGGROUP B;

MEDLINE=20175755; PubMed=10710307;

Tettellin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Clecko A., Parksey D.S., Blair E., Cittcone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                         S.
          Chillingworth T.,
I., Hamlin N., Holroyd
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T. Davies R.M., Davis P. Devlin K., Feltwell T., Hamlin N., HG Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Nelsseria menigitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 GAGAG......GCTTTTGTTAAGGGGAAATTAATCGACGTGGAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 .....AAGGAAAAGTCGTTAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001232; dCTP_deaminse.
InterPro: IPR00128; dUTPase.
InterPro: IPR001428; dUTPase.
Probom: PD004900; dCTP_deaminse: 1.
Hypothetical protein; Complete proteome
Hypothetical Protein; Zomplete proteome
188 AA; 21295 MW; 2CA4459F4678FDF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 CTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 MetileAspProPheGluProAsnGlnIleLysGluAlaAspGlyLysAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 ......GGTTATGACCTCAGAGTGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 gilelleSerTyrGlyThrSerSerTyrGlyTyrAspileArgCysAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AsnPheAspProLysAsnPheValThrValGluAspAspCysCysIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 TCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 AACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 170
Gaps: 4
Percent Identity: 24.118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL162755; CAB84324.1; -. EMBL; AE002438; AAF41260.1; -. TIGR; NMB0849; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:1809-1815(2000).
                                                                                                                                                                                                                    Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 155.00
Ratio: 1.566
Percent Similarity: 58.235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q9JRE8
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US-08-957-709-70 x Q9JRE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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145 AAAGTCGTTATTCCTCCAAGGGAATAC............
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P74073;
                                          47
                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
GAGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGA 405
                                                                                                               151 lyGluGlyValAlaGlnValLeuPhePheGluSerAspGluIleCysGlu 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 alTyrArgGlnMetGlyProGlySerLeulleAspAspGluLysAsn... 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
EMBL; AE000920; AAB86078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 pPheGluGluLeuValGlnProAlaGlyIleAspLeuArgValAspLysV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 TTCTGAAGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGA.
                                                                                                AACCCTTACAGA......GGAAACTATCAGGGGAGCACAAGGTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 AA; 16996 MW; AFA09D55FB371648 CRC64;
                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYCYTIDINE-TRIPHOSPHATE DEAMINASE RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 158
Gaps: 6
Percent Identity: 32.278
                                                                                                                                                                                                                                                    150 AA
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                                                                                                                                                                                                                                                                                                                                                   Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                               Created)
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ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003232; dCTP_deaminse.
Interpro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                 Quality: 153.00
Ratio: 1.719
Harity: 56.329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-957-709-70 x O27642
                                                                                                                                                                                                           seq_name: sp_archea:027642
                                                                                                                                                     447 GTTTTCAAAG 456
                                                                                                                                                                            184 rLeuProLys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=145262
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                               406
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MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                               305
                                                                                                                                                                                                                                                                                     202
                                                                                                                                                           206 CCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAA 255
                                                                                                                                                                                                                                                                                                                                                                 306 AACACTAAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATG 355
                                                                                                                                                                                                                                                                                                                                                                                               356 GAGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGA 405
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......LeuProProLeuGluMetLeuGluProProlleTyrArgLe
                                                                                 60 uGluProGlyLysAlaTyrLeuAlaSerValAspArgMetIleGluIleP
                                                                                                                                                                                                         77 roGluGlyTyrAlaMetLeuTyrLeuProArgSerThrLeuLeuArgSer
                                                                                                                                                                                                                                                               256 GGGGTTATTGGTTTTGCTTGGGTTGACCCAGGATGGGATGGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003232; dCTP_deaminse.
ProbOm; PD004900; dCTP_deaminse; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 193 AA; 21378 MW; BABDF70AD4348330 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 26.087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                   .........GCCTTAATCCTAACCTCGAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last seq
01-UJN-2001 (TrEMBLrel. 17, Last ann
HYPOTHETICAL 21.4 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AACCCTTACAGAGGAAACTATCAG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 .....TyrSerGlySerTyrGln 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: P74073 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   =
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D90912; BAA18149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID P74073 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.426
51.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_bacteria:P74073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-957-709-70 x P74073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
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us-08-957-709-70.rspt

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"Equine infectious anaemia virus proteins with epitopes most frequently recognized by cytotoxic T lymphocytes from infected borses."; J. Gen. Virol. 81:2735-2739(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. McGuire T.C., Leib S.R., Lonning S.M., Zhang W., Byrne K.M., Mealley R.H., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McGuire T.C., Leib S.R., Lonning S.M., Zhang W., Byrne K.M.,
                                                                                                                                                                                                                                                                                                                                                   84 lySerTyrPhelleLeuProAlaHisSerTyrGlyLeuGlyValAlaVal 100
                                                                                                                                                                                                                                                                                                                                                                                                  190 GAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAG 239
                                                                                                                                                                                                                                                                                                                                                                                                                       240 CAGTTTAGCAAGAGAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||||||
165 eGluGlyGluAspCysAspIleSerTyrGluThrArgArgGlyLysTyrG 182
                                                                                                                                                                                                                                                      ......GAAAAGG 139
                                                                                                                                                                                                                                                                                                                            140 AAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 GATGGGATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 GTCGAATTAAGATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 AGAGGGTCCG......GCAAGAAACCCTTACAGAGAAACTATC 427
                                                                                                       .......GGTTATGACCTCAGAGTGGCCAGAGG 102
                                                                                                                                                                                                                67
                                                        67 nPheAsnProHisAsnLeuGluAlaThrGlnLeuHisArgAspAspSerG 84
                                                                                                                          ||| ::::::|||
51 AspPheArgIlePheArgHisIleProGlyThrValValAspProLysAs
                               AGAGCCATTTTCTGAAGAATCGCTC......CAACCAGCA.
                                                                                                                                                                             .03 GCTTTT.....GTTAAGGGGAAATTAATCGACGTG.....
MetIleLysAsnAspIleTrpIleArgAlaGlnAlaAlaGlnGlyMetIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9EGG1 PRELIMINARY; PRT; 1146 AA.
09EGG1.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POL PROTEIN (FRACMENT).
VITUSES: Retroid anemia virus.
VITUSES: Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: sp_virus:09E6G1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 AG 429
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THANSCALLARIY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

EMBL: AF247394; AGG0202.1: -

EMBL: AF247394; AGG0202.1: -

EMBL: AF247394; ASP_Protease.

InterPro: IPR001969; ASP_Protease.

InterPro: IPR001969; ASP_Protease.

R InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May Bell

InterPro: IPR001969; May ASP_PR0TREASE; INTERPRO: IPR001969; May ASP_PR0TREASE; INTERPRO: INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: INTERPRO: INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; May ASP_PR0TREASE; INTERPRO: IPR01969; INTERPRO: IPR01969; INTERPRO: IPR01969; INTERPRO: IPR01969; INTERPRO: IPR01969; INTERPRO: IP
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736 LysIleLysGluGluIleMetLeuAlaTyrGlnGlyThrGlnIleLysGl 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 TTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAGGAAAGGTCGTTATT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 CCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGGATAAAGTTGCC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 CGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAAG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 GGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAGCTTA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      804 lyLeuLeulleAsnGlyGlyIleIleAspGluGlyTyrThrGlyGluIle 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 ACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 AAAATCAGAAAAGAAATACTTATA......GAGCCATTTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               821 GlnValIleCysThrAsnIleGlyLysSerAsnIleLysLeuIleGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality: 126.50 Length: 139
Ratio: 1.524 Gaps: 2
Percent Similarity: 59.712 Percent Identity: 23.022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q9E6G1 from: 1 to: 1146
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854 lnProTrpAspGluAsn 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-957-709-70 x Q9E6G1
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128 lHisAsnAspTyrGlylleTrpLeuSerArgAsnAlaArglleIleGlnL 145
                                                                                                                                                       374 TCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTACAGAGGAAAC 423
                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 CTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTA.
                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 170
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEOUENCE 170 AA; 18473 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00692; dUTPase; 1.
ProDom; PD000946; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF130846; AAD34382.1;
HSSP; P06968; 1EUW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125.50
1.459
60.563
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WHF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-957-709-70 x Q9WHF3
                                                                                                                                                                                                                                                                                                                                     seq_name: sp_virus:09WHF3
                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               424 TATCAGGGG 432
                                                                                                                                                                                                                                                                                         161 TyrLysGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-XJASGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                              Q9WHF3;
                                                                                                                                                                                                                                                                                                                                                                                                         O9WHF3
                       112
                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-VC-16, / DSM 4304 / ATCC 49558;

STRAIN-VC-16, / DSM 4304 / ATCC 49558;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klethum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K. Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of the hyperthermophilic, sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ATCGACGTGGAAAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 ATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: ||||||:::||| ||| |||:::
95 lealaargProArgSerThrLeuIleArgCysGlyAlaAsnValLeuThr 111
                                                                                                                                                       Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GGCAGAGAGGCTTTTGTTAAGGGGAAA......TTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 CTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 GCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAAATGCTCTACAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||||| | |||:::|||
eGlnProAsnGlyPheAspCysThrLeuArgSerValTyrArgLeuArgG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 lyCysGlyArgValAspPheAspAsnSerArgArgGluLeuProGluLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GluGluValGluPheArgAspTrpValTyrLeuProLysGlyValTyrAr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 gAlaLysLeuAsn...GluValValArgLeuGlyAsnAspIleMetAlaI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pram; Pr00692; durpase; 1.
ProDom; PD004900; dCrP_deaminse; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 168 AA; 19227 MW; D99EE0FB943869D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:::|||||| ||||||:::
| 13 ||leGlnLysGluGlyLeuIleArgAspTyrValAspLeuGluThrGlnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 ATCAGAAAAGAAATACTTATAGAGCCATTT.....TCTGAAGAATCGCT
                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 153
Gaps: 5
Percent Identity: 29.412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE001027; AAB90130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: 029157 from: 1 to: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 CCAACCAGCTTATGACCTCAGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.448 56.863
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                                                                                                                                Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-957-709-70 x 029157
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                   NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                         Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
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granulovirus).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus
                                                                                                                                                                                                                                                                                                                                                                                                    Xiulian A., Ning W., Wel Z., Yuhu S.; "The sequence analysis of two BamHI fragments of Agrotis segetum granulovirus DNA."; bothe EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 .ATCGACGTGGAAAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 TTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTCT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 saladlyvalileAspProAspTyrArgGlyHisLeuGlnValLeuLeuP 104
O1-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 18.5 KDA PROTEIN.
Agrotis segetum granulosis virus (AsGV) (Agrotis segetum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||::: |||
54 laLeuValProThrGlyLeuSerIleGluIleProAsnAspCysTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 GATATGAAGATAAGGAGCAGTTTAGCA...AGAGAAGGGGTTATTGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuArgLysAspAlaHisAlaProValArgGlySerValGlyAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       812982A6E508EC0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 27.465
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIATE—98105784; PubMed-9445039;
Petropoulos C.J.;
"Development and characterization of an in vivo pathogenic molecular clone of equine infectious anemia virus.";
(In) Coffin J.M. (eds.);
Retroviruses, pp 757-757, Cold Spring Harbor Laboratory Press,
New York (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIATE-98105784; PubMed-9445039; MEDIATE-98105784; PubMed-9445039; Cook R.F., Leroux C., Cook S.J., Berger S.L., Lichtenstein D.L., Ghabrial N.N., Montelaro R.C., Issel C.J.; "Deveatopment and characterization of an in vivo pathogenic molecular clone of equine infectious anemia virus."; J. Virol. 72:1383-1393(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COOK R.F., Leroux C., Cook S.J., Berger S.L., Lichtenstein D.L.,
COOK R.F., Leroux C., Cook S.J., Berger S.L., Lichtenstein D.L.,
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
-!- PTH: SPECIFIC ENZYMATIC CLEAVAGES IN VIOY YIELD MATURE PROTEI
(BY SIMILARITY).
-!- SIMILARITY:
-!- SIMILARITY: TO REPROVIRAL INFEGRASE, C-TERMINUS.
-!- SIMILARITY: THE PROFESS BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
EMBL; AF016316; AAC03761.1; --
HSSP; P32542; IEQI.
ACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGAGTTTGTG 369
                 121 GlnLeuValCysGluLysIleArgPheProGluAlaValGluLysProLy 137
                                                                                                                                                    .....GCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chappey C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POL POLYPROTEIN.
GAG-POL OR POL.
Viruses: Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroiding viruses.
                                                                                                                                                                                                                                                                                                             PRT; 1138 AA
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Interpro: IPR001969; Asp_prot_retrov.
Interpro: IPR001428; dUTPase
Interpro: IPR001037; Integrase_C.
Interpro: IPR003108; Integrase_C.
Interpro: IPR003165; RuseH.
                                                               370 CAGATCGCATTTATAAGGCTAGAGGGTCCG.
                                                                                                                                                                                                                  443 TAGCGTTTTCAAAGAGAAAGAAACTC 468
                                                                                                                                                                                                                                                                                            documentation_block:
Q9W7U6 PRELIMINARY;
                                                                                                                                                                                                                                                               seq_name: sp_virus:Q9W7U6
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Pfam; PF00552; integrase; 1.
Pfam; PF00552; integrase; 1.
Pfam; PF00055; integrase; 1.
Pfam; PF00075; rose; 1.
Pfam; PF00075; rve; 1.
Pfam; PF00077; rve; 1.
Pfam; PF00078; rvt; 1.
Pfam; PF00171; rv; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS00175; ASP_PROTEASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 GGGTTATTGGTTCTTTTGCTTTGGGTTGACCCCAGGATGGGATGGAAACTTA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 AGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   763 ProvalSerAspThrLysTleIleProThrAspValLysIleGlnValPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::: ::|||| ::: | OProAsnSerPheGlyTrpValThrGlyLysSerSerMetAlaLysGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             796 lyLeuLeulleAsnGlyGlyIleIleAspGluGlyfyrThrGlyGlulle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AAAATCAGAAAAGAAATACTTATA......gAGCCATTTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 AGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 TIGITAAGGGGAAATTAATCGACGTGGAAAAGGAAGGAAAAGTCGTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 CCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 ACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            813 GlnValIleCysThrAsnIleGlyLysSerAsnIleLysLeuIleGluGl
                                                                                                                                                                                                                                                                                                                                                           Ouality: 125.50 Length: 139
Ratio: 1.512 Gaps: 2
Percent Similarity: 59.712 Percent Identity: 23.022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
InterPro; IPR000477; RVTse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 ACCCTTACAGAGGAAAC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::|||:::
846 lnProTrpAspGluAsn 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q9W7U6
                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-957-709-70 x Q9W7U6
                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
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101 AGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAAGGAAAGTC 150
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0.0985
0.1269
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0.1376
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166.07
164.77
148.03
164.78
163.58
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InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
ProDon; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98344137; PubMed=9679194;
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92.00
92.00
92.00
91.50
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US-08-957-709-70 x DCD_PYRHO
                                                                                                                                                                                                                                                                  STANDARD;
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5.020
98.077
                                                                                                                                                                                                                                         seq_documentation_block:
                              SwissProt_39:DUT_LYCES
SwissProt_39:POL_FIVT2
SwissProt_39:DUT_CHLTE
SwissProt_39:DUT_CHVP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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057706;
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02536 helicobacter pylori (d
092kd0 helicobacter pylori j9
197209 buchnera aphidicola (s
1928248 escherichia coli. deox
09zhd8 buchnera aphidicola (s
057872 methanococcus jannasch
09pk29 chlamydia trachomatis.
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066592 aquifex aeolicus. deox
P43792 haemophilus influenzae
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! Q9yys0 avian adenovirus type
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+ 111.50 184.63 0.0012
+ 107.50 193.17 0.0024
+ 105.00 189.30 0.0044
101.00 179.82 0.0118
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Database sequences: 100059
Database length: 3664827
Search time (sec): 26.620000
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Query: US-08-957-709-70
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P32518 lycopersicon escule
P31822 feline immunodefic
1 068992 chlorobium tepidum.
I 041033 paramecium bursaria
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA RES 5:55-76[198].
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 =.DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus horikoshii.
Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TTCTGAAGAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAG 100
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SROUFINCE 156 AA: 17871 MW; 96B2C2C50393A985 CRC64;
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Gaps: 0
Percent Identity: 93.590
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Gaps: 0 Percent Identity: 85.621

4.718 97.386

to: 154

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Align seg 1/1 to: DCD_PYRAB from: 1
                            alignment_block:
US-08-957-709-70 x DCD_PYRAB
 Ratio:
Percent Similarity:
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
PROBABLE DEDXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DCD OR PAB1164.
Pyrococcus abyssi.
Pyrococcus abyssi.
NCBL_TAXID-29292;
                                                                                                                                GTTATICCICCAAGGAATACGCCTTAATCCTAAACCCTCGAGAGGATAAA 200
                                                       GTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAA 250
                                                                                            GAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGA 300
                                                                                                       ATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGG 400
                                                                                                                                                                                401 CAAGAAACCCTTACAGAGGAACTATCAGGGGAGCACAAGGTTAGCGTTT 450
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InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR004238; dUTPase.
Pfam: PF00692; dUTPase; 1.
Pr050m; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete protecome.
SEQUENCE 154 AA; 17758 WW; C031BEE419094DDB CRC64;
                                                                                                                                                                                                                                                                                                                    154 AA.
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Quality: 703.00
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STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
                                                                                                                              301 AACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAG 350
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NCBI_TaxID=2303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 TTATAAGGCTAGAGGTCCGGCAAGAAACCCTTACAGA......GGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 TCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 GTTGACCCAGGATGGGATGGAACTTAACACTAATGCTCTACAATGCCTC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 AGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 .CTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GlyArgGlnTyrSerGluPheGluIleGlyLysAsnValHisPheLeuVa 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATA......
                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase, Complete proteome.
SEQUENCE 183 AA; 20245 MW; 41D1992A99CD6682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 155
Gaps: 5
Percent Identity: 41.290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 183
                                                                                                                                                                                                                                                              EMBL; AL445064; CAC11737.1; -.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-957-709-70 x DCD_THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257.50
2.500
66.452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
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180 AA.

PRT;

STANDARD;

seq_documentation_block:

DCD_AQUAE 067539;

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                                                                                                                                                                                                                                                                                                                                                                                             Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::||||||| ||| ::: ::::: |||||||||||||::: 84 erLeuProProTyrValThrAlaPheValGluGlyArgSerSerLeuGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 TCAGAGTGGGCAGAGAG...GCTTTTGTTAAGGGGAAA...TTAATCGAC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 ....ATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AGTIGCCCGACGAIGTTAIGGGGGATAIGAAGATAAGGAGCAGTTTAGCA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .... 153
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| 51 ValLysLysGlyThrLysGlyValArgIleLeuGluPheGluGluTyrPh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetileLeuSerAspArgSerIleArgGluLeuIleGluLysGlyGluLe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 ACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                               20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 180 AA; 20544 MW; B2710421A2FA48D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392.353-358(1998).
-!- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 162
Gaps: 5
Percent Identity: 37.654
                                                                                                                                                                                                             Bacteria; Aquificales; Aquificaceae; Aquifex NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000747; AAC07499.1; -. InterPro; IPR003232; dCTP_deaminse. InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: DCD_AQUAE from: 1
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GTGGAAAAGGAAGGAAAAGTCGTT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-957-709-70 x DCD_AQUAE
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67.284
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20-AUG-2001 (Rel. 40, 20-AUG-2001 (Rel. 40, 20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                          Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                       DCD OR AQ_1607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                           DEAMINASE)
                                                                                                                                                                                                                                                                                                                                        STRAIN-VF5
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AGAGAAGGGGTT...ATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGA 296

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34 ATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGA
to: DCD_ACIAM from: 1
   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMED outstation the European Bioinformatics institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last anoctation update)
PROBABLE_DEOXXCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kletzin A.;
Molecular characterisation of a DNA ligase gene of the extremely
thermophilic archaeon Desulfurolobus ambivalens shows close
phylogenetic relationship to eukaryotic ligases.";
Nucleic Acids Res. 20:5389-5396(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acidianus ambivalens (Desulfurolobus ambivalens).
Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Acidianus
NCBL_raxID-2883;
   TGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAAT 346
                                                                                                                            TAAGATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGT 396
                                                                                                                                                                                                                                                         DISTRICT OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF 
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                                                                                                                                                                                                                                                                                                                                             CCGGCAAGAACCCTTACAGAGGAAACTATCAGGGG 432
                                                                                                                                                                                                                                                                                                                                                                              173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, X63438; CAA45033.1; -.
PIR, S26382; S26382.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Lei 10 / DSM 3772;
MEDLINE-93065206; Pubmed-1437556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_39:DCD_ACIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242.00
2.283
67.949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEAMINASE).
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SEQUENCE
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                             101
                                                                                        297
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                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                          397
                                                                                                                                                                                                                                                                                                                                                                                                        151
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Length: 156 Gaps: 35.897

alignment_block: US-08-957-709-70 x DCD_ACIAM

Quality:
Ratio:
Percent Similarity:

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STRAIN-E1.

MEDLINE-9310339; Dubwed-10382966;

MEDLINE-930339; Dubwed-10382966;

Jun-no K., Takahbashi M., Sekine M., Baba S.-I., Ankal A., Kosugi H.,
Jun-no K., Takahbashi M., Sekine M., Baba S.-I., Ankal A., Kosugi H.,
Hesoyama A., Fokui S., Naqazi Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-II., Kubota K.,
Naxamura Y., Nomira N., Sako Y., Kikuchi H.;
"Complete gequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).

-I- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DED ON APEO333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aeropyrum pernix.
Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                            ::|||||| |||:::::: ||||||| |||:::
100 heAlaArgLeuGlyLeuPheValProProThrIleValAspAlaGlyPhe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::|||:::||||||:::
117 GluGlyGlnLeuThrIleGluValLeu...GlySerAlaPheProValLy 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 CCTCAGAGTGGGC.....AGAGAGGCTT 106
                                                                                                                             144
                                                                                                                                                                                                                                                                                                                                                                                        245 TAGCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGATGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 GATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 ATTAAGATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGG 394
17 ileValileSerProLeuThrGlnAspThrIleArgGluAsnGlyValAs 33
                                                                                                                                                                                                                                                        83
                                                                   107 TIGITAAGGGGAAA.....TTAATCGACGTGGAAAAGGAAGGA
                                                                                                                                                      :: :::::|||||||| 50 yrGluAspGlyLysAspProArgSerPheTyrGluIleGluLysGlyAsp
                                                                                                                                                                                                                   145 AAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAG
                                                                                                                                                                                                                                         ::: :::||| |||:::||||::::|||| |||
67 GluPheIleIleTyrProAsnGluHisValLeuLeuValThrGluGluTy
                                                                                                                                                                                                                                                                                                   195 GATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGGAGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 GTCCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_39:DCD_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 GCGTTTTCAAAGAGAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 ThrLeuProLysPheLys 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID DCD_AERPE STANDARD;
AC 09YFA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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NCBI_TaxID=56636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..... 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 lnGluTyrIleArgLeuProGlyTyrValAlaGlyLeuValAsnLeuArg 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......TAAGGGGAAATTAATCGACGTGGAAAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 GGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .88 TCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATAAGG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 SerThrTrpAlaArgThrGlyIleTyrIleProAlaThrValValAspAl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 AGGATGGATGGAACTTAACACTAATGCTCTACAATGCCTCAAATGAAC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 CTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCATTTATAAGG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||:::|||
135 rovalLysLeuTyrProGlyAspArgPheLeuHisLeuValLeuValLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 CTAGAGGGTCCGCCAAGAACCCTTACAGAGGAAACTATCAGGGGAGCAC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 uValValGluProLeuSerGlyAspThrValArgGluAsnGlyLeuAspL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 euAspProArgAlaProGlySerProGlyGluPheTyrGluCysGlyGlu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LeulleLeuSerAspArgAspIleArgAlaLeuLeuAlaIleGlyAspLe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 ACTIATAGAGCCATTITCTGAAGAATCGCTCCAACCAGCAGGTTATGACC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 Gly. AspGluIleIleValGlyProGlyGluHisMetLeuLeuHisThrG 86
                                                                                                                                                                                                    Probon; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 181 AA; 19894 MW; D8B6CBDC1722EFE9 CRC64;
                                                                                                                                                                                                                                                                                                      Length: 174
Gaps: 5
Percent Identity: 34.483
                                                                                                                                                                                                                                                                                                                                                                                                                     to: 181
                                                                                                                                        EMBL; AP000059; BAA79288.1; -.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 TCAGAGTGGGCAGAGAGGCTTTTGT....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 gGlyValArgLeuProLys 174
                                                                                                                                                                                      Pfam; PF00692; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 to: DCD_AERPE
                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-957-709-70 x DCD_AERPE
                                                                                                                                                                                                                                                                                                  235.00
2.136
63.218
                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
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seq_name: SwissProt_39:DCD_STRCO

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                                                                                                                                                                                                                                    Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                       В.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 ........GAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 AAAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 CCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGATA 234
                                                                                                                                                                                                                                                                                                                                                                                                                           Oliver K., Harris D., Bentley S.D., Parkhill J., Barrell Rajandream M.A.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 lArgileAspProPheAspAspSerMetValGlnProSerSerIleAspV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                    zu-aug-2001 (Rel. 40, Last sequence update)
20-Aug-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DEAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 .CTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 TCAGAGTGGGCAGA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 uGlyAspGluProPhelleLeuHisProGlyGluPheValLeuAlaSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 3
Percent Identity: 31.361
                      191 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 191
                         PRT;
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InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: DCD_STRCO from: 1
                                                                         20-AUG-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL078610; CAB44381.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-957-709-70 x DCD_STRCO
                      STANDARD;
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2.077
61.538
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seg_documentation_block
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1902;
                                                                                                                                                                                                           DCD OR SCH35.46.
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                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
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                         STRCO
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Percent Identity: 31.551

9

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alignment_block:
US-08-957-709-70 x DCD_METTH
Percent Similarity: 57.219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. SEQUENTA H.

X. MEDLINE-98037514; PubMed-9371463;
X. MEDLINE-98037514; PubMed-9371463;
X. MEDLINE-98037514; PubMed-9371463;
X. MEDLINE-98037514; Dubwedte-5tamm L.A., DeLoughery C., Lee H.-M., DuBois J.,
X. Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
X. Aldredge T., Bashirzadeh R., Wang Y., Wierzbowski J., Gilbert K.,
X. Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
X. Aldredge T., Shamer G., Goyal A., Pietzbowski J., Glabon R.,
X. Daniells C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
X. Complete genome sequence of Methanobacterium thermoautotrophicum R.
X. Tomplete genome sequence of Methanobacterium thermoautotrophicum R.
X. Bacteriol. 179:7135-7155(1997).
X. L. CATALYTIC ACTIVITY: DELONGS TO THE DCTP DEAMINASE FAMILY.

C. CATALYTIC STILLING TO THE DCTP DEAMINASE FAMILY.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last amortation update)
PROBABLE_DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
Archaea: Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter
NCBI_TaxID=145262;
                                  235 AGGAGCAGTTTAGCAAGAGAGGGGTTATT.....GGTTCTTTTGCTTG 278
                                                                                            GGTTGACCCAGGATGGAAACTTAACACTAATGCTCTACAATGCCT 328
                                                                                                                CAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCA 378
                                                                                                                                                                                                                                                   TTTATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCA 428
                                                                                                                                                                                                                                                                        EMBL; AE000937; AAB86313.1; ALT_INIT.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR00423; dUTPase.
Pfam: PF00692; dUTPase; 1.
Pr050m; PD004900; dCTP_deaminse; 1.
Pydrolase; Complete protecome.
SEQUENCE 197 AA; 22426 MW; 96A019F9DBA3528F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: SwissProt_39:DCD_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID DCD_METTH STANDARD;
AC 027875;
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                                                                                                                                                                                                                                                                                                                               GGGGAGC 435
                                                                                                                                                                                                                                                                                                                                                                    167 rGlySer 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEAMINASE)
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                                                                                                                                                                                                                                                 379
                                                                                            279
                                                                                                                                117
                                                                                                                                                                       329
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187

alignment_scores: Quality: Ratio:

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20-AuG-2001 (Rel. 40, Created)
20-AuG-2001 (Rel. 40, Last sequence update)
20-AuG-2001 (Rel. 40, Last sequence update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DEDAMINASE)
Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteriadae;
Mycobacterias; Corynebacterineae; Mycobacteriadae;
Mycobacterias Firmicutes; Actinobacteriadae;
Mycobacterias Firmicutes; Actinobacteriadae;
Mycobacterianeae; Mycobacteriadae;
                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451
                                                                                                                                                                                   83 ACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATC..... 126
                                                                                                                                                                                                                                                                                                                                                                                                                                    223 GATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 GTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTAC.. 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 rIleAspProLeuAspAspProGluArgGlnIleGlnProSerValA 36
                                                                      3 IleLeuSerAspArgAspIleLysArgTyrIleGluGluGlyLeuIleTh 19
                                     4 CTACTICCAGACTGGAAAATCAGAAAAGAA......atacT 38
                                                                                                             39 TATAGAGCCATTTTCT.....GAAGAATCGCTCCAACCAGCAGGTTATG 82
                                                                                                                                                                                                           |||:::|||
51 LysProCysIleAspProLysAspProSerAspIleGluSerTyrMetGl
                                                                                                                                                                                                                                                                                                                                                            67 uThrPheHisValGluAspGlyProPheIleIleHisProGlyGluPheA
                                                                                                                                                                                                                                                                                                                                                                                                            173 CCTTAATCCTAACCCTCGAGAGATAAAGTTGCCCGACGATGTTATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 TICTITIGCTIGGGTIGACCCAGGATGGGAAGCTTAACACTAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ......gacgrggaa.....
                                                                                                                                                                                                                                                                                                                                      ......AAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......AGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTT
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    to:
Align seg 1/1 to: DCD_METTH from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 CAAAGAGAAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 erArgileLys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN-H37RV;
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135 AAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAA 184
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025136:
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                                                                                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the blology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .........GGCAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 uGlyIleAspProPheAspAspThrLeuValGlnProSerSerIleAspV 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase, Complete proteome.
SEQUENCE 190 AA; 20869 MW; F409329810B64781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGAGTG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv0321; -.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006940; AAK44559.1;
HSSP; P16088; 1DUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 296800; CAB09605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: DCD_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198.00
1.941
60.355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MT0336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                   101 LysSerSerLeuGlyArgLeuGlyLeuLeuThrHisSerThrAlaGlyPh 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAGATCGCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 laAsnLeuProlleThrLeuTrpProGlyMetLysIleGlyGlnLeuCys 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 TITATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 elleAspProGlyPheSerGlyHisIleThrLeuGluLeuSerAsnValA
67 lAspGlyGluProPheValLeuHisProGlyGluPheValLeuGlySerT
                                                                           185 CCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATGAAGATA
                                                                                                                                                                                                                               235 AGGAGCAGTITAGCAAGAGAAGGGGTTATT.....GGTTCTTTTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                  GGTTGACCCAGGATGGAAACTTAACACTAATGCTCTACAATGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori.";
Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AA
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TIGR; HP0372; -.
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MEDLINE=97394467; PubMed=9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: SwissProt_39:DCD_HELPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 GGGGAGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 aGlySer 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=210;
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......TTAATCGACGTGGAAAAGGAAAAGTCGTTATTCCTCC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aksnalaphealaLeuAlaHisThrIleGluTyrPheLysMetProLysA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: ||||:::::||| |||:::::::|||
eGluIleSerAsnThrThrAsnLeuProAlaLysValTyrAlaAsnGluG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTIGECAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCT 411
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18 MetileSerProPheCysGluLysGlnValGlyLysAsnValIleSerTy 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnalaThrLysIleAspalaSerLysGluGlyTyrPheIleLeuProAl 84
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DCA OR JHP1009.
Helicobacter pylori J99 (Campylobacter pylori J99).
                                                                                                                                                                                                                                                                                                                                                                                                           51 euPheAspAsnLysAsnAlaLeuIleAspProLysAsnPheAspProAsn
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                                                                                                                                                                                                                                                                                                             37 CTTATAGAGCCATTTTCTGAAGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......GCTTTTGTTAAGGGGAAA.....
Interpro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
ProbOn; PD00490; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 188 AA; 20904 MW; F45AEE3C3F040876 CRC64;
                                                                                                                                               Length: 168
Gaps: 4
Percent Identity: 27.976
                                                                                                                                                                                                                                                                                                                                                                                    61 .TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_39:DCD_HELPJ
                                                                                                                                                                                                                                                                           to: DCD_HELPY
                                                                                                                                                 181.00
1.792
60.119
                                                                                                                                                                                                                      alignment_block:
US-08-957-709-70 x DCD_HELPY
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ID COLHELPJ STANDAI
DCD_HELPJ STANDAI
DT 20-AUG-2001 (Rel. 40,
DT 20-AUG-2001 (Rel. 40,
DE DEAUG-2001 (Rel. 40,
DE DEOXYCYTIDINE TRIPHOSI
DE DEANINASE).
GN DEO OR JHP109.
OS HELICOBACTER PYJORI J'
                                                                                                                            alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
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                                                                                                                                                                                                                                                                           Align seg 1/1
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    DR DR SO
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                                                                          SEQUENCE FROM N.A.
MEDILINE-99120557; PubMed-9923682;
MEDILINE-99120557; PubMed-9923682;
MAID R.A. Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated isolates of the human
Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 AATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
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Hydrclase; Complete profeome:
SEQUENCE 188 AA, 20883 MW; FB58311156742276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 CTTATAGAGCCATTTTCTGAAGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::|||:::||||||| |||:::
18 MetileAsnProPheCysGluLysGlnValGlyLysAsnValIleSerTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......GCTTTTGTTAAGGGGAAA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 ATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 ATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAACTTAACACT
                                                                                                                                                                                                                                                  gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-i - CATALYITY: DELOTP + H(2)0 = DUTP + NH(3).
-i - SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouality: 180,00 Length: 168
Ratio: 1782 Ratio: 7782 Capt 4
Percent Similarity: 60.119 Percent Identity: 27.976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001529; AAD06585.1; -.
InterPro; IPR00323; dCTP-deaminse.
InterPro; IPR001428; dUTPase.
Pfam: PF00692; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: DCD_HELPJ
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US-08-957-709-70 x DCD_HELPJ
                      Helicobacter.
NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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DCD_BUCAI P57209;

DEAMINASE)

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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang L., Weiss B.;
ded (dCTP deaminase) gene of Escherichia coli: mapping, cloning,
sequencing, and identification as a locus of suppressors of lethal
dut (dUTPase) mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
DEAMINASE).
DCD OR DUS OR PAXA OR B2065.
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        272
                                                                                                                                                                                                                                                                                                                                                              91 ysSerThrPheGluSerIleLysMetProAsnAsnLeuValGlyTrpLeu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                   179 TCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGATATG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 IGCTIGGGTIGACCCAGGAIGGGAIGGAAACTIAACACTAAIGCTCTACA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                       74 ePheSerLysGluGlnProCysPheLeuGlnProGlySerLeuValLeuC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
    ::::::;|| ::: nLysThrLeuIleAsnGlyIleThrValAspIleHisLeuGlyAsnLysP
                                                                                                                                                                                                     58 LysilelleGlyGlyLeuSerLeuThrGluIleMetSerAsnGluIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                        229 AAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATT.....GGTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 aHisArgIleAspProGlyTrpAsnGlyAsnIleValLeuGluMetPheA
                                                                                                              41 heArgPhePheTyrGluHisThrGlySerCysIleAspLeuSerAsnSer
                                                                                                                                                                                                                                              ....GAAAAGGAAAGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 ATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCTTAC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GCTTTTGTTAAG......GGGAAATTAATCGACGTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92380941; PubMed=1324907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 174:5647-5653(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=12;
MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_39:DCD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license eigenent (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20445173; PubMed-10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Genome sequence of the endocellular bacterial symbiont of aphids bushanas on ne ".
362 GATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAACCCT 411
                                                                                           412 TACAGA.......GGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AGAATCGCTC...CAACCAGCATTATGACCTCAGAGTGGGCAGAGG. 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Complete proteome.
SEQUENCE 193 Aa; 21951 MW; DE7DD7FD961FC9FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome acyac...

Buchnera sp. APS.";

Buchnera sp. APS.";

1- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).

1- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 164
Gaps: 5
Percent Identity: 29.268
                                                                                                                                                                                                                                                                                                                                                                                                     193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001118; BAB12827.1; ALT_INIT.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD004900; dCTP_deaminse; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                     seq_name: SwissProt_39:DCD_BUCAI
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US-08-957-709-70 x DCD_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00692; durpase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.812
58.537
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                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TOKYO 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR BU108
                                                                                                                                                                                                                                              453 AAAG 456
                                                                                                                                                                                                                                                                                       184 oLys 185
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HDD TTD DD Align seg 1/1

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to trop T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,

Ra lsono K., Rasai H., Kihura S., Kitakawa M., Kitagawa M.,

Rakino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

Rakade S., Maxmura Y., Nashimoto H., Nishio Y., Coshima T.,

Ra Saito N., Sampel G., Sari Y., Sivasundaram S., Tagami H.,

Ra 460-kb DAM sequence of the Escherichia coli K-12 genome

Res. 3:379-392(1996).

Res. 3:379-392(1996).

C. CATANITIC RATIVITY: DCTP + H(2)0 - DUTP + NH(3).

C. CATANITIC RATIVITY: DETP + H(2)0 - DUTP + NH(3).

C. CATANITIC RATIVITY: DETP H DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: DETP H DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: DETP H DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BELONGS TO THE DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BELONGS TO THE DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BELONGS TO THE DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BELONGS TO THE DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BELONGS TO THE DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BELONGS TO THE DCTP DEANINASE FAMILY.

C. CATANITIC RATIVITY: BISOLOGY TO THE CATANITY THEN THE COLLAboration to the EMBL outstation to the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation of the EMBL outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation outstation 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 TGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCTCTACAATGC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 .......GGGAAATTAATCGACGTGGAAAGGAAGGAAAAGTCGTTATT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 CCT......CCAAGGGAATACGCCTTAATCCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GAATCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAG..... 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 TAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 gThrPheArgGlyHisThrAlaAlaPheIleAspLeuSerGlyProLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00692; dUTPase; 1.
ProDom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
Rydrolase; Complete proteome.
RSEQUENCE 193 AA; 21249 MW; B0044051ADE7F919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 167
Gaps: 5
Percent Identity: 29.940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: D90844; BAA15918.1; --
EMBL: D90845; BAA15918.1; --
EMBL: D90845; BAA15923.1; --
EPIR; A42940; A42040.
EcoGene; EG11418; dcd.
InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPasse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, M90069; AAA23669.1; -. EMBL; AE000296; AAC75126.1; - EMBL; D90844; BAA15918.1; -- EMBL; D90845; BAA15923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-957-709-70 x DCD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: DCD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 53.892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CITCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGA 56
                                                                   ......GGAAACTATCAGGGAGCACAAGGTTAGCGTTTTCAAA 455
                       142 rGlyLysLeuProLeuAlaLeuArgProGlyMetLeuIleGlyAlaLeuS 159
                                                    417
                                                                                                                             Volume, 20.40G-2001 (Rel. 40, Created)
20.40G-2001 (Rel. 40, Last sequence update)
20.40G-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DEAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 AGAATCGCTC...CAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA; 21871 MW; 8E19D4580C7C55E8 CRC64;
327 CICAAAIGAACCIGICGAAITAAGAIAIGGAGAGAGATIIGIGCAGAICG
                                                                                                                                                                                                                                                                                                                                                            Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 181
Gaps: 5
Percent Identity: 25.967
                                                       377 CATITATAAGGCIAGAGGGTCCGGCAAGAAACCCITACAGA
                                                                                                                                                                                                                                                               193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF067228; AAC97363.1; -. InterPro; IPR003232; dCTP_deaminse. InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: DCD_BUCAP from: 1
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                        seq_name: SwissProt_39:DCD_BUCAP
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US-08-957-709-70 x DCD_BUCAP
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1.583
56.354
                                                                                                                                                                                                                                                     seq_documentation_block:
ID DCD_BUCAP STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                       456 G 456
                                                                                                                                                                                                192 s 192
                                                                                                                   418
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Thu Jan 31, 13:32:23 2002

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10-NOV-1997 (Rel. 35, Last sequence update)
20-NGC-2001 (Rel. 40, Last anotation update)
PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
                                                                                                                                                                                                                                                                                                                                                                          .....AAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: ||||||||||||:::||| |||||||:::::::::||| :::
91 heSerThrLeuGluAsnIleThrLeuProAsnAsnLeuValGlyTrpLeu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AspGlyArgSerSerLeuAlaArgLeuGlyLeuMetValHisValThrSe 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 rHisArgIleAspProGlyTrpHisGlyAsnIleValLeuGluPhePheA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 ATGCCTCAAATGAACCTGTCGAATTAAGATATGGAGAGAGTTTGTGCAG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 LeuSerPheGluLeuLeuSerLysProValLeuArgProTyrAsnSerAr 174
                                                                                                                                                                                                                        103 .....GCTTTTGTTAAGGGGAAATTAATCGACGTGGAA.... 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 TCCTAACCCTCGAGGGATAAAGTTGCCCGACGATGTTATGGGGGGTATG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 ATCGCATTTATAAGGCTAGAGGTCCGGCAAGAAACCCTTACAGAGGAAA 422
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Methanococcus.
24 sLysGlnLeuIleAsnGlyIleThrValAspIleHisLeuGlyAsnLysP 41
                                                                                                                                                                                                                                                                                               58 LysGluLysIleAlaLeuAspLeuAsnLysIleValSerCysGluThrIl 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 ePheSerLysLysGluProPhePheLeuLysProGlyAlaLeuAlaLeuP 91
                                                                                                                                             41 heArgPhePheTyrAspHisThrThrSerCysIleAspLeuSerGlySer
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 luGlyGlyValLeuGlyThrThrAsnGluTyrIleGluLeuProAsnAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 hrLeuGluIleVal...AlaPheAspLysProValIleLeuTyrLysAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGTT. 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 GTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTAT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 TGGT.....TCTTTTGCTTGGGTTGACCCAGGATGGGAAACTTAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 CACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGATATGGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 GAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGAAA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AspTyrValThrSerLysArgIleIleIleLysProPheAsnLysAspPh 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 CCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 uGluLysIleAsnTyrPheLysGluLysTyrAsnValAspTyrValValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: :: ||| :::|| ||| ||| 11|::::|| 126 rSerHisGlnThrAlaGlyTrpIleAspAlaGlyPheLysGlyLysIleT
                                                                                                                                                                                 InterPro; IPR003232; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase: 1.
Probom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 204 AA; 23432 MW; 1218368057723371 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 yrAspAspGluValTyrAspLeuSerLysGluLeuAsnTyrLysArgIle
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Gaps: 6
Percent Identity: 25.683
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Ratio:
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156 TCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGT 215
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                                                                                      Search time 38.81 Seconds
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-896-164-11
US-08-365-189-7
US-08-365-189-1
US-08-365-189-1
US-08-365-189-1
US-08-2189-1
US-09-018-628-2
US-09-209-605-2
US-09-209-605-3
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                                                                                      January 31, 2002, 10:47:47
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                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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. Holly Polymerase Enhancing Factor (PEF)
Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentII Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
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                         US-08-403-853-17
US-08-325-547-9
US-08-137-1170-36
US-08-671-978A-11
US-08-803-973-6
US-08-803-973-6
US-08-803-973-11
US-08-803-972-11
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US-08-685-625A-5
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US-08-803-972-1
US-08-063-552-1
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                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                       Sequence 42, Application US/08822774; Patent No. 6183997; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: KULIK, David J.
REGIESTRATION UNDRER: 36,576
REFERENCE/POCKET NUMBER: 1486,
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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CLASSIFICATION: 436
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HOGREFE, HOLL
TITLE OF INVENTION: POLY
TITLE OF INVENTION: EXET
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
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Sequence 36, Application US/08822774

Patent No. 618397

CENERAL INFORMATION:
APPLICANT: HGCREFE, Holly
TITLE OF INVENTION:
TITLE OF INVENTION:
ADDRESSEE: Lenhan, P.L., C.
STREET: 1200 G Street, N.W. Suite 700
STREET: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPACTAL
COMPUTER: IEM PC COMPACTAL
COMPUTER: TEM PC POS/MS-DOS
CONFURENT SYSTEM: PC-DOS/MS-DOS
CSOFTWARE: Patentin Release #1.0, Version #1.25
CSOFTWARE: Patentin Release #1.0, Version #1.25
CSOFTWARE: PAPLICATION DATA:
FILING DATE: 21-MAR-1997
CLASSIFICATION NUMBER: 36,576
ATTONNEY/AGENT INFORMATION:
NAME: KULIK, DAVID J
REGISTRATION NUMBER: 36,576
REFERENCE/POCKET NUMBER: 36,576
REGISTRATION NUMBER: 36,576
REFERENCE/POCKET NUMBER: 36,576
TELEPHONE: (202) 628-8800
TELEFAK: (202) 628-8800
TELEFAK: (202) 628-8800
TELEFAK: (202) 628-8840
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CLARACTERISTICS:
                                                                                                                61 TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAG 98
                                                                                                                                                  147 AGTCGTTATTCCTCCAAGGGAATA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-32-463-14/C
US-08-32-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
Fatent INFORMATION
APPLICANT: DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGTCGNTATTCCTCCAAGGGATA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ss: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO US-08-822-774-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                RESULT 3
US-08-822-774-36
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                                                                                                                                                                                               TATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARELICATION DATE: 21-MR-1997
FILING DATE: 21-MR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
TELECHONE: (202) 628-8800
TELEPAN: (202) 628-8800
INFORMATION FOR SEO ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 base pairs
TYPE: NUMBER: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S: single
unknown
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MOLECULE TYPE:
HYPOTHETICAL:
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APPLICANT: Bower, Patricia A
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       1091 RRRRRRRR 1083
                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 CCTGTCGAATTAAGATATGGAGAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 CCGGCAAGAAACCCTTACAGAGGAAACTATCAGGGGAGCACAAGGTTAGCGTTTTCAAAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 CCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 TGGGTTGACCCAGGATGGAATGGAACTTAACACTAATGCTCTACAATGCCTCAAATGAA
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                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
            APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LAITGHER
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-AG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERROME/COCKET UNDRAGER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICANT: SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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US-08-232-463-14
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                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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411 AAGCAAATTGCTTATGATAATNTCTCAGAAAGATACATTTCATTCCTTTTTTCAACACTT 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAA 60
                                                                                                               ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER AND METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 6.8%; Score 31.8; DB 4;
47.1%; Pred. No. 0.28;
ative 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.50 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/896,164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTORNE: No. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
US-08-896-164-11/c
Sequence 11, Application US/08896164
Patent No. 6218521
GENERAL INFORMATION:
APPLICANT: OBSTA, Yuichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CTAACCCTCGAGAGGATAAAGTTG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 AATAACTTCTCAAGATAAACCTAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-365-189-7; Sequence 7, Application US/08365189; Patent No. 5514576; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: UJJy 17, 1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SED ID NO: 11
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.1%;
                                                                                                                                                                                                                                   ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 491 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
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STRANDEDNESS: double
                                                                                                                                                            TITLE OF INVENTION: DINUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskett
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LENGTH: 2982 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.77
Best Local Similarity 59.65
Matches 53; Conservative
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; MOLECULE TYPE:
US-08-365-189-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 6.7%; Score 31.4; DB 1; Length 2646; Best Local Similarity 59.6%; Pred. No. 0.91; Marches 36; Indels 0 Marches 36; Indels 0
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cloned Pullulanase
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quartes & Brady
STREET: 411 East Wisconsin Avenue
STREET: 411 East Wisconsin Avenue
STATE: Misconsin
COUNTRY: U.S.A.
ZITE: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,189
             NUMBER OF INTENTION
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 14
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: S3202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,189
FILING DATE:
TITLE OF INVENTION: Cloned Pullulanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 68 CTTACGAGGGATGTACATGGAGTGGATGG 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 TTTGCTTGGGTTGACCCAGGATGGGATGG 299
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132,648
FILING DATE: 0ctober 5, 1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,407
REFERENCE/DOCKET NUMBER: 66-005-:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESOLA

5 Sequence 2, Application US/08365189

7 Patent No. 5514576

7 GENERAL INFORMATION:
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TELEFAX: (414) 271-3552
INFORMATION FOR SEO ID NO. 7
SEQUENCE CHARACTERISTICS:
LENGTH: 2646 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-365-189-7
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PRIOR PARICHATION 173:

PRIOR PAPELCATION 1700: 413:

PRIOR PAPELCATION 1700: 413:

PRIOR PAPELCATION 1700: 413:

PARELLANDON WOURSER: 06-005-9567-4

PREPERENCE/OREAT NUMBER: 66-005-9567-4

PREPERENCE/ORGANIZATION NUMBER: 66-005-9567-4

PREPERENCE/ORGANIZATION NUMBER: 66-005-9567-4

PREPERENCE/ORGANIZATION NUMBER: 66-005-9567-4

PREPERENCE/ORGANIZATION NUMBER: 96-005-9567-4

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121 TTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                             US-08-800-264A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                 211 GATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pelfe . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                       Length 2988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.2; DB 4; Length 8 Pred. No. 0.58; 0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUD 5499 - JEL/NDH/SLH
                                                                                                                                         36;
                                                                                                     Score 31.4; DB 1;
Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                       271 TTTGCTTGGGTTGACCCAGGATGGGATGG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08896164
Fatent No. 6218521
GENERAL INFORMATION:
APPLICANT: OBATA, Yuichi
TITLE OF INVENTION: ISOLATED NUCLE:
TITLE OF INVENTION: WITH GASTRIC CARROLL OF INVENTION: DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.68;
                                                                                                       6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Felfe & Lynch
: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 802 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.69
Best Local Similarity 47.13
Matches 96; Conservative
                                                                                                                      Best Local Similarity 59.6
Matches 53; Conservative
double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10022
COMPUTER READABLE FORM:
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                linear
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STRANDEDNESS:
             ; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-365-189-1
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                                                                                                       Query Match
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291 ATCATCAACCTTTCTAATGAAGGCAGCGGCAAAAGTAGTAGAAAGCAAAAGGACAAGGACAAGAAC 232
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                                                                                                                                                                                                                                                                                                                                                                                  AN ALTERED TELOMERE REPEAT BINDING FACTOR AND THEPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
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Pred. No. 0.63;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,264A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTOREX/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET UNBER: 600-1-191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          Sequence 2, Application US/08800264A Patent No. 5859183 GENERAL INFORMATION:
                                                                                                  231 AATAACTTCTCAAGATAAACCTAG 208
                                               181 CTAACCCTCGAGGGATAAAGTTG 204
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APPLICANT: van Steensel, Bas
APPLICANT: Bianchi, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.6%;
Best Local Similarity 47.1%;
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: AN TITLE OF INVENTION: FAC NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
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121 TTAATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATC 180
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APPLICANT: de Lange, Titia
APPLICANT: van Steensel, Bas
APPLICANT: van Steensel, Bas
APPLICANT: van Steensel, Bas
APPLICANT: van Steensel, Bas
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING
TITLE OF INVENTION: RATOR AND THEPEUTIC USE THERBOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USS.

COUNTY: USS.

COUNTY: USS.

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/018,628
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
RECISTRATION NUMBER: 26,742
REPERENDE/DCCKET NUMBER: 600-1-191 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 AATAACTICICAAGATAAACCIAG 641
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Patent No. 6022709
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               Hackensack
: New Jersey
RY: USA
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                                                                                                Sequence 2, Application US/09018628
Sequence 2, Application US/09018628
Fatent No. 5917019
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: van Steensel, Bas
APPLICANT: Bianchi, Alessandro
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING:
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING:
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING:
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING:
TITLE OF INVENTION: AN ALTERED TELOMERE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: FLOOR
CITY: Hackensack
STREET: Now Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER YEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIETCATION:
ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26/742
REFERENCE/DOCKET NUMBER: 600-1-191 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-467-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: TURES: Acuted acid
TYPE: TWO AND THE ACUTED THE 
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US-09-273-378-2
; Sequence 2, Application US/09273378
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                                 RESULT 11
US-09-018-628-2
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TITLE OF INVENTION: FACTOR AND THEPEUTIC USE THEREOF
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APPLICATION NUMBER: US/08/800,264A
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                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-018-628-3
; Sequence 3, Application US/09018628
; Patent No. 5917019
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                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.6
Best Local Similarity 47.1
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. C
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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APPLICANT: de Lang
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HYPOTHETICAL:
                                                                                                                                                               COUNTRY: US
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APPLICANT: van Steensel, Bas
APPLICANT: Bianchi, Alessandro
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING
TITLE OF INVENTION: FACTOR AND THEREUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: van Steensel, Bas
APPLICANT: Nalessandro
TITLE OF INVENTION: AN ALTERED TELOMERE REPEAT BINDING
                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                           ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/209,605

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 600-1-191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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Patent No. 5859183
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,264
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LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 47.1
Matches 96; Conservative
                                                                                                                                                     STREET: Floor
CITY: Hackensack
STATE: New Jersey
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APPLICANT: van Steensel, Bas
APPLICANT: Bianchi, Alessandto TITLE OF INVENTION: AN ALYERED TELOMERE REPEAT BINDING
TITLE OF INVENTION: PACTOR AND THEPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EE: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza, 4th
Floor
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.74;
; Mismatches 108;
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CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIPE: New Jersey

COUNTRY: USA

COMFOURE: FLOPPY disk

MEDIUM TYPE: FLOPPY disk

COMPOTER: IBM FC COMPATIBLE

COMPOTER: IBM FC COMPATIBLE

COMPOTER: IBM FC COMPATIBLE

COMPOTER: DATE: PC-DOS/MS-DOS

SOFTWARE: BACHTIN Release #1.0, Version #1.30

CHRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/018,628

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET UNMBER: 26/742

REFERENCE/DOCKET UNMBER: 200-1-191 CIP

TELEPAN: 201-487-5800

TELEFAN: 201-487-5800

TELEFAN: 201-487-5800

TELEFAN: 201-487-5800

TELEFAN: 201-487-5800

TELEFAN: 201-487-5800

TELEFAN: Jall base pairs

SEQUENCE CHARACTRISTICS:

LENGTH: 131 base pairs

TYPE: MULGIC acid

STRANDEDNESS: double

MULCULE TYPE: NO
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ó 61 TCGCTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAA 120 121 TTAATCGACGTGGAAAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATC 180 Gaps 1 ATGCTACTTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAA 60 DB 2; Length 1311; Ouery Match
6.6%; Score 31.2; DB 2; Length 13
Best Local Similarity 47.1%; Pred. No. 0.74;
Matches 96; Conservative 0; Mismatches 108; Indels Ω qq g ò ò ò

Search completed: January 31, 2002, 10:48:51 Job time: 64 sec

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HS_5376_A AL392601 T3 end of BG353517 ps29c10.y AZ189339 SP_1014.A AL055406 Drcc

AL276801 Tetraodon AL105032 Drosophil D32687 CELK020A6R C70559 C70559 Yuji

HS_5308_A TaLr1136F

BF473989 W AQ753165 H BG905021 T BG906626 T

WHE0839_

Talr1151C LEREP28TR Drosophil 2M0268L03 RPCI-11-9 HS_5536_A QV4-NN114

AQ960094 I AL108045 D AZ986009 2 AZ518463 F

HS_5455_B 1M0067010

AQ693439 1 AZ336783

AZ334611 1 BG623120 6

602646837 IL0-GN021

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AQ747571 B BF365040 C AQ657311 S BG622197 6

HS_3020_A 602755966

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"Web: www.genoscope.cns.rn)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's pil and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genöscope.

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                  CNS046KO
CNS0155Q
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                                  AQ699577
CNS06CJN
BG353517
AZ189339
CNS004YY
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AQ747571
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AQ657311
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BG905021
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CNS017HF
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BF992394
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fruit fly
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TITLE
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SOURCE
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 (without alignments)
4309.401 Million cell updates/sec
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                                                                                 January 31, 2002, 10:02:27; Search time 1174.47 Seconds
                                                                                                                                                           1 ATGCTACTTCCAGACTGGAA.......CAAAGAGAAAGAAACTCTAG 471
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AL062049 D
AL060761 D
AL060767 D
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                       11351937 seqs, 5372889281 residues
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CNS0106X
CNS0106J
CNS0107N
CNS005TE
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                                                          OM nucleic - nucleic search, using sw model
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                                                                                                                                                            Sequence:
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found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

wb75e03.x

O O

٠ 9 Result

Page

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Query Match
Best Local Similarity
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                                                                                                                                                  83
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CNS0106X
LOCUS
DEFINITION
                                                                                                                                               BASE COUNT
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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S Malek, R.L. (Cho,J., White,J., Quackenbush,J. and Lee,N. H. Sultana,R.L. Tsai,J. White,J., Quackenbush,J. and Lee,N. H. Generation of ESTS from Normalized Rat Embryo, Bento Soares'
L Unpublished (2000)
Other_ESTS: EST446205 EST446207
Contest: Lee,N. H.
The Institute for Genomic Research
Tel: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information.
Location/Qualifiers
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Ratus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF281615 336 bp mRNA EST 28-NOV-2000 EST46206 Rat Gene Index, normalized rat, Rattus norvegicus CDNA Rattus norvegicus CDNA clone RGIAN54, mRNA sequence. BF281615 GI:11212685
                                                                                                                                                                                                                                           1077 WWIWWKDRADDRRWAGDADRWAWDGAGTWWTATWWWWWWWAWATWDTWWDKWWWATAAK 1018
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                                                                                                                                                                                                                                                                                                                                                      TATTGGTTCTTTTGCTTGGGTTGACCCAGGATGGGAAACTTAACACTAATGCTCTA 320
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                                                                                                                                                                                            Gaps
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                                                                                                                                                             Length 1101;
                                                                                                       others
                                                                                                                                                             Match 8.6%; Score 40.4; DB 13; Length Local Similarity 13.5%; Pred. No. 0.4; D. Conservative 182; Mismatches 150; Indels 85; Conservative 182; Mismatches 150; Indels
                        // Organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RRCI-98"
/clone="BACROBKIO"
/note="end: TET3"
64 c 131 g 202 t 503 c
Location/Qualifiers
1. .1101
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Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Everamination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a hitp://www.edpp.ebi.ac.uk - This Drosophila melanogaster BAC hitp://www.edpp.ebi.ac.uk - This Drosophila melanogaster BAC dibrary (Dros BAC) was made by Alain Billaud at CEPH (Centre dietude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03X20 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephgoridea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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    .1101
        /organism="Drosophila melanogaster" /plasmid="pBeloBAC11" /db_xref="taxon:7227"

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8.3%; Score 39; DB
Best Local Similarity 52.1%; Pred No. 0.93
Matches 87; Conservative 0; Mismatches
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Pred. No. 2.2;
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/clone="BACN03K20"
/note="end : T7"
107 c 60 q
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Length 1101; Indels

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Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNO3D10 of DrosBAC library from Drosophila melanogaster (fruit
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/clone_lib="DrosBAC"
/clone="bACN03D10"
/note="end : SP6"
    DB 13;
                                                                                           94; Mismatches 218;
                                                     5.6;
Score 37.6;
                                                     Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR01M22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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    Gaps
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR01M22"
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Conservative 154; Mismatches
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S Genoscope.

Laboraticad (02-JUN-1999) Genoscope - Centre National de Sequencage : Submisted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqréfégenoscope.cns.fr - Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information plases see http://www.fiultfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial Ecost Indigestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp., the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                       233 TAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTTTTGCTTGGGTTGACCCAGGAT 292
                                                                                                                                                   293 GGGATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAATTAAGAT 352
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Drosophila melanogaster

Brwayota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 997;
                                                                 Length 1019;
 126 others
                                                              7.9%; Score 37; DB 13; Length 10
llarity 41.8%; Pred No. 3.8; Conservative 10; Mismatches 125; Indels
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/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR12K22"
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Pred. No. 4.3
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Matches 97; Conserv
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Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Map Building
Map Building
Map Building
Unpublished (1997)
Other_GSSS: RPCI-11-179G24_TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Email: bheefighr.ogf
Glones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                            RRGRGAGARRRGRGGRRRGAGARRRRRGRRMRTRRARRRRRAGAGAARRRARGARRR 632
                                                                                                                                         AGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGT 131
                                                                                                                                                                                                                                                                           GGAAAAGGAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGA 191
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                                                                                                                                                                                                      AKAARARGARRRRGRRRRRGRGRRRRAGRGGRAGRRGRGRGRRRARARARARARAR
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/db_xref="GDB:7568519"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 973)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
           /Glone="RPCI-11-179524"
/clone=lib="RPCI-11"
/sex="Maile"
/cell_type="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2: EcoRI; Site_3: EcoRI; Sit
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10324 row: j column: 16
High quality sequence stop: 705.
Location/Qualifiers
1. 973
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/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 CTCCAACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ATCGACGTGGAAAAGGAAGGAAAGTCGTTATTCCTC-CAAGGGAATACGCCTTAATCCT 182
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602373061F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4484463
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.4; DB 13; Length 577;
Pred. No. 5.4;
0; Mismatches 127; Indels 1
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Contact: Robert Strausberg, Ph.D. Emall: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
/db_xref="taxon:9606"
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BG261309.1 GI:12771125
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Web: www.genoscope.cns.fr.n.
Web: www.genoscope.cns.fr.n.
Web: www.genoscope.cns.fr.n.
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Gosegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                     286 CCAGGATGGGATGGAAACTTAACACTAATGCTCTACAATGCCTCAAATGAACCTGTCGAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 TTAAGATATGGAAGATTTGTGCAGATCGCATTTATAAGGCTAGAGGGTCCGGCAAGA 405
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                   85;
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1 Similarity 17.6%; Pred. No. 8.5;
60; Conservative 128; Mismatches 153;
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                                                                                                                                                                                                                               7.6%; Score 36; E
50.6%; Pred. No. 7.
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  167
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Direct Submitsaton

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr )

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila malanogaster BAC library (Droso BAC) was made by Alain Billaud at CEPH (Centre d'Etde du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                                                                            272 TTGCTTGGGTTGACCCAGGATGGGAACTTAACACTAATGCTCTACAATGCCTCAA 331
                                                                                                                                                                                                211
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  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fruit fly..
Plasand Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                     AAADKWKDAKKWDGAKKATKTKKKDKKAAWAAADKKDRKKGGKKGKKGKKGKKKKKK
                                                                                                                                    AAATACTTATAGAGCCATTTTCTGAAGAATCGCTCCAACCAGCAGGTTATGACCTCAGAG
                                                                                                                                                                                                TTATTCCTCCAAGGGAATACGCCTTAATCCTAACCCTCGAGAGGATAAAGTTGCCCGACG
                                                                                               TGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCGACGTGGAAAAGGAAAGGAAAGGTCG
                                                                                                                                                                                                                                                                                             212 ATGTTATGGGGGATATGAAGATAAGGAGCAGTTTAGCAAGAGAAGGGGTTATTGGTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 1204
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/plasmid="pBeloBACil"
/db.xref="Exxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 ATGAACCTGTCGAATTAAGATATGGAGAGAGATTTGTGCAG 372
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172 c
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68; Conserv
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LOCUS
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AUTHORS
TITLE
JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2275)
Tripodis, N. and Ragoussis, J. Generation of a transcription map in the region immediately centromeric to human MRC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1608 SRYRRYMAKCRGCSKSCWRCWRSYSSYSCKRCKWYKKTGSTSMKSAGGWGRWRARAARWR 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon2 contig, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 AACCAGCAGGTTATGACCTCAGAGTGGGCAGAGAGGCTTTTGTTAAGGGGAAATTAATCG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 ACGTGGAAAAGGAAAGGAAAAGTCGTTATTCCTCCAAGGGAATACGCCTTAATCCTAACCC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TTCCAGACTGGAAAATCAGAAAAGAAATACTTATAGAGCCATTTTCTGAAGAATCGCTCC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Tripodis and Ragoussis)"
599 t 149 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guys Hospital
7th floor, Guy's Tower, London SE1 9RT, UK
Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 35.2; DB 10; 23.0%; Pred. No. 13; ative 78; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mar - vrint
/clone="ntcon2 contig"
/clone_lib="Human mRNA
619 c 470 g 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                    AF034173.1 GI:2707735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%
Best Local Similarity 23.0%
Matches 58; Conservative
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Bukaryotta; Viridiphantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryotta; Viridiphantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 721)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Lessie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11209182.
                                                                                                                              GA_Eb0038K19f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Eb0038K19f, mRNA sequence.
BF278028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="ARA"
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/db_xref="texon.29729"
/clone="GA_Eb0038K19f"
/clone="GA_Eb0038K19f"
/clone=lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence SP6 end of BAC BACN12634 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 AAAGTIGCCCGACGATGTTATGGGGGAFATGAAGATAAGGAGCAGTTTAGCAAGAGAAGG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 GGTTATTGGTTCTTTGCTTGGGTTGACCCAGGATGGGATGGAAACTTAACACTAATGCT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
124 c 173 g 199 t 22 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 650.
Location/Qualifiers
1. 721
/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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53.3%; Pred. No. 18;
cive 0; Mismatches
/lab_host="E. coli"
                                                                                                                                                                                                                     BF278028
BF278028.2 GI:13248985
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                                                                                                                                                                                                                                                                                              Gossypium arboreum.
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Matches 73; Conservative
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                                                                                                RESULT 13
                                                                                                                                                                  DEFINITION
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KEYWORDS
SOURCE
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CNS014RI
                                                                                                                         BF278028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 1445 Std Error: 0.00
Seq primer: -40UP from Gloco
High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anotem Vector: pi7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 467)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Itssue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                         EST 17-DEC-1999 sapiens cDNA clone IMAGE:2311516 3',
  379 TTTATAAGGCTAGAGGGTCCGGCAAGAACCCTTACAGAGGAAACTATCAGGGGAGCACA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 TCGAGAGGATAAAGTTGCCCGACGATGTTATGGGGGGATATGAAGGATAAGGAGCAGTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2311516"
/clone_lib="NCI_CGAP_GC6"
/tisne_type="pooled germ cell tumors"
/lab_host="PH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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61.8%; Pred. No. 18
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/organism="Homo sapiens"
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wb75e03.x1 NCI_CGAP_GC6 Homo
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                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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source

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human.

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TITLE

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DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ö

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ACCESSION

439 AGGTTAGCGTTTTCAAAGAGAAAGAAACT 467

Query Match

Matches

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BASE COUNT ORIGIN

and

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Figure 1. Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
University of Mashington
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 516)
Mahairas, GG., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                          mapping and
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52.6%; Pred. No. 20;
tive 0; Mismatches
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High quality sequence stop: 516.
Location/Qualifies
1. 516
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.adgp.ebi.ac.uk - This Drosophila melanogaster BAC | Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Geneviewe Payan. It has been constructed in the vector
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Homo sapiens
"Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Plaamid Drosophila melanogaster
Plaamid Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota: Neoptera: Endopteryota: Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACN12G24"
/note="end: SP6"
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TSAR binding domai Mugwort pollen all Mugwort pollen all Peptide #1838 enco Peptide #1929 enco Peptide #1847 enco

AAW30997 AAW30931 AAW512154 AAK513184 AAW31085 AAW31065 AAW31065 AAW31065 AAW31065 AAW31086 AAW31986 AAW31986 AAW31986 AAW31986

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Copyright (c) 1993 - 2000 Compugen Ltd.
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for Polymerase enhancing factor proteins, extracts and complexes -improve the polymerisation activity of nucleic acid polymerases, use in amplification, sequencing and replication Polymerase enhancing factor; PEF; dUTPase; PCR; amplification; sequencing; replication. Herpesvirus dUTPase uridine-binding motif AAW72857 standard; Peptide; 14 AA. 97US-0957709. 98WO-US05497 (first entry) Hansen CJ, Hogrefe H; WPI; 1998-542284/46. (STRA-) STRATAGENE.

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Result ş

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                                                           are provided (see AAM72849-57) of the uridine-binding motifs of the dUTPBASES and dCTP deaminases of Pyrococcus furiosus (see also AAM72847), wetherebrichia coli, yeast, human and herpesvirus; a consensus (see AAM72847), wethenococcus jannaschii, Desulfurolobus ambivalens, Escherichia coli, yeast, human and herpesvirus; a consensus (see AAM72848) is also provided. A claimed method of enhancing a nucleic acid polymerase reaction comprises performing the reaction in the presence of one or more of the following: a polymerase enhancing factor (PEF), a dUTPBASE, a protein that turns-over dUTP and a protein having one or more of the sequences provided in AAM72848-57. Rits are provided for replicating sequences given in AAM72848-57. Kits are provided for replicating sequencing or for site-directed mutagenesis, for nucleic acid sequencing or for amplification (preferably PCR or RT-PCR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 14; DB 19; Length 14; 100.0%; Pred. No. 1.4e-08; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG90573 standard; Protein; 152 AA
Claim 71; Page 47; 161pp; English.
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2000JP-0159162.
2000JP-0280988.
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Best Local Similarity 100.
Matches 14; Conservative
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Senoh A,
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07-APR-2000;
03-AUG-2000;
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Tatelshi N,
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analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from Coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
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SDF; genetic mapping; identification; promoter; structural gene; UTR,
untranslated region; expression control.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 6; DB 22;
100.0%; Pred. No. 29;
tive 0; Mismatches (
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          152 AA;
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| 145 idpgfq 150
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The invention provides a functional site descriptor (FSD) that defines a spatial configuration of a functional site (other than a divalent metal ion binding site) in a protein (1), for use in an inexact threedimensional (3D) structure model of (1) to determine if (1) possesses for at least one atom in each of at least two amino acid (aa) residues that comprise the functional site of (1) and at least one as is identified as a particular as (or set of aa). The atoms are: (i) amide nitrogen, alpha or carbonyl carbon, or carbonyl oxygen within the polymer backbone; (ii) a beta-carbon of aa, or (iii) a pseudoatom, with at least one being of type (i). FSD are used to predict biological activities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins, e.g. enzymatic, ligend-binding protein interaction activities, of animal, plant, prokaryotic or viral origin. They may also be used to validate/confirm results from other predictive methods. The method can be used even with inexact (computed) models of protein structure, deduced from protein or nucleic acid sequence data, i.e. an accurate 3D model of the whole protein is not required, rather just the 3D orientation of the active site. Sequences AAY77991-Y78000 and AAY77923-924 represent peptides used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                             Functional site descriptor for proteins, useful for predicting protein arrivity.
                                                                               Functional site descriptor; FSD; enzyme; protein structure; three-dimnsional structure; active site.
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5. 33;
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100.0%; Pred. No. 33;
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                                              Amino acid sequence of RNAS_ASPGI.
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99US-0120311.
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              23-JUN-2000 (first entry)
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Best Local Similarity
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| 169 qgelkl 174
                                                                                                                                                                   WO200011206-A1.
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                                                                                                                                 Unidentified
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16-FEB-1999;
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                                                             42.9%; Score 6; DB 2
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90JP-0244181.
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Length 177; 0; Indels Functional site descriptor; FSD; 3-dimensional; 3-D; structural model;

Functional site descriptor protein RNAS_ASPGI.

AAY78000 standard; protein; 177 AA.

RESULT
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ID AAY7
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AAY78000

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This invention describes a novel functional site descriptor (FSD) that defines a spatial configuration for a functional site of a protein.

The functional site corresponds to a biological function other than a divalent metal ion binding site. The FSD is applied to an inexact.

The functional site defined by the FSD is applied to an inexact. The protein possesses the biological function corresponding to the constraints for one or more atoms in each of 2 or more amino acid functional site defined by the FSD. The FSD comprises a set of geometric constraints for one or more atoms in each of 2 or more amino acid residues comprising a functional site of a protein other than a divalent constraints for one or more atoms in each of 2 or more amino acid residues, where at least one of the 2 or more amino acid acid residues, where at least one of the atoms is an amide nitrogen, alpha-carbon, carbonyl carbon, or carbonyl expen, within a polypeptide calpha-carbon, carbon, carbon, carbonyl expen, within a polypeptide backbone. The remaining atoms maybe any of the atom as above or beta-carbons of amino acid residues, or pseudoatoms. The FSDs can be used to identify or screen for a novel function in one or more consection, or to provide further information of a protein. The methods confirm a previously identified or suspectific functional confirms a previously identified or suspectific functional site in a protein. Using the methods it is not necessary to accurately confedict its function. Instead, prediction of biological function of a predict its function of the protein under investigation. Afficial function using concerning used to describe in a region responsible for the particular or the particular or function of the protein under investigation. Afficial function in the method of the protein under investigation. Afficial function in the protein under investigation. Afficial function in the protein under investigation.
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Zhang B;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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modifying a plants environmental stress. The transcription factor is encoded by environmental stress. The transcription factor is encoded by environmental stress tolerance gene derived from Arabidopsis thaliana. The transcription factors and the genes encoding them are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, papaya, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, onion, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, blueberry, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. These sequences are also used for modifying traits associated with environmental stress tolerance, such as freezing, chilling, heat, drought, water saturation, sailt, photoconditions, radiation and ozone. The transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                          The present amino acid sequence is Arabidopsis thaliana transcription factor homologue. This novel transcription factor is useful for modifying a plant's phenotype in desirable ways, such as
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                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                       Pred. No. 44;
Mismatches
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 Claim 4; Page 99-100; 116pp; English.
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plant structure; plant development.
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Keddie J;
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                                                                                                                                           DB 21; Length 268;
                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 68075.
                                                                                                                                          Score 6; DB 2]; Pred. No. 46; 0; Mismatches
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Matches 6; Conservative 0;
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PR 24-SEP-1999; 99US-015540.

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PR 13-CCT-1999; 99US-0155773.

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PR 25-OCT-1999; 99US-0161406.
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PR 29-OCT-1999; 90US-0161999.
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Search completed: January 31, 2002, 13:18:16 Job time: 177 sec

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4.837 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-176-500-36

US-08-471-052A-36

US-08-471-939-36

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US-08-471-98-86

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US-08-564-972-57

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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                Sequence
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT PAPLICATION DATE:
APPLICATION NUMBER: US/07/912,740D
FILING DATE: 13-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 1586-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                          US-09-315-444-82

US-08-461-3704-26

US-08-462-3908-26

US-08-462-3908-26

US-08-462-346-26

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US-09-277-54-9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 48, Application US/07912740D
Patent No. 5439815
GENERAL INFORMATION:
APPLICANT: FITTON, John E.
APPLICANT: TIMMS, David
ITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 100 NORTH GLEBE ROAD
CITY: ARLINGTON
STRATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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TOPOLOGY:
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Gaps

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., 0

Length 150;

DB 1;

42.9%; Score 6; DB 1 100.0%; Pred. No. 19; tive 0; Mismatches

Gaps

Length 346; 0; Indels

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WESULT 4

WESULT 4

Sequence 761, Application US/0815939A

Batent No. 6037135

GENERAL INFORMATION:

APPLICANT: Grey, Howard M.

APPLICANT: Gelis, Esteban

TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254

NUMBER OF SEQUENCES: 1254

NUMBER OF SEQUENCES: 1254

ADDRESSEE: Townsend and Townsend and Crew LLP

STREE: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

CITY: San Francisco

CITY: San Francisco

COMPUTER: IBM Compatible

OPERATING STYTEM: DOS

SOFTWARE: FastSEO for Windows Version 2.0

COMPUTER: IBM Compatible

OPERATING STYTEM: DOS

SOFTWARE: FastSEO for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/159, 339A

FILING DATE: 05-NOV-1993

CLASSIFICATION NUMBER: US 08/2027, 746

FILING DATE: 05-NAG-1993

APPLICATION NUMBER: US 08/23, 746

FILING DATE: 05-NAG-1993

APPLICATION NUMBER: US 08/23, 746

FILING DATE: 05-NAG-1993

ATTORNEY/AGENT NUMBER: 32, 76

FILING DATE: 06-NAG-1993

ATTORNEY/AGENT NUMBER: 32, 76

FILING DATE: 106-NAG-1993

ATTORNEY/AGENT NUMBER: 32, 76

FILING DATE: 36

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                             : INFORMATION FOR SEQ ID NO: 28
: SEQUENCE CHARACTERISTICS:
: LENGTH: 346 amino acids
: TYPE: amino acid
: TYPE: amino acid
: TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.9
Best Local Similarity 100
Matches 6; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111111
21 PGFQGE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 PGFQGE 11
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APPLICANT: Laid, breeth
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Young, Y. Tom
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Nail C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 283;
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                                                                                                                                                                                                                       GENERAL IN CONTROLL OF THOMAS
APPLICANT: Gaffney, Thomas
APPLICANT: Gaffney, Albert
APPLICANT: Gates, Krist
APPLICANT: Gates, Krist
APPLICANT: Ayad-Durieux, Yasmina
APPLICANT: Ayad-Durieux, Yasmina
APPLICANT: Philippsen, Peter
TITLE OF INVENTON: Fungal Target Genes and Methods
FILE REFERENCE: PBA-30908A
CURRENT APPLICANT: NUMBER: US/09/588,256
CURRENT FILIG DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 24
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%; Score 6; DB 4 Best Local Similarity 100.0%; Pred. No. 31; Batches 6; Conservative 0; Mismatches
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                              pplication US/09588256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSog for Wir CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZOP: 1012
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Ashbya gossypii
US-09-588-256-8
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249 TGLIDP 254
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ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                           Sequence 46, Application US/08564972
Patent No. 5843462
General Information
APPLICANT: Conti-Fine, B. M.
TITLE OF INVENTION: DIPTHERIA TOXIM EPITOPES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,972
FILING DATE: 30-NOV-1995
CLASSIFICATION: 424
PRIOR APPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600.344US1
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Patent No. 6150081
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAN HEERDE, GEORGE V.
VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE WOLF, FREDERIK A. MOOBROEK, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WERTEN, MARC W.T WIND, RICHELE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: single
|inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                               ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                 USA
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TOPOLOGY, 'in
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  2 GFOGE 6
                                                                                                                                                                                                                                                                                          STATE: M
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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                                                                                           Length 10;
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                                                                                                                                                                                                                                                                                                      Sequence 762, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Cells, Esteban.
TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: USes
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REJECOMMUNICATION:
                                                                                               DB 3;
                                                                                 35.7%; Scc. 100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids TYPE: amino acid
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                                                                                           Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                ; MOLECULE TYPE: peptide US-08-159-339A-761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide us-08-159-339A-762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
TOPOLOGY: linear
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ZIP: 94111-3834
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US-08-159-339A-762
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| GFQGE 9
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                                                                                                                                                                                                            Length 38;
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                                                                                                                                                                                                     Query Match 35.7%; Score 5; DB 1
Best Local Similarity 100.0%; Pred..No. 63;
Matches 5; Conservative 0; Mismatches
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US-08-199-331-36
Sequence 36, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
WOLECULE TYPE: peptide
US-08-176-500-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide
US-08-471-052A-36
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18 DPGFQ 22
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18 DPGFQ 22
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APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALLIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUTABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
FITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-176-500-36
US-08-176-500-36
Sequence 36, Application US/08176500
Patent No. 5498538
GENERAL INFORMATION:
APPLICANT: FOALKS, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS: 141
CORRESPONDENCE ADDRESS: 145
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COMPUTER: Flopy disk
COMPUTER: Elopy disk
COMPUTER: Elopy disk
COMPUTER: Elopy disk
COMPUTER: Elopy disk
COMPUTER: Elby Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/176,500
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/13,416
FILING DATE:
ATTORNEY APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/13,416
FILING DATE:
ATTORNEY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Formula OTHER INFORMATION: sequence NAME/KEY: MOD_RES LOCATION: (3)
OTHER INFORMATION: His or Met NAME/KEY: MOD_RES LOCATION: (6)
COCATION: (7)
COCATION: (7)
COCATION: (8)
COCATION: (8)
COCATION: (9)
COCATION: (9)
COCATION: (10)
COCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 35.7%; Score 5; DB 4
Best Local Similarity 100.0%; Pred. No. 41;
Best Local Similarity 0.0%; Mismatches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lesile
REGISTRATION NUMBER: 18,872
REEFERCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9090
                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11111
18 PGFQG 22
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Patent No. 5852167
GENERAL INFORMATION:
APPLICANT: RAY, B. K.
APPLICANT: ROWLNES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
COMPRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471;800
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                            Score 5; DB 2;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
  US 08/013,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/013,416
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                           NAME: Misrock, S. Leslie
REGISTRATION UNDABER: 18,972
REFERENCE/DOCKET UNDABER: 1101
TELECOMMUNICATION INFORMATION:
TELEFAN: 212 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                       FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity luv...
5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-939-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: unknown
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||
18 DPGFQ 22
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US-08-471-800-36
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APPLICANT: Kay, B. K.
APPLICANT: FOWINES, D. M.
APPLICANT: POWINES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/08471939
Patent No. 5844076
GENERAL INFORMATION:
APPLICANT: RAY, B. K.
APPLICANT: FOWLKES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 38;
                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AURENT APPLICATION DATA:
AUBLICATION NUMBER: US/08/189.331
FILING DATE: Concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Pennie & Edmonds
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/471,939
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%; Sco...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslins
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUICATION INFORMATION:
TELEPHONE: 212 790-9030
TELERX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.
                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-13.1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-189-331-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 DPGFQ 22
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US-08-471-939-36
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STATE:
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APPLICANT: MANFREDI, John
APPLICANT: MANFREDI, John
APPLICANT: MALEIN, CIRISTISTIST
APPLICANT: MURPHY, Andrew
APPLICANT: MURPHY, Andrew
APPLICANT: PAUL, JESEN
APPLICANT: TRUBHRART, JOSHUA
APPLICANT: TRUBHRART, JOSHUA
APPLICANT: TRUBHRART, JOSHUA
APPLICANT: TRUBHRART, JOSHUA
CORRESPONDENCE ADDRESSEE 119
CORRESPONDENCE ADDRESSEE 119
CORRESPONDENCE ADDRESSEE 119
CORRESPONDENCE ADDRESSEE 119
CONTRET: WAS A COMPACTED TO SERVE ADDRESSEE 119
CONTRET: WAS A COMPACTED TO SERVE ADDRESSEE 119
COMPACTER: THE PER PROBABLE FORM:
COMPACTER: THE PER PROBABLE FORM:
COMPACTER: THE PER PAUL CATION DATA:
COMPACTER: THE PER PAUL CATION DATA:
COMPACTE: TO SEE 1994
APPLICATION NUMBER: US 08/322,137
FILING DATE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
S. 08-46.1-598-86
S. Sequence 86, Application US/08461598
S. Setent No. 5876951
GENERAL INFORMATION:
APPLICANT: FOWIKES, Dana M. APPLICANT: RROACH, Jim
APPLICANT: KLEIN, Christine APPLICANT: KLEIN, Christine APPLICANT: WANFRED, John
APPLICANT: WANFRED, John
APPLICANT: WANFRED, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-464-531-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GELKL 14
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41 GELKL 45
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US-08-471-068-36
Sequence 36 Application US/08471068
Sequence 36 Application US/08471068
Sequence 36 Application US/08471068
Sequence 36 Application US/08471068
Sequence 36 Application US/08471068
SPAPLICANT: RAY, B. K.
APPLICANT: RAY, B. K.
APPLICANT: RAY, B. K.
APPLICANT: ROURES: 186
CORRESPONDENCE DADRESS: 186
STARE: New YORK
STARE: New YORK
COUNTRY: U.S.A.
ZIP: 1036-2711
COMPUTER: New YORK
STARE: New YORK
COMPUTER: New YORK
STARE: New YORK
STARE: New YORK
COMPUTER: New YORK
STARE: STARE: 110 NO: 36: STRANDENDESS: SIGGE
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STRANDENDESS: SIGGE
NG-08-471-068-36
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                                                                                                  Length 38;
                                                                                                                                                           0; Indels
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches
                                                                                                  Query Match 35.7%; Score 5; DB 2; Best Local Similarity 100.0%; Pred. No. 63; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-464-531-86
US-08-464-531-86
Sequence 86, Application US/08464531
Patent No. 5789184
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M.
APPLICANT: BROACH, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 DPGFQ 9
                                                                                                                                                                                                                                                                    11111
18 DPGFQ 22
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APPLICANT: TRUEHEARY, JOSHUA
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STREET: D.C.
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER LADUALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,598
FILING DATE: 05-JUN-1995
CLASSIFICATION 0435
PRIOR APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
PRIOR APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-JAN-1994
PRIOR APPLICATION NUMBER: US 08/14,431
FILING DATE: 31-MAR-1993
ATPORTEY-AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: COMPRES-2F
TELECOMMUNICATION NIFORMATION:
TELECOMMUNICATION NIFORMATION:
TELECOMMUNICATION NIFORMATION:
TELECOMMUNICATION NIFORMATION:
TELECOMMUNICATION NIFORMATION:
TELECOMMUNICATION NIFORMATION:
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TELECOMMUNICATION NIFORMATION:
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 86
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-461-598-86
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                                            Gaps
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                                              0; Indels
Query Match 35.7%; Score 5; DB 2; Length 67; Best Local Similarity 100.0%; Pred. No. 99; Matches 5; Conservative 0; Mismatches 0; Indels
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|||||| 41 GELKL 45

Search completed: January 31, 2002, 13:15:16 Job time: 97 sec

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GenCore version.4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

January 31, 2002, 13:20:20 ; Search time 78.64 Seconds (without alignments) 13.561 Million cell updates/sec Run on:

US-08-957-709-81 14 1 TGLIDPGFQGELKL 14 Perfect score:

Sednence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

0 Word size :

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_68:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

|   | Description    | dUTP pyrophosphata | hypothetical prote |        | ىد     | O)     |        | hypothetical 21.2 |        |        | ۵      | dihydropteroate sy | _      | probable protein k | PAS7 protein homol | testosterone-resis | collagen alpha 1(I | hydrogenase expres | protein F20N2.10 [ | apolipoprotein N-a | collagen alpha 2(V | ase AE | probable secreted | collagen alpha 1(I |        |        | alpha 2( |        | >      | ool division one |
|---|----------------|--------------------|--------------------|--------|--------|--------|--------|-------------------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|--------|--------|----------|--------|--------|------------------|
|   | ID             | WZBEP1             | T42968             | S55649 | T50123 | NRASSG | E86004 | H65134            | S64849 | A72568 | S73832 | A82849             | G64060 | A84831             | T42423             | A58583             | S16907             | E75031             | A96599             | B83148             | A5713:1            | D82739 | B81281            | CGHU4B             | CGMS4B | ССНОЗВ | A33526   | A54121 | 877568 | DMOAGE           |
|   | h DB           | 87 1               |                    | 9      |        |        | 9      | •                 | •      | 2      |        |                    |        |                    | 19 2               |                    |                    |                    | 5 2                |                    |                    |        | 1 2               |                    |        |        |          | 7      | ٣      | a                |
|   | Length         | 28                 | 28                 | 289    | 7      | 17     | 18     | 18                | 25     | 27     | 29     | 29                 | 29     | 30                 | 31                 | 34                 | 35                 | 36                 | 445                | 51                 | 63                 | 699    | 1041              | 1669               | 1669   | 1670   | 1707     | 174    | e      | ٧                |
| æ | Query<br>Match | 100.0              | 78.6               | •      | ٠      | 42.9   | 42.9   | 42.9              | 42.9   |        | 42.9   |                    | •      |                    | 42.9               | 42.9               |                    |                    | ٠                  | 42.9               | •                  | •      | 42.9              |                    |        | •      | 42.9     | ς.     | •      | 35 7             |
|   | Score          | 14                 | 11                 | 7      | 9      | 9      | 9      | 9                 | 9      | ø      | ø      | 9                  | 9      | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9      | 9                 | 9                  | 9      | 9      | 9        | 9      | 2      | ď                |
|   | Result<br>No.  | -                  | 7                  | ю      | 4      | Ŋ      | 9      | 7                 | 80     | 6      | 10     | 11                 | 12     | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21     | 22                | 23                 | 24     | 25     | 26       | 27     | 28     | 20               |

| hypothetical prote | cytochrome P450 (c | hypothetical prote | DNA-binding protei | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | probable dioxygena | hypothetical prote | hypothetical prote | brain and muscle A | hypothetical prote | hypothetical prote | universal stress p | universal stress p |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 383795             | 535170             | T11975             | ONZRHM             | 537190             | 264543             | E75074             | H71090             | 75334              | 12857              | A69268             | PC4289 .           | T16510             | E86759             | 164096             | 382368             |
| 2 B                | 2 83               | 2 T]               | 1<br>D             | 2 83               | 2<br>C             | 2 E7               | 2 H7               | 2 F.               | 2 TJ               | 2 A6               | 2 PC               | 2 TJ               | 2 E                | 2 A6               | 2<br>D8            |
| 29                 | 65                 | 72                 | 06                 | 91                 | 95                 | 102                | 102                | 103                | 111                | 112                | 113                | 118                | 135                | 141                | 141                |
| 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               |
| 2                  | 2                  | S                  | ស                  | 2                  | 2                  | ហ                  | ß                  | ഹ                  | Ŋ                  | 2                  | Ŋ                  | ഗ                  | Ŋ                  | S                  | 2                  |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 4.2                | 43                 | 44                 | 45                 |

## ALIGNMENTS

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RESULT
WZBEP1
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| 11)                     |                      |
|-------------------------|----------------------|
| (strain                 |                      |
| -                       |                      |
| herpesvirus             |                      |
| saimiriine herp         |                      |
| ١                       | ,                    |
| $\overline{}$           |                      |
| 1.23                    |                      |
| .6.1.23                 | Court into           |
| 3.6.1.23)               | Otto Care            |
| (EC 3.6.1.23            | borre in a contract  |
| hosphatase (EC 3.6.1.23 | Curing Consolination |
| ohosphatase (EC 3       | ** . * . *           |
| ohosphatase (EC 3       | ** . * . *           |
| (EC 3                   | ** . * . *           |

C;Species: sainiriine herpesvirus 1 A;Note: host Sainiri sciureus (common squirrel monkey) C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999

C; Accession: G36811 R; Albrecht, J.

submitted to the EMBL Data Library, January 1992 A. Description: Primary structure of the herpesvirus saimiri genome. A; Reference number: A36806 A; Accession: G36811

A. Molecule type: DNA
A. Residues: 1-287 < ALB>
A. Residues: 1-287 < ALB>
A. Residues: 1-287 < ALB>
A. Crossreferences: GB. X64346; NID: g60320; PIDN: CAA45677.1; PID: g60375
A. Crossreferences: GB. X647-5058, 1992
J. Virol. 66, 5047-5058, 1992
A. Title: Primary structure of the herpesvirus saimiri genome.
A. Reference number: A37309; MUID: 92333688
A. Contents: annotation: possible protein-coding frames
A. Note: neither amino acid nor nucleotide sequence is given

C; Superfamily: herpesvirus dUTP pyrophosphatase C; Keywords: hydrolase

Gaps ; Query Match 100.0%; Score 14; DB 1; Length 287; Best Local Similarity 100.0%; Pred. No. 6e-08; Matches 14; Conservative 0; Mismatches 0; Indels

ö

1 TGLIDPGFQGELKL 14 δy

74 TGLIDPGFOGELKL 87 qq

RESULT

T42968

hypothetical protein - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
A;Variety: strain 73
C;Bace: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000
C;Accession: T42968
R;Albrecht, J.C.; Fleckenstein, B.
B;Albrecht, J.C.; Fleckenstein, B.
B;Daritted to the EMBL Data Library, August 1998
A;Description: Primary structure of the herpesvirus ateles genome.
A;Reference number: 222274

A, Accession: T42968
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1.287 cALB>
A, Cross-references: EMBL: AF083424; PIDN: AAC95579.1

QQ

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hypothetical protein yrfE [imported] - Escherichia coli (strain 0157:H7)
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Accession: E86004
C; Accession: E86004
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A; Tiller: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Accession: E86004
A; Accession: E86004
A; Reference number: A84480; MUID:21074935; PMID:11206551
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-186 <STO>
A; Experimental source: strain 0157:H7, substrain BDL933
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Genetics: A; Genetics: A; Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Genetics: Gen
ribonuclease alpha-sarcin (EC 3.1...) precursor - Aspergillus giganteus C. Species: Aspergillus giganteus constens: Aspergillus giganteus constens and a papergillus constens and a papergillus constens a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus constens and a papergillus and a papergillus constens and a papergillus and a pa
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A; Molecule type: protein
A; Molecule type: 28-177 CARC>
C; Comment: Alpha-sarcin is specific for purines in both single- and double-stranded
the 60S subunit of ribosomes.
C; Genetics:
A; Gene: Sar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-177 < < CKA>
A; Cross-references: 1517 < < CKA>
A; Cross-references: 18: D13704; GB: D00516; NID: 9217810; PIDN: BAA02863.1; PID: 9217811
B; Sacco, G.; Drickamer, K.; Wool, I.G.
J. Biol. Chem. 258, 5811-5818, 1983
A; Title: The primary structure of the cytotoxin alpha-sarcin.
A; Reference number: A00802; MUID: 83213554
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C;Superfamily: ribonuclease Tl
C;Superfamily: ribonuclease; extracellular protein; hydrolase; toxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-177/Froduct: ribonuclease alpha-sarcin #status experimental <WAT>
F;38-177/Froduct: ribonuclease alpha-sarcin #status experimental <WAT>
F;38-177,123,103-159/Disulfide bonds: #status predicted
F;75,77,123,148,164/Active site: Tyr, His, Glu, Arg, His #status predicted
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Tebol23
Peroxisomal targeting signal 2 receptor (pts2 receptor) peroxin-7 [imported] - fission peroxisomal targeting signal 2 receptor (pts2 receptor) peroxin-7 [imported] - fission c; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Accession: T50123
B; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A; Reseger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A; Reseger, R.; Barris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A; Accession: T50123
A; Accession: T50123
A; Accession: T50123
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residuas: 1-24 SEEP
A; Cross_references: EMBL: ALIS7734; PIDN: CAB75780.1; GSPDB:GN00066; SPDB:SPAC1834.12
A; Experimental source: strain 972h(-); cosmid c1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
355564
Geoxyuridine triphosphatase 54 - equine herpesvirus 2
Geoxyuridine triphosphatase 54 - equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: $5564
M. R.F. Marson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A.Title: The DNA sequence of equine herpesvirus 2.
A.Accession: $5564
A.Accession: $5564
A.Accession: $5564
A.Accession: $5564
A.Accession: $5564
A.Accession: $5564
A.Accession: $5564
A.Accession: $5564
A.Accession: $6804
A.Seperiminary: nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
A.Residues: 1-289 <TEL>
A.Corsos references: $68120824; NID:g695172; PIDN:AAC13842.1; PID:g695227
A.Corsos references: $68120824; NID:g695172; PIDN:AAC13842.1; PID:g69527
A.Sorsos references: $68120824; NID:g695172; PIDN:AAC13842.1; PID:g69527
A.Sorperfamily: herpesvirus dUTP pyrophosphatase
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                                                                                                                                                                                                                              Length 287;
                                                                                                                                                                                                                              Ouery Match 78.6%; Score 11; DB 2; Length 287 Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 11; Conservative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 2.6;
Conservative 0; Mismatches
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100.0%; Pred. No. 2.1;
iive 0; Mismatches
            A; Experimental source: strain 73
C; Superfamily: herpesvirus dUTP pyrophosphatase
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Best Local Similarity 100.
Matches 7; Conservative
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A.Gene: SPDB:SPAC1834.12
A.Map position: 1
C.Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGLIDPGFOGE 11
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Best Local Similarity
Matches 6; Conserv
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77 TGLIDPG 83
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2 GLIDPG

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hypothetical protein APE1827 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A72568
R;Kawarabayssi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Asro A; Reference number: A72456; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Accession: S73832
R.Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420, 4449, 1996
A.Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon A.Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon A.Reference number: S73327; MUID:97105885
A.Accession: S73832
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Nolecule type: DNA
A.Residues: 1-294 <HIM>A.Residues: 1-294 <HIM>A.Residues: 1-294 <HIM>A.Note: Lhe nucleotide sequence was submitted to the EMBL Data Library, November 1996 C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80830.1; PID:d1044616; PID:g
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 10-Dec-1999
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R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nu Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID: 20365717
A; Note: for a complete list of authors see reference number A59328 below A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Mycoplasma pneumoniae (strain ATCC 29342)
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C;Superfamily: Mycoplasma hypothetical protein MG237
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A;Molecule type: DNA
A;Residues: 1-272 <KAW>
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231 GFOGEL 236
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A,Residues: 1-250 <OBE)
A;Cross-references: EMBL:273194; NID:91360327; PIDN:CAA97545.1; PID:e245773; PID:9136032
A;Experimental source: strain $288C
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C'Species: Saccharomyces cerevisiae
C'Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 29-oct-1999
C'Accession: S64849; S64844
R'Obermaier, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64845
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    yeast (Saccharomyces cerevisiae)

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Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches
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100.0%; Pred. No. 22;
Live 0; Mismatches
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hypothetical protein YLR022c

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2 GLIDPG 7

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A;Molecule type: DNA
A;Residues: 135-250 <VAN>
A;Cross-references: EMBL:273194; MIPS:YLR022c
A;Experimental source: strain \$288C
C;Genetics:

A; Map position: 12R

Conservative

Best Local Similarity Matches 6; Conserv

Query Match

111111 TGLIDP 220

215

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1 TGLIDP 6

R; Vandenbol, M.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, A; Reference number: S64742

A; Accession: S64844

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A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Recession: A84420; MUID:20083487
A,Accession: A84831
A,Accession: A84831
A,Accession: A84831
A,Accession: AB4831
A,Accession: ACSA
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Ross references: GB:AE002093; NID:g2651301; PIDN:AAB87581.1; GSPDB:GN00139
C,Genetics: AC24,0550
A,Role position: 2
C,Superfamily: Aquifex aeolicus serine/threonine-specific protein kinase; protein kin
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C:Species: Mas musculus (house mouse)
C:Decies: Nas musculus (house mouse)
R:Kruecken, J.; Schmitt-Wrede, H.P.; Markmann-Mulisch, U.; Wunderlich, F.
B:Kruecken, J.; Schmitt-Wrede (H.P.; Markmann-Mulisch, U.; Wunderlich, F.
A;Title: Novel gene expressed in Spleen cells : mediating acquired testosterone-resista
A;Accession: A58883
A;Molecule type: mRNA
A;Residues: 1.346 < KRUV
A;Residues: 1.346 < KRUV
A;Cross-references: GB:Y08026; NID:g1550784; PIDN:CAA69283.1; PID:e266428; PID:g15507
A;Experimental source: Spleen cell
C;Comment: This protein is a plasma membrane protein with two membrane-spanning domai chabaudi malaria.
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42.9%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches
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F;148-167/Domain: transmembrane #status
F;320-335/Domain: transmembrane #status
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18 PGFQGE 23
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A; Residues: 1-298 <a href="https://doi.org/10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-10.1007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-2007/pnc.2007-
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G64060
conserved hypothetical protein H10301 - Haemophilus influenzae
C.Species: Haemophilus influenzae
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C.Species: Haemophilus H.C.; Fine, L.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. R.Fleischmann, J.D.; Scotlar, R.C.; Fine, L.D.; Fittler, L.D.; Fultmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A.Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A.Reference number: A64000; MuID:95350630
A.Accession: G64060
A.Accession: G64060
A.Accession: G64060
A.Status: nucleic acid sequence not shown; translation not shown
A.Residues: 1-299 <TIGRS
A.C.Scoss references: GB:U32716; GB:L42023; NID:g1573268; PIDN:AAC21966.1; PID:g1573270; TA:Experimental source: strain Rd KW20
C; Superfamily: hypothetical protein b0658
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A48431
Probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-eb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: A84831
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.;
Existant M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Micrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
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Pred. No. 26;
0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 26;
Best Acthes 6; Conservative 0; Mismatches
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Local Similarity 100.0%; P
es 6; Conservative 0;
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| cal                                                                                  | PGF         | PGFQGE |  |
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Q9iad4 xenomystus

Q91g00 arabidopsis Q9c5n4 arabidopsis Q9fks9 arabidopsis

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Q91wjl oryza sativ
Q9cpi4 pasteurella
Q9cpi4 pasteurella
Q9rbk2 xanthomonas
Q9462 caulobacter
Q9865 penicillium
Q91983 gallus gall
Q9mt5 campylobact
Q9vx90 drosophila
Q9ut9 leishmania
Q9ut9 leishmania
Q9ut9 drosophila
Q946w9 drosophila
Q946w9 drosophila
Q94f homo sapien
Q964c bomo sapien
Q964c strongyloce
P6530 alcaligenes
Q9uml5 homo sapien
Q96dy strongyloce
P6530 alcaligenes
Q9uml5 homo sapien
           069141 streptococc
099xv1 streptococc
091tt4 arabidopsis
09fb00 streptococc
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Albrecht J.-C., Fleckenstein B.;
Albrecht Structure of the Herpesvirus Ateles Genome.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083424; AAC95579.1;
InterPro: IPR001428; dUTPase.
Pfam: PF00692; dUTPase: 1.
SEQUENCE 287 AA, 32154 MW; 3A819076115FC280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
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Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Q9A462
Q9P8D5
Q9I9K3
                    Q99XV1
Q9LTT4
Q9FB00
Q9LG00
Q9C5N4
Q9FKS9
                                                                                               Q9CPI4
Q9PER1
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Q9V6W9
Q9H4R9
Q9BQT2
Q26640
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Ateline herpesvirus 3.
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Q9bz45 homo sapien
Q9ph55 xylella fas
Q22879 arabidopsis
Q9be81 macaca fasc
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Q66656 equine herp
P88991 murid herpe
Q91n05 arabidopsis
Q9srr8 arabidopsis
Q65243 african swi
Q65199 african swi
P87063 aspergillus
Q9ky25 streptomyce
P70224 mus musculu
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Q9sqq6 arabidopsis
Q9uzb3 pyrococcus
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Milligan S., Efstathiou S., Stewart J.P., Nash A.A., Davison A.J.; Genetic content of murine gammaherpesviruses."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; X09660; CAA70269.1; -- EMBL; W19553; AmB66412.1; -- EMBL; AF105037; AAF19318.1; -- EMBL; PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpase. PF00692; duTpas
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STRAIN-WUMS, AND G2.4;
MEDLINE-9736649; PubMed-9223479;
Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E., Dal Canto A.J., Speck S.H.;
"Complete sequence and genomic analysis of murine gammaherpesvirus 68.";
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MEDILNE-3135774; PubMed-9191940;
Mackett M., Stewart J.P., de V Pepper S., Chee M., Efstathiou S.,
Nash A.A., Arrand J.R.;
"Genetic content and preliminary transcriptional analysis of a
representative region of murine gammaherpesvirus 68.";
J. Gen. Virol. 78:1425-1433(1997).
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Mackett M., Stewart J.P., Pepper V., Chee M., Efstathiou S.,
Nash A.A., Arrand J.R.;
J. Gen. Virol. 0:0-0(0).
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                                                                                                                                                                                                                     Telford E.A.R.;
Submitted (FEB-195) to the EMBL/GenBank/DDBJ databases.
EMBL; U20824; AAC13842.1;
InterPro; IRF001428; duTPase.
Pfam: PF00652; duTPase;
Pfam: PF00652; duTPase;
SEQUENCE 289 AA; 32957 MW; 6FCEB405630FA996 CRC64;
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murid herpesvirus 4.
furuses: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
NCBI_TaxID=33708;
    Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
NCBL_TaxID=82831;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYURIDINE TRIPHOSPHATASE.
                                                                                   SEQUENCE FROM N.A.
MEDLINE-95302501; PubMed=7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J.,
"The DNA sequence of equine herpesvirus 2.";
J. Mol. Blol. 249:520-528(1995).
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SEQUENCE FROM N.A.

Chart R., Shinn P., Barooks S., Buehler E., Chao O., Johnson-Hopson C.,

Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,

Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,

Theologis A., Ecker J.,

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ACQ26875; AAF79825.1; -.

SEQUENCE 125 AA, 13865 MW; EE7040BDJ98C3935 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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42.9%; Score 6; DB 10; Length 125;
Best Local Similarity 100.0%; Predc. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels
Length 299;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Query Match 50.0%; Score 7; DB 12; Best Local Similarity 100.0%; Pred. No. 6.3; Matches 7; Conservative 0; Mismatches
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN=CV. COLUMBIA;
LIN X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F2103 genomic sequence.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009853; AAR02167.1;
HSSP; P00259; 1GPX.
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STRAIN-MALAWI LIL20 /1;
MEDLINE-94292916; PubMed-8021596;
Dixon L.K., Twigg S.R.F., Baylis S.A., Vydelingum S., Bristow C., Hammond J.M., Smith G.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vydelingum S., Baylis S.A., Bristow C., Smith G.L., Dixon L.K.; "Duplicated genes within the variable right end of the genome of pathogenic isolate of African swine fever virus."; J. Gen. Virol. 74:2125-2130(1993).
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SEQUENCE 162 AA; 17872 MW; FFD71331454A5737 CRC64;
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                                                                                                                                                            Last sequence update)
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Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
African swine fever-like viruses.
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Pred. No. 40;
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MEDLINE=94014996; Pubmed=8409937;
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EMBL; X71982; CAA50839.1; -.
InterPro; IPR001428; dUTPase.
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F2103.19 PROTEIN.
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116 IDPGFQ 123
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75 TGLIDP 80
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Rodriguez J.F., Vinuela E.;
"Immune protection conferred by the baculovirus-related glycoprotein
of Thogoto virus (Orthomyxoviridae).";
                                                                                Gaps
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Gen. Virol. 0:0-0(0).
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MEDLINE-90219205; PubMed-2325203;
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La Vega I., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: family 360.";
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MEDLINE=90219204; PubMed-2325202;
Almendral J.M., Almazan F., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: family 110.";
J. Virol. 64:2064-2072(1990).
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                     Length 162;
                                                                                Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African swine fever virus (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
African swine fever-like viruses.
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                     Score 6; DB 12; Pred. No. 41; 0; Mismatches
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42.9%; Sco.
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MEDLINE=94233765; PubMed=8178480;
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Virology 178:301-304(1990).
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MEDLINE-93281390; PubMed-8506138;
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"African swine fever virus encodes two genes which share significant homology with the two largest subunits of DNA-dependent RNA
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Virology 188:938-947(1992).
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of African swine fever virus.";
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BEDLINE-$4091056; PubMed=8266720;

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MEDLINE-94123986; PubMed-8293992; Rodriguez J.K., Vinuela E., Salas M. Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M. The DNA polymerase-encoding gene of African swine fever virus: sequence and transcriptional analysis."; Gene 136:103-110(1993).
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MEDLINE-92260660; PubMed=1583732;
MEDLINE-92260660; PubMed=1583732;
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"African swine fever virus guanylyltransferase.";
Virology 193:319-328(1993).
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MEDLINE=93174976; PubMed=8438592;
Tanez R.J., Vinuela E.;
Tanez R.J., Mine Ever virus encodes a DNA ligase.";
Virology 193:531-536(1993).
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches
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Kruecken J., Scmitt-Wrede H.P., Markmann-Mulisch U., Wunderlich F.;
"Novel gene expressed in spleen cells mediating acquired testosterone-
resistent immunity to Plasmodium chabaudi malaria.";
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EMBL; AL356892; CAB92841.1; -.
Hypothetical protein.
SEQUENCE 245 AA; 27432 MW; EAE5956CD22B69DE CRC64;
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STAILA-CSTEL/10, AND 129/OLA; TISSUE-SPLEEN;

MEDLINE-9937081; Pubmed-10446218;

Krucken J., Stamm O., Schmitt-Wrede H.P., Mincheva A., Lichter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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EMBL; AJ133125; CAA653101.1; -.
MGD; MGI:109368; Imap38.
SEQUENCE 246 AA; 25867 MW; 3C97194EA7AA9D98 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
IMMUNE ASSOCIATED PROTEIN 38.
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100.0%; Pred. No. 60;
Live 0; Mismatches
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100.0%; Pred. No. 61;
live 0; Mismatches
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SEQUENCE FROM N.A.
STRAIN=C57BL/10; TISSUE=SPLEEN;
MEDLINE=97148595; Pubmed=920038;
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MEDLINE=97367962; PubMed=9224729;
Wirth J., Martinez del Pozo A., Mancheno J.M., Martinez-Ruiz A.,
Mirth J., Onderra M., Gavilanes J.G.;
"Sequence determination and molecular characterization of gigantin,
cytocoxic protein produced by the mould Aspergillus giganteus IFO
                                                                                                                                                                                                                                                                                                                         Aspergillus giganteus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
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Brown S.P., Harris D.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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231EE906F08E46A0 CRC64;
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01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-ocr-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 27.4 KDA PROTEIN.
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100.0%; Pred. No. 45;
Live 0; Mismatches
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EMBL; Y08457; CAA69713.1; -.
HSSP; P04389; 1AQZ.
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SEQUENCE 177 AA; 19827 MW;
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(TrEMBLrel. 05, Last sequence update)
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1-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TY-2001 (TrEMBLrel. 17, Last annotation update)
DIHYDROPTEROATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                            298 AA.
                                                                                                                                                            PRT;
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InterPro; IPR000489; DHPS.
Pfam; PF00809; DHPS; 1.
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PROSITE; PS00792; DHPS_1; 1.
PROSITE; PS00793; DHPS_2; 1.
                                                                                                                                                            PRELIMINARY;
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SEQUENCE 298 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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       119 LIDPGF 124
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022879;
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022879
ID 022879
AC 022879
DT 01-JAN
DT 01-JUN
                                                                                              RESULT 13
Q9PH55
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MEDINE-9310339; PubMed-10382966; ... Manazaki S., Haikawa Y.,

MEDINE-9310339; PubMed-10382966; ... Manazaki S., Haikawa Y.,

Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,

Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,

Takamiya M., Mauda S., Punahashi T., Tanaka T., Kudoh Y.,

Namazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,

Makamura Y., Nomura N., Sako Y., Kikuchi H.;

"Complete genome sequence of an aerobic hyper-thermophilic

Crenarchaeon, Aeropyrum pernix Kl.";

DNA Res 6:83-101(1999).

EMBL. APUROG62: BAR60830.1; --

EMBL. APUROG62: BAR60830.1; --

SEQUENCE 272 AA: 29959 MW: 740562B65DF3ZA96 CRC64;
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Vertebrata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
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Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
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Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels
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42.9%; Score 6; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels
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09B245; 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
BA307L3.1 (SIMILAR TO NUCLEAR PROTEIN NP95) (FRAGMENT).
                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 30.0 KDA PROTEIN APE1827.
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SEQUENCE FROM N.A.
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NCBI_TaxID=56636;
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231 GFQGEL 236
111111
21 PGFQGE 26
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Gaps ; 0

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PUTATIVE SERINE/THREONINE PROTEIN KINASE.

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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                   RA SQUENCE FROM N.A.

RA Rounsley S.D., Ketchum K.A., Lin X., Crosby M.L., Brandon R.C., RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., R. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

R. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

C.C. = SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AC002336; Arath;3248;26527.

DR Mendel; 26527; Arath;3248;26527.

DR NEOFPRO; IPR000299; Submisse: I. -

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Serime/threonine-protein kinase; Transferase.

SFOITENCE 303 AA; 34936 MW; ICF1723CA7462A89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 36.5 KDA PROTEIN.
MAGGGA fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macharyota Metaras (Crab eating macaque) (Cynomolgus monkey).
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecidae; Macaca
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB056765; BAB39313.1;
Hypothetical protein.
SEQUENCE 321 AA; 36464 MW; IDEDOCCOE0453E2E CRC64;
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100.0%; Pred. No. 74;
tive. 0; Mismatches
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tive 0;
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Best Local Similarity 100.(
Matches 6; Conservative,
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Best Local Similarity 100.
Matches 6; Conservative
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SEQUENCE FROM N.A.
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26 PGFQGE 31
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Search completed: January 31, 2002, 13:37:54 Job time: 179 sec

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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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RNAS_ASPGI
NUDE_ECOLI
YL22_YEAST
Y237_MYCPN
CORC_PASHU
CORC_PASHU
CORC_PASHU
CORC_PASHU
ENT_PSEAE
CA28_HUMAN
SIPI_HUMAN
CA14_MOUSE
CA34_HUMAN
CA14_MOUSE
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BH_RHIME
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ATPD_CYACA
DCD_MYCTU
DCD_STRCO
PIC2_AGRTU
DCD_METTH
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Maximum DB seq length: 2000000000
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                                                                                                         January 31,
                                                                            protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                 Scoring table:
                                                                               OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                              Word size
                                                                                                                                                                                                      sedneuce:
                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                                         Title:
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                                                                                                              Run
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34 5 35.7 246 1 NCAP_SFSV Q9935 homo saplen 36 5 35.7 250 1 YC97_HUMAN Q9935 homo saplen 36 5 35.7 253 1 PCRB_THEAC Q9935 homo saplen 37 5 35.7 254 1 FAEI_ECOLI Q06398 oryza sativ 38 5 35.7 254 1 GTXC_ONYSA Q06398 oryza sativ 40 5 35.7 254 1 GTXC_ONYSA Q06398 oryza sativ 41 5 35.7 263 1 KKA9_STRRI P75981 escherichia 41 5 35.7 264 1 PSBO_SYNEN P55221 synechococc 43 5 35.7 272 1 PSBO_SYNEN P55221 synechococc 44 5 35.7 272 1 NUFM_NEUCR P4919 neurospora 45 35.7 282 1 AQUA_ATRCA P42767 atriplex ca-
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# ALIGNMENTS

| YESULI     |                                                                                                                                            |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------|
| Ĕ,         | OUT_HSVSA                                                                                                                                  |
| 3 5        | SIANDAND, FAI, 201                                                                                                                         |
| 2 5        | 1993 (Rel. 25, Creat                                                                                                                       |
| また         | 01-APR-1993 (Rel. 25, Last sequence update)<br>15-DRC-1998 (Rel. 37, East annotation update)                                               |
| E          | E 5'-TRIPHOSPHAT                                                                                                                           |
| 巴          | (DUTPASE) (DUTP PYROPHOSPHATASE).                                                                                                          |
| Z i        | 54 OR EDRE3.                                                                                                                               |
| ກຸ         | Herpesvirus Salmiri (Strain 11)<br>Virusos, Ashub virusos no BND stans Herbesviridae:                                                      |
| 3.8        | Viluses, usbun viluses, no mm stayt, mirros interest<br>Gammaherpesvirinae; Rhadinovirus.                                                  |
| XC         | NCBI_TaxID=10383;                                                                                                                          |
| RN.        | [1]                                                                                                                                        |
| 2 Z        | SEQUENCE FROM N.A.<br>Meditne=92333689: DibMed=1321287:                                                                                    |
| R A        | Albrecht JC., Nicholas J., Biller D., Cameron K.R., Biesinger B.,                                                                          |
| ΚĀ         | Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,                                                                         |
| RA<br>E    | Honess R.W.;                                                                                                                               |
| RI.        | J. Virol, 66:5047-5058(1992).                                                                                                              |
| RN         | [2]                                                                                                                                        |
| КÞ         | SEQUENCE FROM N.A.                                                                                                                         |
| Z i        | MEDLINE=92230228; PubMed=131495/;                                                                                                          |
| Y E        | NICHOLAS U., Calmierton N.K., Coleman n., Newman C., Nomes N.F.,<br>"Analysis of mucleotide sequence of the rightmost 43 kbp of            |
| E E        | herbesvirus saimiri (HVS) L-DNA: general conservation of genetic                                                                           |
| RT         |                                                                                                                                            |
| RL         | Virology 188:296-310(1992).                                                                                                                |
| ပ္ပ        | -!- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT                                                                         |
| ຍ          | PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES                                                                            |
| ပ္ပ (      | AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUIF SO THAI                                                                           |
| ပ္ပ        | URACIL CANNOT BE INCORPORATED INTO DIMA.                                                                                                   |
| ე <u>წ</u> | -:- CATALILE CALIVILI: DUE + n(Z)O - DOME + FINCENCIE.<br>-:- CATALILE PRIORIC TO THE DITPASE FAMILY.                                      |
| )<br>      |                                                                                                                                            |
| ပ္ပ        | This SWISS-PROT entry is copyright. It is produced through a collaboration                                                                 |
| ည          | between the Swiss Institute of Bioinformatics and the EMBL outstation                                                                      |
| ပ္ပ (      | the European Bioinformatics Institute. There are no restrictions on the                                                                    |
| ပ္ပင္      | use by non-profit institutions as iong as its concent is in no man modified and this statement is not removed. Usage by and for commercial |
| ) <u>C</u> | minimizer a license agreement (See http://www.isb-sib.ch/announce,                                                                         |
| 20         | or send an email to license@isb-sib.ch).                                                                                                   |
| ပ္ပ        |                                                                                                                                            |
| DR         | EMBL; X64346; CAA45677.1;                                                                                                                  |
| DR.        | PIR: (336811; WZBEP1.                                                                                                                      |
| DR         | InterPro; IPR001428; dUTPase.                                                                                                              |
| DR         | Pfam; Pr00692; dUTPase; 1.                                                                                                                 |
| X C        | Hydrolase; Nucleotide metabolism                                                                                                           |
| g          | SEQUENCE 28/ AA; 3230/ MW; 33604330/42/4611 CNCO+,                                                                                         |

- u - s >- - >

Length 287;

Score 14; DB 1; I Pred. No. 1.9e-08; 186 AA

STANDARD;

us-08-957-709-81.rsp

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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-AUG-2001 (Rel. 40, Last annotation update)
ADP COMPOUNDS HYDROLASE NUDE (EC 3.6.1.-).
                      169 QGELKL 174
     9 QGELKL 14
                                                                                        NUDE_ECOLI
P45799;
                                                                RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 28-177.

MEDLINE-83213554; PubMed-6343394;

MEDLINE-83213554; PubMed-6343394;

MEDLINE-83213554; PubMed-6343394;

The primary structure of the cytotoxin alpha-sarcin.";

J. 840.1 Chem. 228:5811-5811-5818(1983).

I- DOUBLE-STRANDED RNA. ITS TOXIC ACTION ON EUKARYOTIC CELLS IS THE RESULT OF CLEAVAGE OF A SINGLE PHOSPHODIESTER BOND IN THE 60S SUBUNIT OF RIBOSOMES.

I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE PHOSPHODIESTER LINKAGE BETWEEN GUARACYTIC POSITION IN THE 28S RNA FROM RAT RIBOSOMES.

IN THE 28S RNA FROM RAT RIBOSOMES.
     Gaps
                                                                                                                                                                                                  Aspergillus giganteus.
Makaryota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
MCBI_TaxID=5060;
    .
0
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-90245591; Pubmed-2336369;
Oka T., Natori Y., Tanaka S., Tsurugi K., Endo Y.;
"Complete nucleotide sequence of cDNA for the cytotoxin alpha sarctin.";
    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e; Protein synthesis inhibitor; Signal.
27
177 RIBONUCLEASE ALPHA-SARCTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.9%; Score 6; DB 1; Length 177; Best Local Similarity 100.0%; Pred. No. 7; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MDH 18894.
Whendt S., Felske H., Henze P.P., Ulbrich N., Stahl U.,
Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBONUCLEASE ALPHA-SARCIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
19724 MW; 6C711D9482DC9DD1 CRC64;
                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
RIBONUCLEASE ALPHA-SARCIN PRECURSOR (EC 3.1.27.10).
SAR.
                                                                                                                177 AA
 0; Mismatches
                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 18:1897-1897(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D13704; BAA02863.1; -. EMBL; X6070.0; -. PIR; S12582; NRASSG. PIR; S21866; S21866. PIRSSP. P04389; 1AQZ. Hydrolase; Protein symptoclase; Nuclease; Protein symptoclase; Nuclease;
14; Conservative
                                                                                                                STANDARD;
                                   74 TGLIDPGFQGELKL 87
                         1 TGLIDPGFQGELKL 14
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177 AA;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                               RNAS_ASPGI
ID RNAS_ASPGI
AC P00655;
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SEQUENCE
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Matches
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The Factor of the North Service of the North Service of Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

REDLINE-98123081; bubMed-9452430;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Dunn C.A., Bessman M.J.;

RAD O'Handley S.F., Frick D. No., Prick D. No
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                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-KIZ. 7 MG1657.
STRAIN-KIZ. 7 MG1657.
STRAIN-KIZ. 7 MG1657.
SIBLATENE-97426617.
SIBLATENE F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                  Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Hydrolase; Magnesium, Complete proteome.
BO 101 NUDIX BOX.
SEQUENCE 186 AA; 21153 MW; D959AD8ECF73FCC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 42.9%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18997; AAA58194.1; --
EMBL; AE000415; AAC76422.1; --
ECOGENE; EG12926; nudE.
InterPro; IPR000086; NUDIX_hydrolase.
Pfam; PF000293; mutr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION
                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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NUDE OR B3397
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                                                                                                                                           Escherichia
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Gaps

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and the EMBL outstation

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6; Conservative
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      170 PGFQGE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae Rd."
                                                                                                                                                                                                                                                                                                                               6 PGFQGE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORC OR HI0301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORC_HAEIN
Q57368;
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
CORC_HAEIN
00000008¥8000008
                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The First are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 28.3 KDA PROTEIN IN PPRI-SNF7 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 134-250 FROM N.A. Vandenbol M., Portetelle D., Hilger F.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.-:- SIMILARITY: BELONGS TO THE UPF0023 FAMILY.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Obermaier B., Piravandi E., Rinke M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein.
250 Aa; 28283 MW; EFC799ADEFF73E0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL PROTEIN MG237 HOMOLOG (F10_ORF294).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6; DB 1;
Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%; Scot.
100.0%; Pred. No.
                 250 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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SGD; S0004012; YLR022C.
InterPro; IPR002140; UPF0023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01172; UPF0023; 1.
ProDom; PD009796; UPF0023; 1.
PROSITE; PS01267; UPF0023; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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P75455;
               YL22_YEAST
Q07953;
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Y237_MYCPN
AC P7545M, AC P7545M, AC P7545M, AC P754CM, AC P764CM, AC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation between the Bropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial
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between the Swiss Institute of Bioinformatics and the EMBL outstative the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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InterPro; IPR000644; CBS.
Pfam; PF00571; CBS; 2.
SMART; SM00116; CBS; 2.
Magnesium; Cobalt; Transport; CBS domain; Repeat; Complete proteome.
73 129 CBS 1.
CBS 2.
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-!- FUNCTION: PLAYS A ROLE IN THE TRANSPORT OF MAGNESIUM AND COBALT IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE UPF0053 FAMILY.
-!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 294;
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                                                                                                                                                                                                                                                                EMBL; AE000050; AAB96154.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 294 AA; 34135 MW; DB9F1896E24073AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM AND COBALT EFFLUX PROTEIN CORC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%; Score 6; DB 1; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA
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EMBL, ABC06144; ARK03117.1; ...

EMBL, ABC0644, CBS.

SWART; SM00116; CBS; 2.

SWART; SM00116; CBS; 2.

Magneslum; Cobalt; Transport; CBS domain; Repeat; Complete proteome.

DOMAIN 138 191 CBS 1.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                             Length 299;
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20-AUG-2001 (Rel. 40, Last sequence update)
AC-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM AND COBALT EFFLUX PROTEIN CORC.
                                  DB 1;
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42.9%; Scc.
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SEQUENCE FROM N.A.
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27 FQGELK 32
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29 FOGELK 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
Studitted (FEB-1200) to the EMBL/Genbank/DDBJ databases.
-!- BUNCTION: BINDS TO THE N-TERMINAL PTS2-TYPE PEROXISONAL TARGETING
SIGNAL AND PLAYS AN ESSENTIAL ROLE IN PEROXISONAL PROTEIN IMPORT.
-!- SUBUNIT: INVERACTS WITH PEXS ( BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 6 WD REPEATS (TRR-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APOLIPOPROTEIN N-ATTRANSFERASE (EC 2.3.1.-) (ALP N-ACYLTRANSFERASE)
(COPPER HOMEOSTASIS PROTEIN CUTE HOMOLOG).
Pseudomonas aeruginosa.
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DR EMBL; D69147; BAA1809.1; ALT_INIT.

DR EMBL; AL157734, CAR75780.1;

DR PRINTS; DR00320; WA40; 6.

DR PROSITE; PS00032; WD_REPEATS_1;

DR PROSITE; PS00032; WD_REPEATS_1;

DR PROSITE; PS00924; WD_REPEATS_1;

DR PROSITE; PS00924; WD_REPEATS_1;

DR PROSITE; PS00926; WD_REPE
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Qi H.-Y., Gupta S.D., Wu H.C., Rick P.D.;
"Identification of N-acyltransferase (Int) gene from Pseudonomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                             Yoshioka S., Kato K., Okayama H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 42.9%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 12; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 511 AA.
                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE OF 1-24 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PGFQGE 11
                                                                                                                                                                                                                        STRAIN-PR745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNT_PSEAE
Q9ZI86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
LNT_PSEAE
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1

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"The alpha 2(VIII) collagen gene. A novel member of the short chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 1161-1214 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 PGFQGE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 PGFQGE 11
  Olsen B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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DOMAIN
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DOMAIN
DOMAIN
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                                 STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
MEDLINE-2043737; Pubmed-10984043;
Strover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).

-- FUNCTION: TRANSFERS THE FATTY ACYL GROUP ON MEMBRANE LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                -1- PATHWAY: LIPOPKOTEINS BIOSYNTHESIS.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                         (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE APOLIPOPROTEIN N-ACYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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InterPro: IPR003010; CN_hydrolase.
Pfam; PF00795; CN_hydrolase; 1.
Transferase: Acyltransferase; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-91210292; PubMed=2019595;
Muragaki Y., Jacenko O., Apte S., Mattei M.-G., Ninomiya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
           Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9DAE98422EBF8B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 6; DB 1
100.0%; Pred. No. 18;
tive 0; Mismatches
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGLIDP 6
 aeruqinosa.";
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                                                                                                                                                                                                                                                                    FAMILY
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ID CA28_HR
CA28_HR
DT CA28_HR
DT 01-MAY.
DT 20-MUG
DE COLLAGG
GN COLRAGG
GN COLRAGG
GN HUMAN
COC MARIMALIAN
RN SEQUEN
RN MEDLINI
RA MITAGAIN
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collagen family located on the human chromosome 1.";

J. Biol. Chem. 266:7721-7727(1991).

-!- FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.

-!- SUBUNIT: MAY FORM HUMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION INTH ALPHA 1(VIII) TYPE COLLAGENS.

-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-!- SIMILARITY: STRONG, TO ALPHA 1 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Prediction of the coding sequences of unidentified human genes. I) the complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
SMART: SM00110; C10; 1.
PROSITE; PS01113; C10; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIP1_HUMAN STANDARD; PRT; 1214 AA. 060315; Q9UED1; 20-AGG-2001 (Rel. 40, Created) 20-AGG-2001 (Rel. 40, Last sequence update) 20-AGG-2001 (Rel. 40, Last annotation update) ZINC FINGER HOMEBBOX PROTEIN 1B (SMAD INTERACTING PROTEIN 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 6; DB 1; Length 635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22A261164754F771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60527 MW;
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MIM; 120252; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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468
635
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Structural organization of the gene for the alpha 1 chain of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AB011141; BAA25495.1; -
BEMBL, AB015341; BAA3798.1; -
BEMBL, AB015341; BAA3798.1; -
BEMBL, AB015341; BAA37798.1; -
BEMBL, AB015341; BAA37798.1; -
BEMBL, AB015341; BAA37798.1; -
INTERPRO; IPRO0082; Znf-C2H2.
Ffam; PR00089; ZINCFINGER.
PRINTS; PR00048; ZINCFINGER.
PRNSTT; SW00389; HOX; 1.
SWART; SW00389; LINCFINGER.
PROSITE; PS50157; ZINC_FINGER.
PROSITE; PS50157; Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                             MEDLINE=99068504; PubMed=9853615;
UGK1 N. , Odd T., Kondo M., Yano K., Noguchi T., Muramatsu M.A.;
UGK1 N., Odd T., Kondo M., Yano K., Noguchi T., Muramatsu M.A.;
Nat. Biotechnol. 16.138-134.2(1998)
... Selection system for genes encoding nuclear-targeted proteins.";
Nat. Biotechnol. 16.138-134.2(1998)
... CACCT-3' IN DIFFERENT PROMOTERS (BY SIMILARITY).
... SUBURIT. BINDS ACTIVATED SMADI, ACTIVATED SMADI, AND ACTIVATED SMADIS: BINDING WITH SMAD4 IS NOT DETECTED (BY SIMILARITY).
... SUBCELLIGAR LOCATION: NUCLEAR (BY SIMILARITY).
... SIMILARITY: BELONGS TO DELTA-EFI/ZFH-1 FAMILY OF TWO-HANDED ZINC FINGER/HOMEODOMAIN PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLANI.
COLANI.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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SEQUENCE FROM N.A.
MEDLINE-89340433: Pubmed-2701944;
Soininen R., Huotari M., Ganguly A., Prockop D.J., Tryggvason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1214;
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W; B578FD91339C3FDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE (ATYPICAL).
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HOMEOBOX-LIKE.
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01-FBB-1996 (Rel. 33, Last sequence update)
0-0-MC-2001 (Rel. 40, Last annotation update)
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1669 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homeobox; Repressor; DOMAIN 437 48 21 22 ZN_FING 241 26 ZN_FING 241 26 ZN_FING 310 3310 3310
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1055 107
1084 121
1214 AA;
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SEQUENCE OF 1-28 FROM N.A. MEDLING-89034231; Pubmed-3182844; MEDLING-89034231; Pubmed-3182844; Solinine R., Huotari M., Hostikka S.L., Prockop D.J., Tryggvason K.; "The structural genes for alpha 1 and alpha 2 chains of human type IV collagen are divergently encoded on opposite DNA strands and have an overlapping promoter region."; J. Biol. Chem. 263:17217-17220(1988).
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MEDLINE=89005112; PubMed=2844531;
Siebold B., Deutzmann R., Kuehn K.;
Siebold B., Deutzmann R., Kuehn K.;
"The arrangement of intra- and intermolecular disulfide bonds in the carboxyterminal, non-collagenous agraegation and cross-linking domain of basement membrane type IV collagen.";
Eur. J. Blochem. 176:517-624 (1988).
- I. FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF CLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'
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MEDLINE=8802941; PubMed=3311751;
Brazel D., Oberbaeumer I., Dieringer H., Babel W., Glanville R.W.,
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basement membrane collagen (type IV) reveals 21 non-triplet
interruptions located within the collagenous domain.";
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Babel W., Glavdille R.W.;
Structure of human-basement-membrane (type IV) collagen. Complete
amino-acid sequence of a 914-residue-long pepsin fragment from the
alpha 1(IV) chain.",
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MEDLINE=85207819; PubMed=2581969;
Pihlajaniemi T., Tryggvason K., Myers J.C., Kurkinen M., Lebo R.,
Cheung M.-C., Prockop D.J., Boyd C.D.;
"cDNA clones coding for the pro-alphal(IV) chain of human type IV
procollagen reveal an unusual homology of amino acid sequences in
halves of the carboxyl-terminal domain.";
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Biol. Chem. 260:7681-7687(1985).
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MEDLINE-88216555; PubMed-2582422;
Brinker J.M., Gudas L.J., Loidl H.R., Wang S.-Y., Rosenbloom J.,
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procollagen chains."
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type IV collagen.";
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-! SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
MITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

-! DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN NETWORK.

DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN NETWORK.

GG-Y-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELICAL SOMAIN.

-!- PTM: LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT ARE HYDROXYLATED IN ALL CASES AND BIND CARBOHYDRATE.

-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

-!- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THESE. LOCATED IN THE NCI DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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MEDIINE=8811221; PubMed=3338568;
Wood L., Theriault N., Vogeli G.;
"CDNA clones completing the nucleotide and derived amino acid
sequence of the alpha 1 chain of basement membrane (type IV) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                               AMINO-TERMINAL PROPEPTIDE (7S DOMAIN).
COLLAGEN ALPHA 1(IV) CHAIN.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
N-LINKED (GLCNAC. . .).
OR 1548.
OR 1551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                   Extracellular matrix; Connective tissue; Basement membrane;
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10-JUL-1999 (Rel. 38, Last annotation update)
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
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MEDLINE-85127033; Pubbled=2578961;
Oberbaeumer I., Laurent M., Schwarz U., Sakurai Y., Yamada Y.,
Oberbaeumer I., Laurent M., Schwarz U., Sakurai Y., Yamada Y.,
Oberbaeumer I., Laurent M., Schwarz U., Sakurai Y., Yamada Y.,
Nogeli G., Voss T., Siebold B., Glanville R.W., Kuhn K.;
"Amino acid sequence of the non-collagenous globular domain (NC1) of the alpha IIV) chain of basement membrane collagen as derived from Complementary DNA.";
Eur. J. Blochem. 147:217-224(1985).
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MEDLINE-87250460; PubMed=3597383;
Kurkinen M., Condon M.R., Blumberg B., Barlow D., Quinones S.,
Saus J., Pihlajaniemi T.;
"Extensive homology between the carboxyl-terminal peptides of mouse
alpha 1(IV) and alpha 2(IV) collagen.";
J. Biol. Chem. 262:8496-8499(1987).
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MEDLINE-8843732, Pubmed-3739041;

Killen P.D., Burbelo P., Sakurai Y., Yamada Y.;

"Structure of the amino-terminal portion of the murine alpha 1(IV)

"Structure of the amino-terminal portion of the gene.";

J. Biol. Chem. 263:8706(1988).

-!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR.STRUCTURAL COMPONENT OI GLOMERULAR BASEMENT EMBRANES (EBM), FORMING A 'CHICKEN-WIRE'

MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
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BELLINE-86196099;
Sakural Y., Sullivan M., Yamada Y.;
Alpha I type IV collagen gene evolved differently from fibrillar collagen genes ";
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between the Swiss Institute of Bioinformatics and the EMBi outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SW00111; C4; 2.
Srtracellular matrix; Connective tissue; Basement membrane; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
SIGNAL
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COLLAGEN ALPHA 1(1V) CHAIN.
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EMBL, J04644, AAA50292.1;

EMBL, X06777;

EMBL, X02021.2

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EMBL, M16822, AAA7340.1;

EMBL, M18322, AAA7342.1;

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MEDLINE-93015826; PubMed-1400291; Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.; Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.; Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpasture antigen (alpha 3(IV)NC1). Identification of a potentially antigenic region at the triple helix/NC1 domain junction."; J. Blol. Chem. 267:19780-19784(1992).
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J. Clin. Invest. 89:592-601(1992).
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                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bernal D., Quinones S., Saus J.; "The human mRNA encoding the Goodpasture antigen is alternatively
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"Alternative splicing of the NCl domain of the human alpha 3(IV) collagen gene. Differential expression of mRNA transcripts that predict three protein variants with distinct carboxyl regions.";
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COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR (GOODPASTURE ANTIGEN)
                                                                                                                                                                                                                Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                  Biol. Chem. 269:23013-23017(1994).
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                                                                                                                                                                                                                                                                                                                                                                                    chain of type IV collagen.";
n. J. Hum. Genet. 49:545-554(1991)
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MEDLINE=93280184; Pubmed=8505332;
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MEDLINE=92147878; PubMed=1737849;
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MEDLINE-94124597; PubMed-8294492;
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MEDLINE=98196854; PubMed=9537506;
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                                                                                SEQUENCE FROM N.A.
                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                    Heidet L., Arrondel C., Forestier L., Cohen-Solal L., Mollet G., Gutierrez B., Stavrou C., Gubler M.C., Antignac C.; Stavrou C. fabler M.C., Antignac C.; Stavroture of the human type IV collagen gene COL4A3 and mutations in autosomal Albort syndrome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV COLLAGENS ARE COLOCALIZED AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDNEY, EYE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE: ANTIBODIES AGAINST THE NC1 DOMAIN OF ALPHA3(IV) MEDIATE THE HUMAN AUTOIMMUNE DISEASE, GOODPASTURE SYNDROME, WHICH IS CHARACTERIZED BY HEMATURIA AND PULMONARY HEMORRHAGE.
DISEASE: DEFECTS IN COLDA3 ARE ASSOCIATED WITH THE TYPE I AUTOSOMAL RECESSIVE FORM OF ALPORT SYNDROME, AN HEREDITARY GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE RENAL FAILURE, HEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS BQUALLY BETWEEN
                                                   Lemmink H.H., Mochizuki T., van den Heuvel L.P.W.J., Schroeder C.H., Barrientos A., Monnens L.A.H., van Oost B.A., Brunner H.G., Reeders S.T., Smeets H.J.M.;
Mutations in the type IV collagen alpha 3 (COL4A3) gene in autosomal recessive Alport syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA 6(1V), EACH OF WHICH CAN FORM 4 TRIPLE HELIX STRUCTURE WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
-!- SUBCELLIGLAR LOCATION: CELL SURFACE (POTENTIAL).
-!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHOWN HERE), 2/V AN 3/LS; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THEIR C-TERMINAL NC1 DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  autosomal Alport syndrome.";
J. Am. Soc. Nephrol. 12:97-106(2001).
-!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT (CLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                  Hum. Mol. Genet. 3:1269-1273(1994).
                                                                                                                                                                                                                                                                                                          MEDLINE=21064696; PubMed=11134255;
VARIANT PRO-1474.
MEDLINE=95078827; PubMed=7987301;
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U02520; AAA18943.1; -
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CLEAVAGE (BY COLLAGENASE)

(BY SIMILARITY).

CELL ATTACHMENT SITE (POTENTIAL).

N-LINKED (GLONAC...) (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

OR 1548 (BY SIMILARITY).

OR 1551 (BY SIMILARITY).

BY SIMILARITY.

OR 1662 (BY SIMILARITY).

BY SIMILARITY.

OR 1665 (BY SIMILARITY).

BY SIMILARITY

CREELEKTRYPERFECHGRGTCNYYS

NSYSENDASSERRENTE STYRAGELEKTISKCOVCMK

KRH -> KASINCESWGTRKINNKSLSGVHEBKTLKKKTA

ELVFFILKNRVWEBAVIR IN ISOTOCHMEASRIDYSYWISTPRI

MPNNMAPITGRALEPYISRCTVCGGPAINIAVHSOTTDIPP

CPHGWISSINGTRANDRASSENDYSYWISTPRI

GGLGSCLOGFTTMPFLECHONVUNDVORFASRIDYSYWISTPRI

GGLGSCLOGFTTMPFLECHONVUNDVORFASRIDYSYWISTPRI

GGLGSCLOGFTTMPFLECHONVUNDVORFASRIDYSYWISTPRI

GGLGSCLOGFTTMPFREEDRICKERPASPELECHERRA

SPELECHGRGTCNYYSNSYSFWLASSTPUN

AGELERIA ISRCQVCMKKRH -> DALEVKVLRSP (IN
InterPro; IPR000087; Collagen.

Pfam; PF01413; C4; 2.

Probom; PP01413; C4; 2.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation; C4 Tycoprotein; Basement membrane; Collagen; Signal; Cell adhesiton; Calternative splitcing; Polymorphism; Phosphorylation; Disease mutation; SIGNL

CHAIN

29 1670 COLLAGEN ALPHA 3(IV) CHAIN.

DOMAIN

43 1439 1670 NONHELICAL REGION.
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                                                                                            POTENTIAL.
COLLAGEN ALPHA 3(IV) CHAIN.
7S DOMAIN.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (GOODPASTURE ANTIGEN) (BY SIMILARITY).
EPITOPE (RECOGNIZED BY GOODPASTURE ANTIBODIES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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/FTId=VAR_011202.
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G -> E (IN AS).
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100.0%; Pred. No. 54;
:lve 0; Mismatches
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CA24_MOUSE
TO CA24_MOUSE
TO CA24_MOUSE
DT 01-AUG
DT 30-MAY
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COC Mammal
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ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE IV COLLAGENS.
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DR EMBL; X02899; CAA26657.1; -
DR EMBL; W02899; CAA26658.1; -
DR PIRL; A33526; A33526.

DR PIR; A33526; A33526.

DR PIR; A33526; A33526.

DR HSSP; P19972; IVAD.

DR HSSP; P19972; IVAD.

DR HSSP; P19972; IVAD.

DR HSSP; P19972; IVAD.

DR PGD: MGI: 88455; Collagen.

DR Fini; PF01391; Collagen; 19.

R SMART; SM00111; C4; 2.

R SMART; SM00111; C4; 2.

W Extracellular matrix; Connective tissue; Repeat; Hydroxylation; W Glycoprotein; Basement membrane; Collagen; Signal.
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
OR 1585 (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY).
OR 1700 (BY SIMILARITY).
OR 1703 (BY SIMILARITY).
NR 1701 (BY SIMILARITY).
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100.0%; Pred. No. 55;
tive 0; Mismatches
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1707 AA; 167391 MW;
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EMBL; M23333; AAA51626.1; JOINED.
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AAA37438.1;
CAA28308.1;
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CAB51614.1;
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Matches 6; Conserv
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Search completed: January 31, 2002, 13:39:26 Job time: 86 sec This Page Blank (uspto)

OM protein - protein search, using sw model

January 31, 2002, 13:39:24 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec Run on:

US-08-957-709-80 14 1 AGVIDEDYRGNVGV 14

Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues

Searched:

Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description           | P14597 orf virus ( | m       | 9         | -         | P21035 vaccinia vi | P33826 variola vir | Q03479 dictyosteli |            |            |           | P19331 schistosoma |            |            |            |            | Q05201 drosophila | P57483 buchnera ap | schizosad  | P40064 saccharomyc | P33842 variola vir | P03621 bacteriopha | . Q29214 sus scrofa | P08929 bombyx mori | _          | Q09384 caenorhabdi | P29174 cavia porce |            | P08826 bombyx mori | Q10262 schizosacch | P08825 bombyx mori |           | ~         | P18663 glycine max |
|-----------------------|--------------------|---------|-----------|-----------|--------------------|--------------------|--------------------|------------|------------|-----------|--------------------|------------|------------|------------|------------|-------------------|--------------------|------------|--------------------|--------------------|--------------------|---------------------|--------------------|------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|-----------|-----------|--------------------|
| SUMMARIES             | DUT ORFN2          | DUT_RAT | DUT_HUMAN | DUT_VACCV | DUT_VACCC          | DUT_VARV           | MYSE_DICDI         | OMPA_RICCN | PSAN_ARATH | DUT_ADEG1 | IM23_SCHMA         | DAPB_MYCBO | YHDF_BACSU | SERA_ARATH | RRP1_IAFOM | EYA_DROME .       | SYA_BUCAI          | YAK1_SCHPO | N157_YEAST         | VA19_VARV          | COAB_BPPF1         | RLAO_PIG            | CHA3_BOMMO         | VP16_NPVOP | YS88_CAEEL         | UNR_CAVPO          | YHFY_ECOLI | CHA1_BOMMO         | YD2E_SCHPO         | CHA2_BOMMO         | DUT_SCHPO | DUT_CHVP1 | RK2_SOYBN          |
| Length DB             | 159 1              | 205 1   | 252 1     | 144 1     | 147 1              | 147 1              | 1003 1             | 2021 1     | 171 1      | 178 1     | 218 1              | 271 1      | 289 1      | 624 1      | 757 1      | 766 1             | 878 1              | 1365 1     | 1391 1             | 76 1               | 82 1               | 93 1                | 100                | 103 1      | 109 1              | 114 1              | 120 1      | 129 1              | 131 1              | 132 1              | 140 1     | 141 1     | 143 1              |
| %<br>Query<br>Match L | 100.0              | 100.0   | 100.0     | 71.4      | 71.4               | 71.4               | 50.0               | •          | ς.         |           | 42.9               | •          | 42.9       | ٠          | ٠          | 'n                |                    | ٠          | 42.9               | 35.7               | 35.7               | 35.7                | 35.7               | 35.7       | 35.7               | 35.7               | 35.7       | 35.7               | 35.7               | 35.7               | 35.7      | 35.7      | 35.7               |
| Score                 | 14                 | 14      | 14        | 10        | 10                 | 10                 | 7                  | 7          | 9          | 9         | 9                  | 9          | 9          | 9          | 9          | 9                 | 9                  | 9          | 9                  | S                  | S                  | ស                   | S.                 | ഗ          | S                  | 2                  | 'n         | S                  | Ŋ                  | 5                  | Ŋ         | ഗ         | 2                  |
| Result<br>No.         |                    | 7       | e         | 4         | 5                  | 9                  | 7                  | Φ.         | σ,         | 10        | 11                 | 12         | 13         | 14         | 15         | 16                | 17                 | 18         | 19                 | 20                 | 21                 | 22                  | 23                 | 24         | 25                 | 26                 | 27         | 28                 | 29                 | 30                 | 31        | 32        | 33                 |

| 048500 bacteriopha | P43580 saccharomyc | P38839 saccharomyc | P16792 human cytom | Q03740 mus musculu | P43058 candida alb | Q9yys0 avian adeno | Q9zk53 helicobacte | 025776 helicobacte | P32518 lycopersico | P08209 bos taurus | P07320 homo sapien |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| DUT_BPT5           | YFB2_YEAST         | YHT6_YEAST         | UL51_HCMVA         | CRGF_MOUSE         | DUT_CANAL          | DUT_ADEG8          | FLAV_HELPJ         | FLAV_HELPY         | DUT_LYCES          | CRGD_BOVIN        | CRGD_HUMAN         |
| 48.1               | 48 1               | 48 1               | 157 1              | 58 1               | 59 1               | 53 1               | 54 1               | 54 1               | 59 1               | 73 1              | 73 1               |
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| 35.7               | 35.                | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7              | 35.7               |
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| 34                 | 35                 | 36                 | . 37               | 38                 | 39                 | 40                 | . 41               | 42                 | 43                 | 44                | 45                 |

# ALIGNMENTS

| 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-DEC-1998 (Rel. 14, Last sequence update) 15-DEC-1998 (Rel. 137, Last annotation update) DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6 (DUTPASE) (DUTP PROPHOSPHATENE). Orf Virus (Strain NZ2) (OW NZ-2). VIRUSES; dSDNA VIRUSES, NO RNA stage; POXVIRIDASE (CHORD PARADDAXVIRUS. NCBL_TAXID=10259; (1) SEQUENCE FROM N.A. MEDLINE=9001200; PubMed=2678731; Mercer A.A., Fraser K.M., Stockwell P.A., Robinson A.J.; Menclogy 172:665-668(1989) |     | DIT ORFN2    | STANDARD      | RD.       | - ТЯО     | 159 2 | 44      |       |         |              |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|--------------|---------------|-----------|-----------|-------|---------|-------|---------|--------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | 14597;       | VOICE OF      | ,         | rur'      |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | 1-APR-1990   | (Rel. 14,     | Created   | u ocuonit | אלפהת | -       |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | 5-DEC-1998   | (Rel. 37,     | Last an   | jacacc u  | apan  | te)     |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | EOXYURIDINE  | 5'-TRIPH      | OSPHATE   | NUCLEOTI  | DOHYI | ROLASE  |       | 3.6.1.2 | 3)           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | OUTPASE) (D  | UTP PYROP     | HOSPHATA  | SE).      |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | cf virus (s  | train NZ2     | OV NZ     | -2).      |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | iruses; dsD  | NA viruse:    | s, no RN. | A stage;  | Pox   | riridae | cho : | rdopoxv | irinae;      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | arapoxvirus  |               |           | 1         |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | CBI_TaxID=1  | 0259;         |           |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | 1.           |               |           |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | SQUENCE FROM | M N.A.        |           |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | EDLINE-9002  | 1200; Publ    | Med=2678  | 731;      |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | ercer A.A.,  | Fraser K      | .M., Sto  | ckwell P  | . A.  | Robins  | on A. | J.;     |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | A homologue  | of retro      | viral ps  | eudoprot  | eases | i in th | e par | apoxvir | us, orf      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | irus.";      |               |           |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | irology 172  | : 665-668(    | 1989).    |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | - FUNCTION   | : THIS EN     | ZYME IS   | INVOLVED  | IN    | UCLEOT  | IDE M | ETABOLI | SM: IT       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | PRODUCES     | DUMP, THI     | E IMMEDIA | ATE PREC  | URSOF | OF TH   | IMIDI | NE NUCL | EOTIDES      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ပ္ပ | AND IT D     | ECREASES :    | THE INTR  | ACELLULA  | R CON | CENTRA  | TION  | OF DUTP | DUTP SO THAT |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ပ္ပ | URACIL C     | ANNOT BE      | INCORPOR  | ATED INT  |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     |              | C ACTIVITY    | Y: DUTP . | + H(2)0   |       | 1P + PY | ROPHO | SPHATE. |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     |              | TY: BELON(    | GS TO THI | E DUTPAS  |       | IILY.   |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | -            | WAS ORIG      | INALLY T  | HOUGHT T  |       | A PROT  | EASE- | LIKE PR | OTEIN        |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 22  | (PSEUDOP     | ROTEASE).     |           |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | -1           |               |           |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | is SWISS-P   | ROT entry     | is copy   | right. I  | t is  | produc  | ed th | rough a | collabo      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | etween the   | Swiss In      | stitute ( | of Bioin  | forms | tics    | and t | he EMB  | L outst      |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | ne European  | Bioinform     | matics In | nstitute  | Ē     | ere ar  | e no  | restri  | ctions       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | se by non    | -profit       | institut  | ions as   | long  | as it   | s con | tent i  | s in         |
| entities requires a license agreement (See or send an email to license@isb-sib.ch).  EMBL; M30023; AAA46786.1;  HSSP; P06968; IDUD.  InterPro; IPR001428; dUTPase. Pfam; PP0692; dUTPase; HYdrolase: Nucleotide metabolism.                                                                                                                                                                                                                                                                                                             |     | dified and   | this star     | tement is | s not re  | томес | I. Usa  | de p  | y and   | for com      |
| or send an email to license@                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | _   | ntities req  | uires a l     | icense a  | greement  | (See  | http:   | /www  | isb-si  | b.ch/an      |
| EMBL; M30023; AAA4678<br>HSSP; P06968; IDUD.<br>InterPro; IPR001428;<br>Pfam; PF006623; durpas<br>Hvdrolase: Nucleoride                                                                                                                                                                                                                                                                                                                                                                                                                 |     | send an el   | mail to 1     | icense@i  | sb-sib.c  | h).   | •       |       |         |              |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | terPro; IP   | R001428; (    | dUTPase.  |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | fam: PF0069  | 2; dUTPase    | e: 1.     |           |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | drolase; N   | ucleotide     | metabol   | ism.      |       |         |       |         |              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | SOUENCE      | 59 AA: 16     | 6893 MW:  | 080085    | 27472 | IE17AD  | CPC64 |         |              |

ration tion -n its way ercial

; Query Match 100.0%; Score 14; DB 1; Length 159; Best Local Similarity 100.0%; Pred. No. 2.9e-08; Matches 14; Conservative 0; Mismatches 0; Indels

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Gaps

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~ RESULT DUT\_RAT

Euteleostomi;

Hominidae; Vertebrata;

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TISSUE-Lymphocytes;

MEDINE-9321661;

A Strabler J. R., Zhu X., X., Wang Y.K., Hora N., Andrews P.C.,

A Strabler J. R., Zhu X., X., Wang Y.K., Hora N., Andrews P.C.,

A Roseman N.A., Neel J.V., Turka L., Hanash S.M.;

Roseman N.A., Neel J.V., Turka L., Hanash S.M.;

In human T cells.,

In human T cells.,

In human T cells.,

PRODUCES DUWP, THE IMMEDIATE PRECURSOR OF THYMIDINE WICLEOTIDES

AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT

URACIL CANNOT BE INCORPORATED INTO DNA.

COPACIOR: MAGNESIUM.

COPACIOR: MAGNESIUM.

COPACIOR: MAGNESIUM.

COPACIOR: MAGNESIUM.

COPACIOR: MAGNESIUM.

COPACIOR: MAGNESIUM.

COPACIDER LOCATION: DUT- N IS NICLEAR, DUT-M IS MITOCHONDRIAL.

COPACIDER LOCATION: DUT-N IS NICLEAR, DUT-M IS MITOCHONDRIAL.

COPACIDER DRODUCED BY ALTERNATIVE SPLICING.

ARE PRODUCED BY ALTERNATIVE SPLICING.

ARE PRODUCED BY ALTERNATIVE SPLICING.

COPACIONER DRODUCED BY ALTERNATIVE SPLICING.

COPACIONER DRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92390380; PubMed=1325640; McIntosh E.M., Ager D.D., Gadsden M.H., Haynes R.H.; "Human duTp pyrophosphatase: cDNA sequence and potential biological importance of the enzyme."; proc. Natl. Acad. Sci. U.S.A. 89:8020-8024(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96205967; PubMed=8631816;
Ladner R.D., McNulty D.E., Carr S.A., Roberts G.D., Caradonna
"Characterization of distinct nuclear and mitochondrial forms
human deoxyuridine triphosphate nucleotidohydrolase.";
J. Biol. Chem. 271:7745-7751(1996).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (DUT-N).
Cohen D., Heng H.H.Q., Shi X.M., McIntosh B.M., Tsui L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                        Ladner R.D., Caradonna S.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McIntosh E.M., Ager D.D., Gadsden M.H., Haynes R.
Proc. Natl. Acad. Sci. U.S.A. 90:4328-4328(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (DUT-N)
(EC 3.6.1.23) (DUTPASE) (DUTP PYROPHOSPHATASE) DUT.
                                                                                           Craniata; Ve
Catarrhini;
                                                                                                                                                                                         SEQUENCE FROM N.A. (DUT-M AND DUT-N).
                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 112-252 FROM N.A
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (DUT-M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEPENDENT MANNER
                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      Cohen D., Her
Pearlman R.E.
                                                                                                                                                                                                                     Pearlman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRATUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chu R.Y., Lin Y.L., Rao M.S., Reddy J.K.;
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

L. Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

ENGUGES DUMP. THE INTROCACED IN NUCLECTIDE METABOLISM: IT PROPUES DUMP. THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT DUES AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT OF PROLIFERATOR ACTIVATED RECEPTOR (PPAR) ACTIVITY BY BINDING OF ITS NATERIARD TO PPAR, PREVENTING THE LATTER'S DIMBRIZATION WITH COPACITOR: MAGNESIUM (BY SIMILARITY).

C.-I- CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

C.-I- CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

C.-I- CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

C.-I- CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

C.-I- CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

C.-I- CATALYTIC ACTIVITY: EXPRESSED IN ALL TISSUES EXAMINED. HIGHER

C.-I- STMILARITY: BELONGS TO THE DUTPASE FAMILY:

C.-I- SIMILARITY: BELONGS TO THE DUTPASE FAMILY:
                                                               01-NOV-1997 (Rel. 35, Created)
20-NG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
(DUTPASE) (DUTP PYROPHOSPHATASE) (PPAR-INTERACTING PROTEIN 4). (PIP4).
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
MCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARANG-SPRAGUE-DAMELY; TISSUE-Liver;
MEDLINE-97066956; PubMed-8910358;
Chu R.Y., Lin Y.L., Rao M.S., Reddy J.K.;
Cloning and identification of rat deoxyuridine triphosphatase as inhibitor of peroxisome proliferator-activated receptor alpha.";
J. Blol. Chem. 271:27670-27676(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUT_HUMAN STANDARD;
PRT; 252 AA.
913316; 016860; 016708; 014785;
01-FEB-1994 (Rel. 28, Created)
115-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE S'-TRIPHOSPHATE NUCLEOTIODHYDROLASE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide metabolism; Magnesium.
205 AA; 22003 MW; A9D54EBF5ED015C4 CRC64;
                      205 AA
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001428, dUTPase.
Pfam, PF00692, dUTPase; 1.
Hydrolase; Nucleotide metabol
SEQUENCE 205 AA; 22003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U64030; AAC34734.2; -. HSSP; P16088; 1DUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                      STANDARD;
                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AGVIDEDYRGNVGV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGVIDEDYRGNVGV 14
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es 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS.
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DUT_HUMAN
ID DUT_H
AC P3331
DT 01-FE
DT 20-AU
DE DEOXYI
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-i- TISSUE SPECIFICITY: FOUND IN A VARIETY OF TISSUES.
-i- PTM: PHOSPHORYLATION IN MATURE T-CELLS OCCUR IN A CELL CYCLE-
                                                                                                                                                -!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF018432; AAB71393.1; -.
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EMBL; M34368; AAA48246.1; ALT_INIT.
EMBL; M25392; AAA48238.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUTPASE) (DUTP PYROPHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                      71.4%; S
                                                                                                                                                                                                    InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                              Pfam; PF00692; dUTPase; 1
                                                                                                                                                                                                                                                                     Query Match 71.4
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10249, 31531;
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                        PIR, A32907; PRVZWR.
PIR, A31310; A31310.
PIR, H36213; H36213.
HSSP; P16088; 1DUT.
                                                                                                                                                                                                                                                                                                                              2 GVIDEDYRGN 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                              DUT_VACCC
P21035;
                                                                                                                                                                                                                                                                                                                                                                                  DUT_VACCC
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                                                                                                                                                                                                           Hydrolase; Nucleotide metabolism; Phosphorylation; Magnesium; Alternative splicing; Nuclear protein; Mitochondrion; Transit peptide. TRANSIT 1 69 MITOCHONDRION.
                                                                                                                                                                                                                                                                                MTPLCPRPALCYHFLTSLLRSAMQNARGTAEGRSRGTLRAR
                                                                                                                                                                                                                                                                                           PAPRPPAAQHGIPRPLSSAGRLSQGCRGASTVGAAGWKGEL
PKAGGSPAPGP -> MPCSE (IN ISOFORM DUT-N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89264577; PubMed-2657744;
Slabaugh M.B., Roseman N.A.;
Slabaugh M.B., Roseman N.A.;
Fretrovial protease-like gene in the vaccinia virus genome.";
Proc. Natl. Acad. Sci. U.S.A. 86:4152-4155(1989).
-!- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT
PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES
AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
URACIL CANNOT BE INCORPORATED INTO DNA.
-!- CATALYTIC ACTIVITY: DUTP + H(2)0 = DUMP + PYROPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE-91020979; Pubmed=2219701;
MEDISOBORD N.A., Slabaugh M.B.;
"The vaccinia virus HindIII F fragment: nucleotide sequence of the left 6.2 kb.";
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 14; DB 1; Length 252; 100.0%; Pred. No. 4.3e-08;
                                                                                                                                                                                                                                              DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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9D3E69031D2FECC7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
, AF018429; AAB71393.1; JOINED.
, AF018430; AAB71393.1; JOINED.
, AF018431; AAB71393.1; JOINED.
, AF018432; AAB71394.1; JOINED.
, AF018429; AAB71394.1; JOINED.
, AF018430; AAB71394.1; JOINED.
, AF018431; AAB71394.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DUTPASE) (DUTP PYROPHOSPHATASE)
                                                                                                 . U90224; AAB93867.1; ... U52891; AAC51123.1; ... U31930; AAC5418.1; ... M89913; AAA58441.1; ... L11877; AAA36801.1; ...
                                                                                                                                                                                                                                                                                                                           26706 MW;
                                                                                                                                                                                          IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 178:410-418(1990).
                                                                              AAB94642.1;
                                                                                          AAB93866.1;
                                                                                                                                                                                                   Pfam; PF00692; dUTPase; 1
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    186 AGVIDEDYRGNVGV 199
                                                                                                                                                                                                                                                                     93
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                                                                                                                                                       PIR; A46256; A46256.
HSSP; P16088; 1DUT.
MIM; 601266; -.
                                                                                                                                                                                                                                                                                                                 233 ;
252 AA;
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P17374;
                                                                                                                                                                                          InterPro;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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Vaccinia virus (strain Copenhagen), and Vaccinia virus (strain L-IVP).
Viruses; dsDNA viruses, no RNA stage; poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRODUCES DUMP, THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT - FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT - PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
-!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
-!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A PROTEASE-LIKE PROTEIN
(PSEUDOPROTEASE).
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Cochel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
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Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mikryukov N.N., Chizhikov V.E., Prikhod'Ko G.G., Urmmanov I.M., Serpinskii O.I., Blinov V.M., Nikulin A.E., Vasilenko S.K.; "Structural-functional organization of segment of vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Nucleotide metabolism.
SEQUENCE 144 AA: 16012 MW; E0825682340ABD5C CRC64;
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; Pred. No. 0.00042;
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Virology 179:247-266(1990).
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the BMIS. Outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regulares a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-SOMALIA-1977, CONGO-1965, AND GARCIA-1966;
MASSING R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M., Potmenin A.V., Shchelkunov S.N., Esposito J.J.; vo. Shchelkunov S.N., Esposito J.J.; vo. Shchelkunov S.N., Fromerited (DEC-1994) to the Emily General databases.
-- FUNCTION: THIS ENZYME IS INVOLVED IN NOCLECTIOR METABOLISM: IT
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STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE-93202281; PubMed-8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";
FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variola virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
URACIL CANNOT BE INCORPORATED INTO DNA.
CATALYTIC ACTIVITY: DUTP + H(2)0 = DUMP + PYROPHOSPHATE.
SIMILARITY: BELLONGS TO THE DUTPASE FAMILY.
CAUTION: WAS ORIGINALLY THOUGHT TO BE A PROTEASE-LIKE PROTEIN (PSEUDOPROFEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         venter C.J.;
"Potential virulence determinants in terminal regions of variola
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SERAILE-BAGGLADESH-1975;
MEDLINE-94088747; PubMed-8264798;
MASSUNG R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
(DUTPASE) (UUTP PYROPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
(DUTPASE) (OR E2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 10; DB 1; Length 147
100.0%; Pred. No. 0.00042;
Live 0; Mismatches 0; Indels
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ture 366:748-751(1993).
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Best Local Similarity 100.
Matches 10; Conservative
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NCBI_TaxID=10255;
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES AND IT DESCREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT URACIL CANNOT BE INCOPERATED INTO DNA.
CATALYTIC ACTIVITY: DUTP + H(2)0 - DUMP + PYROPHOSPHATE.
SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
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"The Dictyostellum myosin IE heavy chain gene encodes a truncated
lsoform that lacks sequences corresponding to the actin binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR001428; dUTPase.
Pfam. PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism.
SEQUENCE 147 AA; 16464 MW; D918ED4F482ECDA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYSE DICDI STANDARD; PRT; 1003 AA. 003479; (PEB-1994 (Rel. 28, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) MYOE OR DMIE.
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MEDLINE=93277957; PubMed=8504170;
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EMBL, 122579; AAA60774.1; -.
EMBL, U18340; AAA69437.1; -.
EMBL, U18337; AAA69331.1; -.
PIRE, P36839; F56839.
HSSP; P16088; IDUT.
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Best Local Similarity 100.
Matches 10; Conservative
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J. Clin. Microbiol. 34:2058-2065(1996)
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MEDLINE-94171067; PubMed-8125327;
Crooquet-valdes P.A., Weiss K., Walker D.H.;
"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
Gene 140:115-119(1994).
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MEDLINE=97015921; PubMed=8862558;
Roux V., Fournier P.E., Raoult D.;
"Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMPA_RICCN STANDARD; PRT; 2021 AA. 052668; 052669; , 052657; P95591; P95592; P95594; Q52667; Q52668; Q52669; , Q52670; Q52674. C52674. C52664. Created) 20-AuG-2001 (Rel. 40, Last sequence update) 20-AuG-2001 (Rel. 40, Last annotation update) OUTER MEMBRANE PROTEIN A PRECURSOR (190 KDA ANTIGEN) (CELL SURFACE OWARD A). ROMPA OR RC1273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A.
STRAIN=Malish 7;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                    10 1.
10 a.
NO ALPHA-HELICAL, C-TERMINAL DOMAIN.
ATP (BY SIMILARITY).
                                              Dictybb; DO0149; myoE.
InterPro: IPR0016049; myoE.
InterPro: IPR0016049; myoE.
InterPro: IPR001609; myoEn_head.
Pfam: PF001612; IQ, 2.
Pfam: PF000613; myoSin_head; 1.
PRINTS: PR00193; myoSin_head; 1.
SMART: SM00045; myoSin_head; 1.
SMART: SM00045; MYOSIn_head; 1.
SMART: SM00045; MYOSIn_head; 1.
SMART: SM00045; MYOSIN_SC: 1.
PROSITE: PS50096; IQ; 2.
MYOSIN: Actin_binding; ATP-binding; Calmodulin-binding; Rèpeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsieae
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1003;
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MW; B6E758BEC035766F CRC64;
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                                                                                                                                                                                                                                                                     MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 7; DB 1; 100.0%; Pred. No. 3.3;
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EMBL; L06805; AAA33201.1; -. PIR; S33760; S33760.
HSSP; P08799; 1MND.
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Best Local Similarity
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DOMAIN 1
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OMPA_RICCN
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YI -> II (IN STRAIN INDIAN TICK TYPHUS).
D -> A (IN STRAINS INDIAN TICK TYPHUS, MI
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M -> I (IN STRAIN INDIAN TICK TYPHUS).

Q -> K (IN REF. 1).

I -> V (IN REF. 1).

V -> I (IN REF. 1).

G -> D (IN REF. 1).

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SEQUENCE OF 953-2012 FROM N.A. STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan; Strain-Indian tick typhus, MI, Malish 7, and Moroccan; Raoult D., Fournier P.E., Roux V.; Phylogenetic analysis of spotted fever group rickettsiae by study
                                                                                            of the outer surface protein rompa.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ELICITS PROTECTIVE IMMONITY (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY SLAYER WITH HEXAGONAL SYMMETRY.
-!- PTM: GLYCOSYLATED (BY SIMILARITY).
-!- PTM: GLYCOSYLATED (BY SIMILARITY).
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D -> Y
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Pfam; PF02708; rOmpA_rOmpB; 1.
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EMBL; U43794; AAB49549.1; --
EMBL; U43806; AAB49550.1; --
EMBL; U45244; AAB49550.1; --
EMBL; U4544; AAB49566.1; --
EMBL; U465418; AAA886663.1; --
EMBL; U46418; AAC35176.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U83443; AAC35179.1; -. EMBL; U83448; AAC35184.1; -. EMBL; U83453; AAC35189.1; -.
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SERING P.C., FETI R.J.;
SERING P.C., FETI R.J.;
Nucleotide sequence of an Arabidopsis thaliana cDNA clone encoding
the complete precursor for a homolog to the barley extrinsic thylakoid
lumenal polypeptide PSI-N ";;
(In) Plant Gene Register Poss-088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 34, Last sequence update)
PHOTOSYSTEM I REACTION CENTRE SUBBURT N PRECURSOR (PSI-N).
PSAN OR ATSGEGGATO OR WHI24.2.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabata S.:

"Structural nallysis of Arabidopsis thaliana chromosome 5. III.

"Structural nallysis of Arabidopsis thaliana chromosome 5. III.

physically assigned Pi clones.";

DNA Res. 4:401-414 (1997).

-!- FUNCTION: MAY FUNCTION IN MEDIATING THE BINDING OF THE ANTENNA COMPLEXES TO THE PSI REACTION CENTRE AND CORE ANTENNA.

-!- SUBCELLULAR LOCATION: ON THE LUMENAL SURFACE OF THE THYLAKOID MEMBRANE.

-!- SIMILARITY: BELONGS TO THE PSAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST (BY SIMILARITY).
PHOTOSYSTEM I REACTION CENTRE SUBUNIT N.: 82FE2AFF7C599C07 CRC64;
                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE-98162728; Pubmed-9501997;
MAKAmura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
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EMBL, AB008266; BAB10272.1; -.
Mendel: 7192; ATH:PSAN:
Photosystem I; Photosynthesis; Chloroplast; Transit peptide;
75 T -> P (IN REF. 1).
36 MS -> LP (IN REF. 1).
36 E -> A (IN REF. 1).
70 MTAPLP -> ITPPLS (IN REF. 1).
203328 MW; 327PC42D7CB24668 CRC64;
                                                                                                                                                                                                                                           Length 2021;
                                                                                                                                                                                                                                                                                                 0; Indels
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100.0%; Pred. No. 6.2;
ive 0; Mismatches
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171 AA; 18429 MW;
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Best Local Similarity 100.
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Length 171;

DB 1;

Score 6;

42.98;

Query Match

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"The Comp.rec. ....
adenovirus CELO.";
J. Virol. 70:2939-2949(1996).
J. VIROL. 70:2939-2949(1996).
J. VIROL. THIS INAMEDIATE DECURSOR OF THYMIDINE NUCLEOTIDES
PRODUCES DUMP, THE INMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES
AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
INCALL CANNOT BE INCORPORATED INTO DNA (BY SIMILARITY).
J. CATALYTIC ACTIVITY: DUTP + H(2)0 = DUMP + PYROPHOSPHATE.
J. CATALYTIC ACTIVITY: DUTP + H(2)0 = DUMP + PYROPHOSPHATE.
J. SIMILARITY: BELONGS TO THE DUTPASE FAMILY.

J. SIMILARITY: BELONGS TO THE DUTPASE FAMILY.

THIS PRODUCED THYMID A COLLABOR.
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                                                                   Gaps
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[2] SEQUENCE FROM N.A. MEDLINE-96186720; PubMed=8627769; Chiocca S., Kurzbauer R., Schaffner G., Baker A., Mautner V.,
                                                                                                                                                                                                                                                                                                                                           DUT_ADEGI STANDARD; PRT; 178 AA.
089662; 086612;
080662; 0. Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 34), Last sequence update)
DEOXYURIDINE 5'-TRIPHOSPHATE UNCLEOTIDOHYDROLASE (EC 3.6.1.23)
(DUTPASE) (DUTP PYROPHOSPHATES).
Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO).
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete DNA sequence and genomic organization of the avian
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EMBL; S61107; AAB26434.1; -.
EMBL; U46033; AAC54895.1; -.
HSSP; P06968; IDUD.
InterPo.; IPRO01428; durpase.
InterPo.; IPRO01428; durpase.
InterPo.; IPRO01428; durpase.
InterPo.; IPRO01428; durpase.
IS 6 18 2 -> F (IN REF. 1; AAB26434).
SEQUENCE 178 AA; 19219 MW; 477C885A944D16F1 CRC64;
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100.0%; Pred. No. 8;
Live 0; Mismatches
                           Pred. No. 7.7;
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100.08; Pr
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Best Local Similarity 100.
Matches 6; Conservative
                           Best Local Similarity 100.
Matches 6; Conservative
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86 AGVIDE 91
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IM23_SCHMA
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TOTAL 20

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271 AA.

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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
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Pfam; PF01113; DapB; 1.
ProDom; PD004105; DapB; 1.
PROSITE: PS01298; DAPB; 1.
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Matches 6; Conservative
 STANDARD;
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                                                                                                     Mycobacterium bovis.
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                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=1765;
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| AGVIDE
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ID YHDF_BACSU
AC O07575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                 "Schistosoma mansoni: characterization of the gene encoding Sm23, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90217533; Pubmed-2324498;
Wright M.D., Henkle K.J., Mitchell G.F.;
"An immunogenic Mr 23,000 integral membrane protein of Schistosoma
                                                                                                                                                                                                                                                                                                                                                                 Lee K.W., Shalaby K.A., Medhat A.M., Shi H., Yang Q., Karim A.M., Loverde P.T.;
         P1931; 026585;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
23 KDA INTEGRAL MEMBRANE PROTEIN (SM23).
Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
D -> N (IN REF. 2).
                                                                                                                  Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea;
Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                         mansoni worms that closely resembles a human tumor-associated antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                             integral membrane protein.";
Exp. Parasitol. 80:155-158(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 218;
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218 AA.
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                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95121434; PubMed=7821405;
                                                                                                                                                                                                                                                                                      Immunol. 144:3195-3200(1990).
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151 D
23684 MW;
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STANDARD;
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=6183;
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                                                                                                                                                                                                                                                                                                                                                                                                                        pathway of mycobacteria.";
J. Bacteriol. 176:4424-4429(1994).
-!- CARALYTIC ACTIVITY: 2,3,4,5-TETRAHYDRODIPICOLINATE + NAD(P)(+) = 2,3-DIHYDRODIPICOLINATE + NAD(P)H.
-!- PATHWAY: BIOSYNTHESIS OF DIAMINOPIMELATE AND LYSINE FROM ASPARTATE SEMIALDEHYDE; SECOND STEP.
                                                                                                                                                                                                                                                                                                 STRAIN=BCG / PASTEUR;
MEDILINE=94292473; PubMed=8021227;
Cirillo J.D., Weisbrod T.R., Banerjee A., Bloom B.R., Jacobs W.R. Jr.;
"Genetic determination of the meso-diaminopimelate biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE DIHYDRODIPICOLINATE REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diaminopimelate biosynthesis; Lysine biosynthesis; Oxidoreductase;
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN CITA-SSPB INTERGENIC REGION
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDRODIPICOLINATE REDUCTASE (EC 1.3.1.26) (DHPR)
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its more by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STAIN-CV. COLUMBLA.
STAIN-CV. COLUMBLA.
MEDLINE-21016719; PubMed-11130712;
Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A. Ecker J.R., Palm C.J., Bowan C.L., Brooks S.Y.,
White O., Alonso J., Altafi H., Araujo R., Bowan C.L., Brooks S.Y.,
White O., Alonso J., Chen H., Cheuk R.F., Chin C.W.
A buen F., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Etgu P., Feldblyum T.V., Feng B., Hujar K.,
A bunn P., Etgu P., Feldblyum T.V., Feng B., Hujar L.,
A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
A Hunter J.L., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
And Iltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
A hiltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
A sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (EC 1.1.1.95) (PGDH).
ATIGIT740 OR FILAG. 8.
ATRADIAGOPSIS thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eddicotyledons; core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-99085035; PubMed-9867856;
HO C.-L., NOji M., Saito M., Saito K.;
"Regulation of serine blosynthesis in Arabidopsis. Crucial role of plastidic 3-phosphoglycerate dehydrogenase in non-photosynthetic tissues.";
J. Biol. Chem. 274:397-402(1999).
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REMBL; 299109; CAB12784.1;
RISSP; 0126341; 1980.
Subtilist; BG13012; yhdF.
InterPro; IPR002198; ADH_short.
Pfam; PP00106; adh_short.1;
Pfam; PP00106; adh_short.2.
PFam; PP000678; adh_short.1.
PFam; PP000678; adh_short.1.
PFAM: PROSIFE: PS00061; ADH_SHORT; 1.
PFAM: PROSIFE: PS00061; ADH_SHORT; 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
NP BIND
49 73 MAD OR NADP (BY SIMILARITY).
SEQUENCE 289 AA; 31509 MW; 4EC98C62B9241BCI CRC64;
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30-MAY 2000 (Rel. 39, Last sequence update)
30-MAY 2000 (Rel. 39, Last sequence update)
30-MAY 2000 (Rel. 39, Last annotation update)
RNA-DIRECTED RNA POLYMERASE SUBUNIT P1 (EC 2.7.7.48) (POLYMERASE BASIC IPROTEIN), (PB1).
Influenca virus (strain A/Fort Monmouth/1/47).
Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;
Influenca virus A and B group; Influenca A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97033391; PubMed=8879138; MEDLINE=97033391; PubMed=8879138; Medline=97033391; PubMed=8879138; Mutations in the hemagglutinin and matrix genes of a virulent influenza virus variant, A/FM/1/47-MA, control different stages in pathogenesis: "; A/FM/1/47-MA, control different stages in pathogenesis: "; SUBUNIT: INFLUENZA RNA POLYMERASE IS COMPOSED OF THREE SUBUNITS:
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., tlerback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROPLAST (POTENTIAL).
D.3-PHOSPHOGLYCERATE DEHYDROGENASE.
SUBSTRATE-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
T24370F870DEA310 CRC64;
                                                                                                                                        THEALAGE 408.8;
NATURE 408.8;
NATURE 408.8;
-I- CATALYTIC ACTIVITY: 3-PHOSPHOGLYCERATE + NAD(+) = 3-PHOSPHOHYDROXYPYRUVATE + NADH.
-I- SUBCELLULAR LOCATION: CHLOROPLAST.
-I- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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InterPro: IPR002162; D_2_hydroxyacid_DH.
Ffam; PR00389; 2-Hacid_DH; 1.
Ffam; PR003842; ACT; 1.
FROSITE; PS000670; D_2_HYDROXYACID_DH_1; 1.
FROSITE; PS00671; D_2_HYDROXYACID_DH_2; 1.
FROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
FROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
FROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
FRANSIT 1.

CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.9%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches
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624 AA; 6
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P1 (OR PB1), P2 (OR PA), AND P3 (OR PB2).
SIMILARITY: BELONGS TO THE INFLUENZA VIRUSES POLYMERASE PB2
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X99037; CAA67498.1; -.
InterPro; IPR001407; Flu_PB1.
Pfam; PF00602; Flu_BB1; 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 757 AA; 86671 MW; 7E45D6DE764A7534 CRC64;
                \begin{array}{c} \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{C} \\ \mathcal{
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Search completed: January 31, 2002, 13:39:25 Job time: 85 sec

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Gaps

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Length 757; 0; Indels

Query Match 42.9%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 29; Matches 6; Conservative 0; Mismatches

||||||| 617 DEDYRG 622 5 DEDYRG 10

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:39:23 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec

US-08-957-709-79 14 1 AGVVDRDYTGEVKV 14 Title: Perfect score: Sequence:

Scoring table:

100059 seqs, 36664827 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

0

Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| P30599 ustilago ma | 033773 sulfolobus | P33859 variola vir | P14312 rhizobium l | P96985 rhizobium e | P15530 mus musculu | P40259 homo sapien | Q9wyi7 thermotoga | Q9pla1 chlamydia m | P81296 lentinula e |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| CHS2_USTMA         | HIS7_SULSO        | VC01_VARV          | FIXW_RHILE         | TPIS_RHIET         | C79B_MOUSE         | C79B_HUMAN         | Y352_THEMA        | Y206_CHLMU         | RNL2_LENED         |
| ~ ~                |                   |                    | Н                  | -                  | -                  | -                  | <del>, -</del> 1  | Н                  | 7                  |
| 186                | 193               | 214                | 221                | 226                | 228                | 229                | 234               | 238                | 239                |
| 35.7               | 35.7              | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7              | 35.7               | 35.7               |
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| 34                 | 300               | 3 <i>8</i>         | 39                 | 40                 | 41                 | 42                 | 43                | 44                 | 45                 |

### ALIGNMENTS

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Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                       01-NOV-1997 (Rel. 35, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATPC SYNTHASE EPSILON CHAIN (EC 3.6.1.34).
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Matches 6; Conserv
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SEQUENCE 123 AA
                                                                                                                                                                                                                                                   Helicobacter.
NCBI_TaxID=210;
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"Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";

"Genomic sequence comparison of two unrelated isolates of the human agastric pathogen Helicobacter pylori.";

"I PUNCTION: PROBUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.

"I SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), GAMMA[1), DELTA(1), EPSILON(1). CF(0)

"I STAILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
MEDLINE=99120557; PubMed=9923682;
ALL R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Gulld B.C., delonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor'D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                20-A0G-2001 (Rel. 40, Created)
20-A0G-2001 (Rel. 40, Last sequence update)
20-A0G-2001 (Rel. 40, Last annotation update)
ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34).
ATP COR JHP1059 (Campylobacter pylori J99) (Campylobacter pylori Forteobacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
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0
                                                         100.0%; Score 14; DB 1; Length 147; Ilarity 100.0%; Pred. No. 6e-08; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
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pfam; PF00401; ATP-synt_DB; 1.

Probom; P000944; ATP-synt_DB; 1.

Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 123 AA.
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HSSP; P00832; 1BSH.
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                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                         1 AGVVDRDYTGEVKV 14
                                                                                                                                                                                                                                81 AGVVDRDYTGEVKV 94
                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome SEQUENCE 123 AA
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| 16 YTGEVK 21
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ATPE_HELPY
ID ATPE_HELPY
                                                         Query Match
Best Local Sim
Matches 14;
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Q92K82;
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ATPE_HELPJ
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NATURE 388:539-547(1997).

NATURE 388:539-547(1997).

PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEBRANE.

SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

HAS THREE MAIN SUBUNITS: A, B AND C.

SIMILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.
STRAIN-2669, ATCC 700392;
STRAIN-2669, ATCC 700392;
TOMD J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Felsochmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Octon M.D., Weidman J.M., Fujii C., Bowman C., Watthey E.K., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith.H.O., Fraser C.M., The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interprice Interprice Products of Arp-synt_DE.

Pfan: Prodod1, Arp-synt_DE; 1.

Prodom: Polod044, Arp-synt_EE; 1.

Hydrolase; Arp synthesis; CF(1); Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA; 13357 MW; 19EDDA4D2B3A5461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERR.
Bacillus sp. (strain RC607).
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4

TO MERR BACSR STANDARD; PRT; 132 AA.

AC P22853

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1993 (Rel. 27, Last sequence update)

DT 01-CCT-1993 (Rel. 27, Last annotation update)

DE MERCURIC RESISTANCE OPERON REGULATORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%; Score 6; DB 1;
ilarity 100.0%; Pred. No. 8.2;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000619; AAD08173.1; ALT_INIT. HSSP; P00832; 1AQT. TIGR; HP1131; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96011384; PubMed=7592346;
Sprenger G.A., Schorken U., Sprenger G., Sahm H.;
"Transaldolase De Escherichia coli K-12: cloning of its gene, talb, and characterization of the enzyme from recombinant strains.";
J. Bacteriol. 177:5930-5936(1995).
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95350630; PubMed-7542800; Platic Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutlon G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al protein; Complete proteome.
185 AA; 20954 MW; 23C80042B2F22449 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
-!- SIMILARITY: STRONG, TO PHACE MU PROTEIN GP16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                          (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%; Score 6; DB 1;
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01-JUL-1993 (Rel. 26, Last sequence update)
02-JUL-1993 (Rel. 40, Last annotation update)
TRANSALDOLASE B (EC 2.2.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 AA.
185 AA.
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0; Mismatches
                                                                                                                                                    MU-LIKE PROPHAGE FLUMU PROTEIN GP16.
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         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                           Haemophilus influenzae.
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                30-MAY-2000
30-MAY-2000
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         VG16_HAEIN
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                 Wang Y., Moore M., Levinson H.S., Silver S., Walsh C., Mahler I.; "Nucleotide sequence of a chromosomal mercury resistance determinant from a Bacillus sp. with broad-spectrum mercury resistance."; J. Bacteriol. 171:883-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00422; HTH_MERR; 1.
PROSTIE; PS00525; HTH_MERR_FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric resistance;
Mercury; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helmann J.D., Wang Y., Mahler I., Walsh C.T.; "Homologous metalloregulatory proteins from both gram-positive and gram-negative bacteria control transcription of mercury resistance
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SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
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C->A: LOSS OF HG BINDING.
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6557FBF1FB95B635 CRC64;
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Pred. No. 8.7;
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         Bacillus/Staphylococcus group; Bacillus.
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HG(2+).
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                                                                                         SEQUENCE FROM N.A.
MEDLINE-89123092; PubMed-2536669;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=89123021; PubMed=2492496;
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100.08; Pr
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PIR; A32239; A32239.
InterPro: IPR000551; HTH_MerR.
Pfam; PF00376; merR: 1.
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Matches 6; Conservative
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REGULATORS.

MUTAGENESIS

ò 셤 RESULT 5

Query Match

SEQUENCE MUTAGEN MUTAGEN

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   agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: SIMILARITY: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

-!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN PATCC 700825 / FA 1090, AND MS11;
STRAIN PATCC 700823 PubMed=10417653;
Zhu P., MOGTAB11 G., Achtman M.;
The opcA and (psi)opcB regions in Neisseria: genes, pseudogenes, deletions, insertion elements and DNA islands.";
MOI. Microblol. 33:635-650(1999).
-! CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PRUVATE + L-GLUTAMATE
-! PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
-! PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
                                                                                   Length 316;
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316 AA; 35088 MW; 2D71C44DFCB55523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ANTHEANLIATE SYNTHASE COMPONENT I (EC 4.1.3.27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.9%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 491 AA.
   entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
INIT_MET 0
ACT_SITE 131 1
SEQUENCE 316 AA;
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X JIA J., Schorken U., Lindqvist Y., Sprenger G.A., Schneider G.;
X JIA J., Schorken U., Lindqvist Y., Sprenger G.A., Schneider G.;
X JIA J., Schorken U., Lindqvist Y., Sprenger G.A., Schneider G.;
X "Crystal structure of the reduced Schiff-base intermediate complex of transaldolase B from Escherichia coli: mechanistic implications for the State of 119-124 (1997).

I TENENTIAL SCI. G. 119-124 (1997).

I FOUNTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF METABOLITES IN THE PENTOSE PHOSPHATE + D-GLYCERALDEHYDE CATALITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE CATALITY: SEDOHEPTULOSE 7-PHOSPHATE PATHWAY.

I SUBUNIT: HOMONIMER - D-ERYTHROSE 4-PHOSPHATE PATHWAY.

I SUBUNIT: HOMONIMER IN CATTON: CYTOPLASHIC (PROBABLE).

I SUBCELLULAR INCATION: CYTOPLASHIC (PROBABLE).

I SUBCELLULAR INCATION: CYTOPLASHIC (PROBABLE).

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Jia J., Huang W., Schoerken U., Sham H., Sprenger G.A., Lindqvist Y.,
Schneider G.;
"Crystal structure of transaldolase B from Escherichia coli suggests
a circular permutation of the alpha/beta barrel within the class I
structure 4:715-724(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12 / EMG2;

MEDLINE-9743975; PubMed-9298646;

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties of proteins encoded

in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12:";
Science 277:1453-1474(1997).
                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN+"L2:
MEDLINE=92334977; PubMed-1630901;
Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Yura T., Marbuchi K., Nakata A.;
"Systematic sequencing of the Escherichia coli genome: analysis of
the 0-2.4 min region."
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12 / W3110;
Basqualı C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.
Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.
Hochstrasser D.F.;
SEQUENCE FROM N.A.
STRAIN-K12 / WillO;
Lida A., Teshba S., Mizobuchi K.;
Submitted (ANG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1994) to the SWISS-PROT data bank.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sprenger G.A.;
Unpublished observations (JUN-1993).
[8]
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Gaps

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Length 491;

42.9%; Score 6; I 100.0%; Pred. No.

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Probom; P0000779; Chorismate_bind; 1.
Tryptophan biosynthesis; Lyase; Complete proteome.
SEQUENCE 491 AA; 54722 MW; 035A92E12707B660 CRC64;
    PRINTS; PR00095; ANTSNTHASEI.
                                                                                                                                              Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                RESULT 9
TRPE_NEIMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                             Gaps
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhu P., Morelli G., Achtman M.; The opca and pseudogenes, The opca and pseudo opca regions in Neisseria: genes, pseudogenes, deletions, insertion elements and DNA islands."; Mol. Microbiol. 33:635-650(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelil G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Sagels K.M., Leather S., Moulle S., Mungall K., Quall M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
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SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
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                                                                                                                                                                                             Length 491;
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                                                                                            Tryptophan biosynthesis; Lyase.
SEQUENCE 491 AA; 54748 MW; A810F7B2304FE47F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
                                                                                                                                                                                   DB 1
26;
                                                                                                                                                                                           42.9%; Score 6; DB 1100.0%; Pred. No. 26; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=22491 / SEROGROUP A / SEROTYPE
                   Pfam; PF00425; chorismate_bind; 1. PRINTS; PR00095; ANTSNTHASEI. ProDom; PD000779; Chorismate_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ242841; CAB44973.1; -.
EMBL; AL162755; CAB84502.1; -.
INTERPROPTO: IPRO00350; Chorismate_bind.
Pfam; PF00425; Chorismate_bind; 1.
InterPro; IPR000350; Chorismate_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09XAZ0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
20-AUG-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                    Query Match
Best Local Similarity
Thes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=65699
                                                                                                                                                                                                                                                                                                                                       351 TGEVKV 356
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                                                                                                                                                                                                                                                                                          9 TGEVKV 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=2017555; PubMed=10710307;
MEDLINE=20175555; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONTA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
-!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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-I - PATHRAX: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
-I - SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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SEQUENCE 491 AA; 54702 MW; 815236B1334D122C CRC64;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
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                                                                                                                                                                                                                                                                                                      491 AA.
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100.0%; Pred. No. 26;
iive 0; Mismatches
0; Mismatches
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Conservative 0
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                                                                                                                                                                                                                                                                                                         STANDARD;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                               351 TGEVKV 356
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                                                               9 TGEVKV 14
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P56995;
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                                                                                                                                Neisseria meningitidis (serogroup C).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=135720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROB_UREPA STANDARD; PRT; 1434 AA.
09POVG;
020-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
BNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE RETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 6; DB 1; Length 491; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tryptophan blosynthesis; Lyase.
SEQUENCE 491 AA; 54719 MW; FC7053315D19EA7B CRC64;
                                                                                  30-MAY-2000 (Rel. 39, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
                                                                         491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ242842; CAB44980.1; -.
InterPro: IPR000350; Chorismate_bind.
Pfam; PF00425; Chorismate_bind; 1.
PRINTS; PR00095; ANTSNTHASEI.
ProDom; PD000779; Chorismate_bind; 1.
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Best Local Similarity 100.
Matches 6; Conservative
                                                                        STANDARD;
                  351 TGEVKV 356
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         TGEVKV 14
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                                                                        TRPE_NE
098358;
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RPOB_UREPA
AC 09POV6,
DT 20-AUG
DT 20-AUG
DE DNA-DII
GE BNA-DII
GN RPOB OI
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BETA' CHAIN.

-1. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

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                                                                                                                                                            STRAIN=SEROVAR 3;
MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
"The complete sequence of the mucosal pathogen Ureaplasma
urealyticum."; 7-f62(2000).
-!- FUNCTION: DNA-DEPENDEMT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETALIAW-C1-6 / DSM 4.304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Craham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Fleischmann R.D., Dougherty B.A., McRenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Mowell L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBDNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
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0
Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmatcaea; Ureaplasma.
NCBI_TaxID-134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
42.9%; Score 6; DB 1; Length 1434;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels
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Archaeoglobus.
Archaeoglobus.
Archaeoglobus.
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InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B. 2.
PROSITE; PS01166; RNA_Pol_BE. 2.
Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1434 AA; 162022 MW; 2841BFA50C19BA7A CRC64;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
HYPOTHETICAL PROTEIN AF0737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AA.
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                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE 1434 A
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029521;
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B29272F519B8E068 CRC64;

8444 MW;

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Query Match
Best Local Similarity
'-hes 5; Conserve
      72 AA;
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34 RDYTG 38
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ID CMGC_BACSU
AC P25955;
      SEQUENCE
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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"Sequence of the left end of Mu.";
"In Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.);
Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press,
New York (1987).
                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
NCBL_TaxID=10677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 67;
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Stoddard S.F., Howe M.M.;
Submitted (SEP-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 67 AA, 7296 MW; 6F103AABBBE56630 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN GP18 (E18 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AA.
                                                                                                                                                   reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.7%; Score 5; DB 1
100.0%; Pred. No. 52;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001054; AAB90514.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF083977; AAF01095.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y00419; CAA68476.1; -. EMBL; M64097; AAA32410.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 5; Conservative
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56 GEVKV 60
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038625;
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VG18_BPMU
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MEDLINE=9938931; Pubmed=9723928;
Chung Y.S., Breidt F., Dubnau D.A.;
Clang Y.S., Breidt F., Dubnau D.A.;
"Cell surface localization and processing of the ComG proteins, required for DNA binding during transformation of Bacillus subtilis.";
mol. Microbiol. 29:905-913(1998).
-!- FUNCTION: REQUIRED FOR TRANSFORMATION AND DNA-BINDING.
-!- SUBCELLULAR LOCATION: THE UNPROCESSED FORM IS AN INTEGRAL MEMBRANE PROTEIN WITH ITS C-TERMINUS OUTSIDE THE MEMBRANE. UPON CLEAVAGE,
IT IS TRANSLOCATED TO THE OUTER FACE OF THE MEMBRANE.
-!- PTM: PROCESSING OF COMGC IN COMPETENT CELLS REQUIRES COMC.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90170868; PubMed=1968455;
Breitling R., Dubnau D.A.;
"A membrane protein with similarity to N-methylphenylalanine pilins is essential for DNA binding by competent Bacillus subtilis.";
J. Bacteriol. 172:1499-1508(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chung Y.S., Dubnau D.A.; "All seven comG open reading frames are required for DNA binding during transformation of competent Bacillus subtilis."; J. Bacteriol. 180:41-45(1998)
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90008773; PubMed=2507524; Albano M., Breitling R., Dubnau D.A.; "Nucleotide sequence and genetic organization of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168 / JH642;
Kobayash, T., Mizuno M., Masuda S., Takemaru K., Hosono S.,
Sato T., Takeuchi M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                0; Indels
         Length 72
                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-AMC-1992 (Rel. 40, Last annotation update)
COMG OPERON PROTEIN 3 PRECURSOR.
DB 1
55;
                                            0; Mismatches
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         Score 5; I
Pred. No.
                                                                                                                                                                                                                     PRT;
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J. Bacteriol. 171:5386-5404(1989).
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         35.7%; S
                                                Conservative
                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    COMGC OR COMG3.
Bacillus subtilis
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EMBL; M29691; AAA83369.1; -.

REMBL; D64432; BAA1235.1; -.

REMBL; D64432; BAA1402.1; -.

R PIR; D30338; D30348; D30408; PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROMED PROM
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METHYLATION (BY SIMILARITY).
17B8152CAFE2E4C9 CRC64;
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illarity 100.0%; Pred. No. 72;
Conservative 0; Mismatches
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98 AA; 10850 MW;
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Best Local Similarity
Matches 5; Conserv
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92 GEVKV 96
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DR Pfam; PP00379; insect_cuticle; 1.

DR PRINTS; PR00247; CUTICLE.

DR PROSTE; PS00243; CUTICLE; 1.

KW Structural protein; Cuticle; Signal; Polymorphism.

FT SIGNAL

FT CHAIN

Search completed: January 31, 2002, 13:39:24

JOB time: 84 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:39:22 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec

US-08-957-709-78 14 1 VGLIDSDYQGQLMI 14 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

100059

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description      | P06968 escherichia |           | 2 haemophil |           |           | P49306 rhizobium m | ~        | _          |            | P17255 saccharomyc | P23334 swinepox vi |            | P47093 saccharomyc | O41033 paramecium | m         |            | Q9z9c2 chlamydia p | Q9x3x5 zymomonas m |          | P54191 drosophila | •          |            | Q9yys0 avian adeno | Q06254 xenopus lae | P57115 buchnera ap | P94965 mycobacteri | 057213 haemophilus | P97769 mus musculu | Q55593 synechocyst | 060258 homo sapien | O70627 mus musculu | _          | P39590 bacillus su |
|-----------|------------------|--------------------|-----------|-------------|-----------|-----------|--------------------|----------|------------|------------|--------------------|--------------------|------------|--------------------|-------------------|-----------|------------|--------------------|--------------------|----------|-------------------|------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|
| SUMMARIES | ID               | DUT_ECOLI          | DUT_BUCAI | DUT_HAEIN   | DUT_PASMU | DUT_COXBU | YMO2_RHIME         | HO_YEAST | SYFB_MYCPN | AMPN_LACLA | VATA_YEAST         | PAP2_SPVKA         | YGAV_ECOLI | YJZ2_YEAST         | DUT_CHVP1         | DUT_SPVKA | YL23_ARCFU | DUT_CHLPN          | DUT_ZYMMO          | DUT_BPT5 | PBP1_DROME        | PTP2_NPVOP | SP2G_BACTK | DUT_ADEG8          | CRG1_XENLA         | HSLV_BUCAI         | RECX_MYCSM         | YE74_HAEIN         | MSG1_MOUSE         | KTHY_SYNY3         | FGFH_HUMAN         | FGFH_MOUSE         | PAP2_CAPVK | YWBG_BACSU         |
|           | Length DB        | -                  | 154 1     | 151 1       | 151 1     | 152 1     | 293 1              | 586 1    | 805 1      | 848 1      | 1071 1             | 69 1               | 99 1       | 128 1              | 141 1             | 142 1     | 143 1      | 145 1              | 146 1              | 148 1    | 148 1             | 160 1      | 161 1      | 163 1              | 1.75 1             | 175 1              | 188 1              | 199 1              | 203 1              | 212 1              | 216 1              | 216 1              | 220 1      | 241 1              |
| , de      | Query<br>Match L | 100.0              | 100.0     | 71.4        | 71.4      | 71.4      | 42.9               | 42.9     | 42.9       | 42.9       | 42.9               | 35.7               | 35.7       | 35.7               | 35.7              | 35.7      | 35.7       | 35.7               | 35.7               | 35.7     | 35.7              | 35.7       | 35.7       | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7       | 35.7               |
|           | Score            | 14                 | 14        | 10          | 10        | 10        | 9                  | 9        | 9          | 9          | 9                  | 2                  | S          | 2                  | 2                 | S         | 5          | . 2                | S                  | 2        | S                 | Ŋ          | S          | Ŋ                  | ស                  | ហ                  | S                  | S                  | 5                  | S                  | ω                  | S                  | ı,         | ι.                 |
|           | Result<br>No.    | 1                  | 7         | m           | 4         | 2         | 9                  | 7        | 8          | σ          | 10                 | 11                 | 12         | 13                 | 14                | 15        | 16         | 17                 | 18                 | 19       | 20                | 21         | 22         | 23                 | 24                 | 52                 | 56                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32         | 33                 |

| P42360 streptococc<br>P42729 rhizobium l |                          | Q03417 zymomonas m<br>Q26230 methanobact | Q9zmv6 helicobacte<br>P56080 helicobacte | P13801 bacillus su | 29/630 Ducineta ap<br>Q94660 plasmodium | Q9zchl rickettsia |
|------------------------------------------|--------------------------|------------------------------------------|------------------------------------------|--------------------|-----------------------------------------|-------------------|
| YSC1_STRGC<br>TFXG RHILT                 | GLK2_XENLA<br>Y4OV_RHISN | SCRK_ZYMMO<br>DHYS_METTH                 | Y117_HELPJ<br>Y117_HELPY                 | SP2G_BACSU         | RLAO_PLAF8                              | FABH_RICPR        |
|                                          |                          |                                          |                                          | ٦,                 |                                         | -                 |
| 251                                      | 285<br>285               | 301                                      | 308                                      | 309                | 316                                     | 317               |
| 35.7                                     | 35.7                     | 35.7                                     | 35.7                                     | 35.7               | 35.7                                    | 35.7              |
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| 34<br>35                                 | 36                       | 38<br>39                                 | 40                                       | 42                 | 43                                      | 45                |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=RD, KW20, KW20, ATCC 51907;
STRAIN=RD, KW20, ATCC 51907;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tromb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Wenter J.C.;
Wenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).

-!- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT PRODUCES DUMP, THE IMMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT URACIL CANNOT BE INCORPORATED INTO DNA (BY SIMILARITY).

-!- CATALYTICA CATIVITY: DOTP + H(2)0 - DUMP + PYROPHOSPHATE.

-!- PATHWAX: DE NOVO SYNHESIS OF THYMIDYLATE.

-!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DECXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dota m. 12.2. influenzae.
Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}.^{\mathrm{n}}:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 14; DB 1; Length 154; 100.0%; Pred. No. 1.3e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            EMBL; AP001119; BAB13250.1; ...
InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
Hydrolase; Nucled metabolism; Complete proteome.
SEQUENCE 154 AA: 16936 MW; E5BSFDEBFB09E920 CRC64;
              SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUTPASE) (DUTP PYROPHOSPHATASE)
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Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VGLIDSDYQGQLMI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUT OR HI0954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUT_HAEIN
P43792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
DUT_HAEIN
ID DUT_HAEIN
AC P43791
DT O1-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchhera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria: Proteobacteria: gamma subdivision; Buchnera.
NCBL_TaxID=118099;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00692; dUTPase; 1
Hydrolase; Nucleotide metabolism; 3D-structure; Complete proteome.
SEQUENCE 151 AA; 16155 MW; 98FA3DE0BC70FFB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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1957623.
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE 5-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 14; DB 1; Length 151; 100.0%; Pred. No. 1.3e-08; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X01114; CAA25859.1; EMBL, X01578; CAA24897.1; EMBL; L10128; AAA61993.1; EMBL, AE000441; AAC76664.1; PIR; Q000497; WPDS; LDUP; 01-SEP-95; PDB; LDUP; 01-SEP-95; PDB; LDUP; 01-SEP-95; PDB; LDUP; 03-MAY-00. SWISS-2DPAGE; P06968; COLI. ECOZDBASE; CO17.2; 6TH EDITION. ECOGENE; EG010251; dut. InterPro; IPR01428; dutrpase. Pfam; PF00692; durpase: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DUTPASE) (DUTP PYROPHOSPHATASE).
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                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
Coxiella group; Coxiella.
NCBL_TaxID=777;
                                          15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 AA; 16213 MW; 00041727C1882C57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism.
                                                                                        (DUTPASE) (DUTP PYROPHOSPHATASE).
                             15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%; 100.0%;
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Best Local Similarity 100.
Matches 10; Conservative
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STANDARD;
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                                                                                                                     Coxiella burnetii.
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P49306:
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
DUT OR PM1154.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                     71.4%; Score 10; DB 1; Length 151; 100.0%; Pred. No. 0.00026; Pred. No. 0.10026; ive 0; Mismatches 0; Indels
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         TIGR; H10954; -...
InterPro; IPR001428; duTPase.
Pfam; PF00692; duTPase; 1.
Hydrolase; Nucleotide mctabolism; Complete proteome.
SEQUENCE 151 AA; 16445 MW; 78A45c50518FCDE2 CRC64;
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SEQUENCE 151 AA: 16170 MW; 99B088FFADD2F843 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
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                                                                                                                                                    Conservative
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Matches 10; Conservative
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                                                                                                                                     Best Local Similarity
Matches 10; Conserv
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P57914;
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RESULT 4

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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 32.3 KDA PROTEIN IN MOCC-MOCA INTERGENIC REGION (ORF293).
RhizoDium melliOti (Sinorhizobium melliOti).
Barcteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rossbach S., Kulpa D.A., Rossbach U., de Bruijn F.J.;
"Molecular and genetic characterization of the rhizopine catabolism
(MOCABRC) genes of Rhizobium meliloti L5-30.";
Mol. Gen. Genet. 245:11-24(1994).
                                                                       ő
Length 152;
Score 10; DB 1; Le
Pred. No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                      293 AA
                                                                   0; Mismatches
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RESULT 5

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WALCHING."

WELL BLAYNOL. 194:132-146(1991)

I PUNCTION: INITIATION OF MATING TYPE INTERCONVERSION. THIS PROTEIN

IS A SITE-SPECIFIC ENDONUCLEASE THAT CLEAVES A SITE IN THE MAT

LOCUS ON CHROMOSOME III. THE DOUBLE-STRAND BREAK IS FOLLOWED BY A

UNIDIRECTIONAL GENE CONVERSION EVENT THAT REPLACES THE INFORMATION

AT THE MAT LOCUS BY INFORMATION COPIED FROM ETHER OF THE TWO

HONOLOGOUS LOCI (HMR AND HML) THAT RESIDE AT THE EXTREMITY OF THE

CHROMOSOME III. ENDONUCLEASE EXPRESSION TAKES PLACE IN LATE GI

JUST BEFORE CELLS ENTER S PHASE.

I- MISCELLAREOUS: THE METAL-BINDING DOMAIN FORM ZINC-FINGERS THAT ARE

INVOLVED IN BINDING OF THE DNA

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-87089786; PubMed-3025649;
Russell D.W., Jensen R., Zoller M.J., Burke J., Errede B., Smith M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meiron H., Nahon E., Raveb D.;
Meiron H., Nahon E., Raveb D.;
"Identification of the heterothallic mutation in HO-endonuclease of
S. cerevisiae using HO/ho chimeric genes.";
Curr. Genet. 28:367-373(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herskoutz I.;
Herskoutz I.;
"Structure of the Saccharomyces cerevisiae HO gene and analysis of
its upstream regulatory region.";
Mol. Cell. Biol. 6:4281-4294(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HO_YEAST STANDARD; PRT; 586 AA.
010931; 012183; 012183; 0190932; 012183; 0109932; 012183; 0109932; 010187.
010-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HOMOTHALLIC SWITCHING ENDONUCLEASE.
HOMOTHALLIC SWITCHING ENDONUCLEASE.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomycetar, Fungi; Ascomycota; Saccharomyceties; Saccharomycetaces; Saccharomycets.
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                                                                                                                                                                                                                                                                                                                                                                 Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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SEQUENCE FROM N.A.
REQUISSED S.W.:
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      EMBL; X78503; CAA55268.1; -.
Hypothetical protein.
SEQUENCE 293 AA; 32308 MW; 2D4A662356EAA2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.9%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 9.6; Matches 6; Conservative 0; Mismatches
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MEDLINE-96120866; Pubmed-8590483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSUKASSAKI F., Motoshima H., Minagawa E., Kaminogawa S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AMINOPEPTIDASE WITH BROAD SUBSTRATE SPECIFICITY TO
SEVERAL PEPTIDES. IT HAS MORE AFFINITY FOR OLIGOPEPTIDES THAN FOR
DIPEPTIDES. IT PLAYS AN ESSENTIAL ROLE IN THE METABOLISM, IT MAY
BE INVOLVED IN NITROGEN SUPPLY OR PROTEIN TURNOVER.
-!- COFACTOR: BINDS ONE ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AN UNKNOWN MECHANISM.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE PEPN SUBFAMILY.
                Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
AMINOPEPTIDASE N (EC 3.4.11.2) (LYSYL AMINOPEPTIDASE) (LYS-AP)
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BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

PROTON DONOR (POTENTIAL).

6EDE1716CF2B1185 CRC64;
                                                                                            Length 805
                                                                                                                           0; Indels
                                               937B7614E789547A CRC64;
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
                                                                                            DB 1;
                                                                                                                                                                                                                                                                     848 AA.
                                                                                         42.9%; Score 6; DB 1
100.0%; Pred. No. 23;
iive 0; Mismatches
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InterPro; IPR01899; Gram_pos_anchor.
InterPro; IPR001899; Gn_MPoptdse.
Pfam; PF01433; Peptidase_M1; 1.
                                             91713 MW;
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EMBL; AE000006; AAB95696.1;
                                                                           Query Match
Best Local Similarity 10v.v.
6; Conservative
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                                                                                                                                                                                                                                                                      STANDARD;
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294
297
316
381
848 AA;
                                               805 AA;
                              Complete proteome.
SEQUENCE 805 AA
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560 VGLIDS 565
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                                                                                                                                                       1 VGLIDS 6
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Q48656;
01-NOV-1997
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METAL
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Length 848;

DB 1;

Score 6; IPred. No.

42.9%; S 100.0%;

Query Match Best Local Similarity

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AEDLINE=5288C / FY1679;
MEDLINE=96021607; PubMed=8533471;
Verhasselt P., Voet M., Volckaert G.;
New open reading frames, one of which is similar to the nifV gene of Azotobacter vinelandi, found on a 12.5 kbp fragment of chromosome IV of Saccharomyces cerevisiae.";
Yeast 11:961-969(1995).
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirata R., Ohsumi Y., Nakano A., Kawasaki H., Suzuki K., Anraku Y.; "Molecular structure of a gene, VMA1, encoding the catalytic subunit of H(+)-translocating adenosine triphosphatase from vacuolar
                                                                                                                                                                      VATA_YEBSY
STANDARD; PRT; 1071 AA.
P17255; 074301;
01-306-1990 (Rel. 15, Created)
01-306-1990 (Rel. 15, Last sequence update)
20-AUG-2001 (Rel. 40, Last amoutation update)
20-AUG-2001 (Rel. 40, Last amoutation update)
VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (EC 3.6.1.34) (V-ATPASE A SUBUNIT) (CONTAINS: ENDONUCLEASE PI-SCEI (EC 3.1.-.-) (VMAI-DERIVED ENDONUCLEASE) (VDE) (SCE VMA INTEIN)]
(VMAI OR TFPI OR CLESS OR YDILSSW OR D1286) AND VDE.
Saccharomyces cerevisiae (Baker's yeast).
EUKAIYOta; Fungl: Ascomycota: Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kane P.M., Yamashiro C.T., Wolczyk D.F., Neff N., Goebl M., Stevens T.H.:
"Protein splicing converts the yeast TFP1 gene product to the 69-kD subunit of the vacuolar H(+)-adenosine triphosphatase."; Science 250:651-657(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mutations at the putative junction sites of the yeast VMA1 protein, the catalytic subunit of the vacuolar membrane H(+)-ATPase, inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 41-1071 FROM N.A.

MEDLINE-89096895; Pubmed-2905423;

Shih C.K., Wagner R., Feinstein S., Kanik-Ennulat C., Neff N.;

Adominant trifluoperazine resistance gene from Saccharomyces cerevisiae has homology with F0F1 ATP synthase and confers calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93285129; pubMed=8508780;
Cooper A.A., Chen Y.-J., Lindorfer M.A., Stevens T.H.;
                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          processing by protein splicing."; them. Biophys. Res. Commun. 188:40-47(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membranes of Saccharomyces cerevisiae."
J. Biol. Chem. 265:6726-6733(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sensitive growth.";
Mol. Cell. Biol. 8:3094-3103(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SPLICING.
MEDLINE=91047969; PubMed=2146742;
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Hirata R., Anraku Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-34 FROM N.A. STRAIN=W303-1A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=X2180-1A;
                                                                             526 DYQGQL 531
                                        7 DYQGQL 12
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TII CATS CAN AND AN ACTIONAL OF PI-SCE I.

RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF PI-SCE I.

RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF PI-SCE I.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A PROST-TRANSLATIONAL EXCISION OF THE VDE REGION FOLLOWED BY
        a
"Protein splicing of the yeast TFP1 intervening protein sequence: model for self-excision.";
EMBO J. 12:2575-2583(1993).
                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF PI-SCE I.
MURDILINE-73704384. PUDNEd-21506747;
MURDIN X., Gimble F.S., Quiocho F.A.;
Crystal structure of PI-Scel, a homing endonuclease with protein splicing activity.";
Cell 89:555-564(1997).
                                                                                                  FUNCTION OF VDE.

**MEDILINE-92269931; PubMed-1534148;

GIMDLE F.S., Thorner J.;

"Homing of a DNA endonuclease gene by meiotic gene conversion in Saccharomyces cerevisiae.";

Nature 357:301-306(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: WE IS HIGHLY SIMILAR TO ENDONUCLEASE HO.
SIMILARITY: VDE IS HIGHLY SIMILAR TO ENDONUCLEASE HO.
                                                                                                                                                                                                                                                                                REVIEW.
Grivell L.A.;
Grivell L.A.;
Curr. Biol. 2:450-452(1992).
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EMBL, X83276; CAA58261.1; --
EMBL, Z74233; CAA98761.1; --
EMBL, Z74233; CAA98761.1; --
EMBL, M21609; AAB63978.1; --
EMBL, X58877; CAA41657.1; --
PIR, A35746; PXBYVA.
PIR, A35746; PXBYVA.
PIR, 10PR, 08-DEC-99.
REBASE, 2615; PI-SCEI.
SGD; S0002344; TFP1.
InterPro; IPR000793; ATPase_AB_C.
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                                                                                                                                                                                                                              A, IST PART.
ENDONOCLEASE PI-SCEI.
VACUOLAR ATP SYNTHASE CATALVTIC SUBUNIT
A, 2ND PART.
ATP (EW SIMILARITY).
CONSERVED MOTIF FOR MITOCHONDRIAL MRNA
MATURASES OF YEAST AND FUNGI.
C->S: INHIBITS SPLICING.
C->S: INHIBITS SPLICING.
G->D (IN REF. 3).
36 MW; 2AACGSD2FS9426FD CRC64;
InterPro; IPR000194; ArPase_alpha_beta.
InterPro; IPR003586; Hintc.
InterPro; IPR003587; Hintc.
InterPro; IPR003587; Hintc.
InterPro; IPR003587; Hintc.
InterPro; IPR003587; Hintc.
InterPro; IPR00305; ArP-synt_ab, I.
SMART; SM00306; ArP-synt_ab, I.
PR031E; PS00152; ArPASE_ALPHA_BETA; I.
PR051E; PS00152; ArPASE_ALPHA_BETA; I.
PR051E; PS00181; PROTEIN_SPICING; I.
PR051E; PS00181; PROTEIN_SPICING; I.
PR051E; PS00181; PR0TEIN_SPICING; I.
I. 283 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT
I. 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILNE-91196265; PubMed=1840707;
MEDILNE-91196265; PubMed=1840707;
Schnitzlein W.M., Tripathy D.N.;
Schnitzlein w.M., Tripathy D.N.;
Identification and nucleotide sequence of the thymidine kinase gene of swinepox virus.";
Virology 181:727-732(1991).
-i- FUNCTION: POLYMERASE THAT CREATES THE 3' POLY(A) TAIL OF MRNA'S.
THE REGULATORY SUBUNIT BINDS TO POLY(A) BUT HAS NO CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY.
-!- SUBUNIT: HETERODIMER OF VP55 (CATALYTIC) AND VP39 (REGULATORY).
-!- SIMILARITY: TO OTHER POXVIRUSES VP39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swinepox virus (strain Kasza) (SPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
POLY(A) POLYMERASE REGULATORY SUBUNIT (PAP) (VP39) (FRAGMENT).
SWF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%; Score 6; DB 1; ilarity 100.0%; Pred. No. 30; Conservative 0; Mismatches
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PIR; D37949; D37949.
HSSP; P07617; 1AV6.
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738
875
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Best Local Similarity
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NCBI_TaxID=10277;
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604 GLIDSD 609
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601
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P23334;
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MUTAGEN
CONFLICT
SEQUENCE
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SIMILAR
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Gaps

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0; Indels Length 99;

H-T-H MOTIF (BY SIMILARITY). 93B9B32C62CC0223 CRC64;

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Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 45; Matches 5; Conservative 0; Mismatches
              41 60
99 AA; 10596 MW;
    proteome.
                                                                                                                                                                         YJZ2_YEAST
P47093;
   Complete pond BIND SEQUENCE
                                                                                                                                                    RESULT 13
YJZ2_YEAST
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ID DUT_C
AC 04103
DT 15-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1655,
STRAIN-KIZ. / MG1657,
Pubbed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae;
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InterPro; IPR001845; HTH_ARSR.
Pfam; PF01022; HTH_5; 1.
SWART; SW00418; HTH_ARSR.
PROSITE; PS00846; HTH_ARSR.FAMILY; FALSE_NEG.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                 0; Indels
                                                                            Length 69;
                                              C6830F285030213E CRC64;
                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YGAV.
                                                                           35.7%; Score 5; DB 1;
100.0%; Pred. No. 33;
iive 0; Mismatches
                                                                                                                                                                                               .99 AA.
InterPro; IPR000176; PolA_polym_reg. Pfam; PF01358; PARP_regulatory; 1. Transferase; Transcription. 69 MW. TER 69 69 MW; C6830F2 SEQUENCE 69 AA; 8069 MW; C6830F2
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000351; AAC75714.1; -.
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                                                                 Ouery Match
Best Local Similarity 100...
5, Conservative
                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGULATORS.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                      8 YQGQL 12
                                                                                                                                         36 YQGQL 40
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P77295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 66-128 FROM N.A.
MEDLINE=96109310; PubMed=8619316;
Zagulski M., Babinska B., Gromadka R., Migdalski A., Rytka J.,
Sulicka J., Herbert C.J.;
"The sequence of 24.3 kb from chromosome X reveals five complete open
reading frames, all of which correspond to new genes, and a tandem
insertion of a Tyl transposon.";
Yeast 11:1179-1186(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 14.5 KDA PROTEIN IN MERZ-BNAI INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de Haan M., Smits P.H.M., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X87611; CAA60945.1; -.
EMBL; Z4522; CAA89547.1; -.
SGD; S0003783; YAT022W.
InterPro; IPR001163; SNRNP_Sm.
Pfam; PF04423; Sm; 1.
Hypothetical protein.
SEQUENCE 128 AA; 14518 MW; F05592F393BEF3DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%; Score 5; DB 1;
100.0%; Pred. No. 57;
tive 0; Mismatches
                                                                                                                                                                                                    128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUT_CHVP1 STANDARD; F 041033; 15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                XJR022W OR J1464 OR YJR83.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Lange 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                 ||||||
66 GLIDS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||
83 VGLID 87
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2 GLIDS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                             Gaps
                                                                                                                      Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dSDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
NCBI_Tax1D=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homologue.";
Virology 197:511-528(1993).
-!- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLECTIDE METABOLISM: IT
PRODUCES DUMP, THE INMEDIATE PRECURSOR OF THYMIDINE NUCLEOTIDES
AND IT DECREASES THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swinepox virus (strain Kasza) (SPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-94060924; PubMed-8249275;
MESSUNG R.F., Jayarama V., Moyer R.W.;
Massung R.F., Jayarama V., Moyer R.W.;
"DNA sequence analysis of conserved and unique regions of swinepox virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
(DUTPASE) (DUTP PYROPHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBLY.
Interpro; IPR001440,
Pfam; PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism.
Hydrolase; Nucleotide metabolism.
Amarence 141 AA; 14879 MW; 3D0734C9C9BD70B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Score 5; DB 1;
100.0%; Pred. No. 61;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DUTPASE) (DUTP PYROPHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U42580; AAC96912.1; -. InterPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suipoxvirus.
NCBI_TaxID=10277;
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79 IDSDY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IDSDY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
DUT_SPWRA

ID DUT_SPWRA

AC P32208;
DT 01-0CT-1993
DF 15-DEC-1993
DE COTTE-1993
DE COTTE-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
URACIL CANNOT BE INCORPORATED INTO DNA.
-!- CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
-!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A PROFEASE-LIKE PROTEIN (PSEUDOPROTEASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                most, Fourdon, Proposes.
Pfam, PF00692; durpase; 1.
Hydrolase; Nucleotide metabolism.
SEQUENCE 142 AA; 15750 MW; 13BCDF9C64AD9635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.7%; Score 5; DB 1;
100.0%; Pred. No. 62;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 31, 2002, 13:39:23 Job time: 83 sec
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L22013; AAC37860.1; -. HSSP; P06968; 1DUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query.Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
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us-08-957-709-77.rsp

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:39:21 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec Run on:

US-08-957-709-77 14 1 AHRIDPGWSGCIVL 14 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

0 Word size :

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | esche     | P57209 buchnera ap | pasteurel | P44534 haemophilus |           | borrelia   | P09261 varicella-z | P43602 saccharomyc | P46531 homo sapien |            |           | 4          |            | P80726 anguilla an | 075340 homo sapien | _          | O54294 salmonella | Q53178 rhodobacter | P55617 rhizobium s | Q53138 rhodococcus | 053191 mycobacteri |            | P78009 mycoplasma |            |            | 9          | _        | Ç          | 013597 septoria ly | 37 human cyt | 664 sacchar | 27404 feline | P27405 feline cali |
|-----------|----------------|-----------|--------------------|-----------|--------------------|-----------|------------|--------------------|--------------------|--------------------|------------|-----------|------------|------------|--------------------|--------------------|------------|-------------------|--------------------|--------------------|--------------------|--------------------|------------|-------------------|------------|------------|------------|----------|------------|--------------------|--------------|-------------|--------------|--------------------|
| SUMMARIES | ID             | DCD_ECOLI | DCD_BUCAI          | DCD_PASMU | DCD_HAEIN          | DCD_BUCAP | Y085_BORBU | CELF_VZVD          | YFJ2_YEAST         | NTC1_HUMAN         | IF1C_MARPO | FER_PSALA | YJIW_ECOLI | HBA4_XENLA | HBAC_ANGAN         | PCD6_HUMAN         | PCD6_MOUSE | CSGD_SALTY        | NAPC_RHOSH         | Y4PL_RHISN         | COBM_RHOSO         | YO64_MYCTU         | YAFJ_HAEIN | EFTS_MYCPN        | Y370_MYCGE | Y370_MYCPN | ML1B_HUMAN | B3_USTMA | RHSA_RHIME | ER24_SEPLY         | TEGU_HCMV    | 1           | COAT_FCVC6   | COAT_FCVF4         |
|           | DB             | Н         | -                  | П         | Н                  | П         | ٦          | -                  | 1                  |                    | 7          | ٦         | 7          | -          | -                  | 7                  | -          | ч                 | ч                  | ч                  | Н                  | 7                  |            | -                 | -          | Н          |            | -        | Н          | -                  | Ħ            | -           | -            | Н                  |
|           | Length         | 193       | 193                | 194       | 195                | 193       | 141        | 340                | 733                | 2444               | 78         | 107       | 132        | 141        | 142                | 191                | 191        | 216               | 227                | 245                | 249                | 268                | 294        | 298               | 323        | 326        | 362        | 410      | 470        | 512                | 549          | 663         | 999          | 899                |
| d         | Query<br>Match | 100.0     | 57.1               | 57.1      |                    | 。         | ~          | 2                  | 2                  | 42.9               | 35.7       | 35.7      | 35.7       | 35.7       | 35.7               | 35.7               | 35.7       | 35.7              | 35.7               | 35.7               | 35.7               | 35.7               | 35.7       |                   |            |            | 35.7       | ٠.       | ٠.         |                    | 5.           | 'n.         | 35.7         | 35.7               |
|           | Score          | 14        | 80                 | 80        | Φ                  | 7         | 9          | 9                  | 9                  | 9                  | ഗ          | S         | S          | 2          | ហ                  | S                  | S          | S                 | 'n                 | S                  | Ω.                 | വ                  | S          | S                 | Ŋ          | S          | 2          | ស        | 2          | S                  | S            | S           | ស            | S                  |
|           | Result<br>No.  | 1         | 7                  | m         | 7                  | 5         | 9          | 7                  | æ                  | σ                  | 10         | 11        | 12         | 13         | 14                 | 15                 | 16         | 17                | 18                 | 19                 | 20                 | 21                 | 22         | 23                | 24         | 25         | 56         | 27       | 28         | 58                 | 30           | 31          | 32           | 33                 |

|            | Q9zky0 helicobacte | P50610 helicobacte | Q46861 escherichia | Q18600 caenorhabdi | P52550 gallus gall | P15558 pseudomonas | P39920 coxiella bu |            | P25733 escherichia | Q11042 mycobacteri | 09p0kl homo sapien |
|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|
| COAT_FCVF9 | FLGE_HELPJ         | FLGE_HELPY         | YGIQ_ECOLI         | YTV2_CAEEL         | MYBA_CHICK         | PAC2_PSES3         | FTSK_COXBU         | AD22_MOUSE | CFAC_ECOLI         | YC78_MYCTU         | AD22_HUMAN         |
| 1          | П                  | П                  | Т                  | Т                  | П                  | П                  | Ţ                  | 7          | г                  | T                  | 7                  |
| 671        | 718                | 718                | 739                | 744                | 757                | 773                | 778                | 857        | 869                | 875                | 906                |
| 35.7       | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7       | 35.7               | 35.7               | 35.7               |
| 5          | Ŋ                  | Ŋ                  | Ŋ                  | Ŋ                  | Ŋ                  | Ŋ                  | Ŋ                  | Ŋ          | 2                  | S                  | ß                  |
| 34         | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42         | 43                 | 44                 | 45                 |

## ALIGNMENTS

194 AA.

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                                                                                                                                                                                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP DEAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=PMON.A.
STRAIN=PMON.
STRAIN=PMON.
STRAIN=PMON.
STRAIN=PMON.
MAY B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- CATALYTIC ACTIVITY: DCTP + H(2)O = DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
NCBL_Tax.D=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE006134; AAK03035.1; -.
InterPro; IPR001323; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase, 1.
ProDom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 194 AA; 21467 WW; AC76D219F5258F94 CRC64;
                                                                                                                                                                      STANDARD;
       124 AHRIDPGW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AHRIDPGW 8
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P44534;
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20-40G-2001 (Rel. 40, Last sequence update)
20-40G-2001 (Rel. 40, Last sequence update)
20-40G-2001 (Rel. 40, Last annotation update)
DEAMINASE).
DEAMINASE).
DCD OR BUIO8
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum Symbiotic bacterium).
Bacteria: Proteobacteria; gamma subdivision; Buchnera.
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                                     , DB 1; Leus
No. 0.012;
0, Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 14; Conservative 0; Mismatches 0; Indels
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ProDom; PD004900; dcTp-deaminse; 1.
Hydrolase; Complete protecome:
SEQUENCE: 193 AA; 21951 MW; DE7DD7FD961FC9FA CRC64;
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Best Local Similarity 100.0%; Pred. No. 0.
Matches 8; Conservative 0; Mismatches
send an email to license@isb-sib.ch).
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InterPro; IPR003332; dCTP_deaminse.
InterPro; IPR001428; dUTPasse.
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STRAIN=RD / KW20 / ATCC 51907;
MEDILINE=59550630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
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DCD OR H10133.
Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                     57.1%; Score 8; DB 1; Length 194; 100.0%; Pred. No. 0.012; ive 0; Mismatches 0; Indels
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DEOXYCYIIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
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Query Match
Best Local Similarity 100..
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     InterPro; IPR001428; dUTPase.
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                                                                                                                                                                                           Query Match 50.0°
Best Local Similarity 100.
Matches 7; Conservative
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Nature 390:580-586(1997).
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                                  Pfam; PF00692; dUTPase;
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Matches 6; Conserv
                                                                                                                 193 AA;
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| 125 HRIDPGW 131
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30-MAY-2000
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58 SGCIVL
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P09261;
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CELF_VZVD
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Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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MEDLINE=9844031; PubMed=9767718;

Clark M.A., Baumann P.;

Clark M.A., Baumann P.;

Buchnera aphidicola (Aphid endosymbiont) contains genes encoding enzymes of histidine biosynthesis.";

Curr, Microbiol. 37:356-358(1998).

-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).

-!- CAMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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20-MG-2001 (Rel. 40, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13) (DCTP
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Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD004900; dCTP_deaminse; 1.
Hydrolase; Complete proteome.
SEQUENCE 195 AA; 21616 MW; 39EE5C2370A6C1CB CRC64;
                                                                                                                                                                                                                     Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: DCTP + H(2)0 = DUTP + NH(3).
-!- SUBUNIT: HOMOTERRAME (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
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100.0%; Pred. No. v...
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InterPro; IPR001428; dUTPase.
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InterPro; IPR003232; dCTP_deaminse.
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STRAIR=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Hanang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 141;
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                                                                                                                                                                                                                                            0; Indels
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SEQUENCE 141 AA; 16214 MW; 1F42B5CABFAA690F CRC64;
                                                                       21871 MW; 8E19D4580C7C55E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                    50.0%; Score 7; DB 1;
100.0%; Pred. No. 0.17;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.9%; Score 6; DB 1; 100.0%; Pred. No. 1.8;
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(Rel. 10, Last sequence update)
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ProDom; PD004900; dCTP_deaminse; 1.
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NTC1_HUMAN
P46531:
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NTC1_HUMAN
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SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

MEDLINE-95400292; PubMed-7670463;

Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,

Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,

Samazaki M., Tashiro H., Eki T.;

"Analysis of the nucleotide sequence of chromosome VI from

Saccharomyces cerevisiae.";

Nat. Genet. 10:261-268(1995).

-: SIMILARITY: TO YEAST RODI, YGRO68C AND TO S.POMBE SPAC31A2.12 AND

SPAC8A4.13C.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
0387FE00EC39C946 CRC64;
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Eukaryota: Kungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID-4932;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
41-YPOTHETICAL 79.7 KDA PROTEIN IN FABI-PES4 INTERGENIC REGION
YER022W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
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                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-8650657; Pubwed-3018124;
Davison A.J., Scott J.E.;
"The complete DNA sequence of varicella-zoster virus.";
J. Gen. Virol. 67:1759-1816(1986).
                                                                    (VZV).
Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL FUSION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 42.9%; Score 6; DB 1; Best Local Similarity 100.0%; Pred. No. 3.7; Matches 6; Conservative 0; Mismatches
     annotation update)
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PIR; E27212; MMBES.
InterPro; IPR002567; Fusion_gly_K.
Pfam; PF01621; Fusion_gly_K; 1.
Fusion protein; Transmembrane; Signal.
SIGNAL
                                                               Varicella-zoster virus (strain Dumas)
Viruses; dsDNA viruses, no RNA stage:
Alphaherpesvirine; Varicellovirus.
VCBI_TaxID=10338;
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55 55 N
65 65 N
340 AA; 38576 MW;
15-DEC-1998 (Rel. 37, Last and
CELL FUSION PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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P43602;
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A BILLIAN BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, BILLOW, 
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (A. Last annotation update)
NEUROCENIC LOCUS NOTCH PROTEIN HOMOLOG I PRECURSOR (TRANSLOCATION-ASSOCIATED NOTCH PROTEIN TAN-1) (FRAGMENT)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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MINST, FOUNDS, LIAM.
MINSTALL PRROBLID: ANK.
LINEAFPO: IPRO00152; ASX.hydroxyl.
LINEAFPO: IPRO00561; EGF-1ike.
LINEAFPO: IPRO00742; EGF-2.
LINEAFPO: IPRO01881; EGF-CA.
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CYOPLASMIC (POTENTIAL).

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EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 1.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9.

EGF-LIKE 11.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13.

CALCIUM-BINDING (POTENTIAL).

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CALCIUM-BINDING (POTENTIAL).

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CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21.

EGF-LIKE 21.

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CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 24.

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CALCIUM-BINDING (POTENTIAL).

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EGF-LIKE 33.

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Nature 323:572-574(1986).
INTIATION: NO SPECIFIC FUNCTION HAS SO FAR BEEN ATTRIBUTED TO THIS INTIATION FACTOR; HOMEVER, IT SEEMS TO STIMULATE MORE OR LESS ALL.
THE ACTIVITIES OF THE OTHER TWO INITIATION FACTORS, IF-2 AND IF-3.
SUBCELLULAR LOCATION: CHLOROPLAST.
SUBCELLULAR ELONGY TO THE IF-1 FAMILY.
SIMILARITY: BELONGS TO THE IF-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Marchantiales; Marchantlaceae; Marchantla.
NCBL_TaxID=3197;
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A. MEDINE-8008687; PubMed=3199436; MEDINE-80086887; PubMed=3199436; Pukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H., Ozeki H., Ohyama K.; Structure and organization of Marchantia polymorpha chloroplast structure and organization of the large single copy region from rbcL to rn1(CAU)."; Jubel 101: 203:333-351(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLETE GENOME.
Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
Umesono K., Shiki Y., Takeuchi M., Chang 2., Aota S., Inokuchi H.,
                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                           Length 2444;
                                                                                                                                                                                                                                                                                              0; Indels
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PIR; A05008; A05008.

HISP: P02998; LABO;
Interpro; IPR03029; S1.

Ffam; PF00575; S1; 1.

SMART; SM0316; S1; 1.

Intitation factor; Protein biosynthesis; Chloroplast.

SEQUENCE 78 AA; 8978 MW; B0C85D43EBA5AFB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-027.1989 (Rel. 12, Created)
01-027-1989 (Rel. 12, Last sequence update)
20-030-2001 (Rel. 40, Last annotation update)
TRANSLATION INITIATION FACTOR IF-1, CHLOROPLAST.
                                                                                                                                                                                                                              DB 1;
SIMILARITY.
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                                                                                                                                                                                                                           42.9%; Score 6; DB 1
100.0%; Pred. No. 18;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marchantia polymorpha (Liverwort).
       BY
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Best Local Similarity 100.
انمو 6; Conservative
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   1008
1019
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   993
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P12134;
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IFIC_MARRO
AC P10234,
DT 101-0234,
   FFF
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P39394;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
HYPOTHETICAL 14.6 KDA PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132).
YJIW OK B437.
BSCHETICAL 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERREDOXIN.
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
F033ACCB00134CC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9411457; pubmed-8286402;

Brul S., Veltman R.H., Lombardo M.C.P., Vogels G.D.;

Brul S., Veltman R.H., Lombardo M.C.P., Vogels G.D.;

Molecular cloning of hydrogenosomal ferredoxin cDNA from the anaerobic amoeboflagellate Psalteriomonas lanterna.";

Blochim. Biophys. Acta 1183:544-546(1994).

"I FUNCTION: FERREDOXINS ARE IRON-501LFUR PROTEINS THAT TRANSFER ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.

"CORACTOR: BINDS A 2FE-2S CLUSTER.
"I SUBCELLULAR LOCATION: HYDROGENOSOMAL.

"I SIMILARITY: TO 2FE-2S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö;
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Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae;
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                                             Indels
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     Length 78;
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PROPEP
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                                                                                                                                                                                                                                                                       P34806.
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FERREDOXIN PRECURSOR.
  35.7%; Score 5; DB 1;
100.0%; Pred. No. 16;
ive 0; Mismatches
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Query Match
Best Local Similarity
Matches 5; Conserv
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es 5; Conserv
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NCBI_TaxID=31290;
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29 GCIVL 33
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Best Local S
Matches 5
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FER_PSALA
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0; Indels

Length 141;

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MEDLINE=95370199; PubMed=7642546;
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rago A., Carratore V., di Prisco G., Feuerlein R.J.,
Rado Carratore R.E.;
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
40, Last annotation update)
HEMOGLOBIN CATHODIC, ALPHA CHAIN.
Anguilla anguilla (European freshwater eel).
Eukaryota: Medazoa: Chordata: Craniata; Vertebrata: Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
NCBL_TaxID=7936;
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PRINTS; PR00612; ALPHAHRM.
PROSITE; PS01033; GLOBIN; 1. Heme; Oxygen transport; Respiratory protein; Erythrocyte; Acetylation. MOD_RES 1 1 ACETYLATION (PROBABLE).
METAL 59 59 IRON (HFMF DISTAL ITCAND.)
                                                                                                                                                                                           IRON (HEME DISTAL LIGAND).
IRON (HEME PROXIMAL LIGAND).
41E6580905BDF546 CRC64;
                             Pfam; PF00042; globin; 1.
PRIMTS: PR00612; ALDHAMABE.
PROSITE: PS01033; GLOBIN; 1.
Heme: Oxygen transport; Respiratory protein; Erythrocyte.
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IRON (HEME DISTAL LIGAND).
IRON (HEME PROXIMAL LIGAND).
F61A7B96A07A41CD CRC64;
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches
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100.0%; Pred. No. 26;
tive 0; Mismatches
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InterPro; IPR000971; Globin.
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   InterPro; IPR000971; Globin.
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Best Local Similarity 100.
Matches 5; Conservative
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92 RIDPG 96
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93 RIDPG 97
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                             "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                      SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE-95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 132;
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SEQUENCE 132 AA; 14576 MW; 3E53097CD17B0C62 CRC64;
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01-APR-1988 (Rel. 07, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HEMOGLOBIN ALPHA-4 CHAIN (ALPHA-T4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000505; AAC77303.1; -. EcoGene; EG12584; yjiw.
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NCBI_TaxID=8355;
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                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                      Blattner F.R.;
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84 GCIVL 88
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P06637;
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TO POOS_ALMAN STANDARD; PRT; 191 AA.

AC 075340.

DT 20-MOG-2001 (Rel. 40, Leat sequence update)
DT 20-MOG-2001 (Rel. 40, Leat sequence update)
DT 20-MOG-2001 (Rel. 40, Leat sequence update)
DT 20-MOG-2001 (Rel. 40, Leat sequence update)
DE ROOMG-2001 (Rel. 40, Leat sequence update)
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10 GCIVL 14

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Best Local Similarity 100.0%, Pred. No. 33;
Matches 5; Conservative 0; Mismatches

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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| 35.7 133 1 PA2D_PSETE 35.7 142 1 OSMC_ECOLI 35.7 144 1 14KD_MYCTU 35.7 146 1 APAA_HUMAN 35.7 147 1 RL15_SYNY3 35.7 149 1 GLB1_MORMR 35.7 149 1 GLB2_PSTMA 35.7 149 1 GLB2_PSTMA 35.7 149 1 GLB2_PSTMA 35.7 149 1 GLB2_PSTMA 35.7 149 1 GLB2_PSTMA 35.7 149 1 GLB2_PSTMA 35.7 149 1 GLB3_PSTMA | ALIGNMENTS | CIAM DCD_ACIAM STANDARD; PRT; 173 AA. 002103; 01-APR-1993 (Rel. 25, Cart sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE | rolobus<br>lobales;                       | [1] SEQUENCE FROM N.A. STAIN=Lei 10 / DSW 3772; MEDLINE-93065206; PubMed=1437556; Kletzin A.; "Molecular characterisation of a DNA ligase gene thermophilic archaeon Desulfurolobus ambivalens s | c relationship to eukaryotic lig<br>ds Res. 20:5389-5396(1992).<br>06934; PubMed=7899076;<br>, Kyrplides N., Sander C.; | NOTES FORTH THE THE TOTAL THE THE THE THE THE THE THE THE THE THE | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb.sib.ch). | EMBL; X63438; CAA45033.1; PIR; S26382; S26382. InterPro; IPR003232; dCTP_deaminse. Interpro; IPR001428; dUTPase. Pfan; PF00692; dUTPase; 1. ProDom; PD004900; dCTP_deaminse; 1. Hydrolase. SEQUENCE 173 AA; 19858 MW; B4D922503CD4B25A | 100.0%; Score 14; DB<br>Similarity 100.0%; Pred. No. 2.66<br>4; Conservative 0; Mismatches | PTIVDAGFEGOLTI 14<br> |
| 33333333333333333333333333333333333333                                                                                                                                                                                                                                                        |            | SUL<br>D_A                                                                                                                                                                            |                                           | RN [1]  RP SEQUENCE FR  SEQUENCE FR  STRAIN-Lei  XN MEDLINE-330  RA Kletzin  RT "Molecular  Thermophili                                                                                          |                                                                                                                         |                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                        | Query Match<br>Best Local Sim<br>Matches 14;                                               | 1 109                 |
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MEDLINE-99310339; PubMed=10382966;

Junno K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Junno K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukuti S., Magai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Namazaki J., Kushida N., Oguchi A., Aoki K., T., Kubota K.,
Namaura Y., Nomura N., Sako Y., Kikuchi H.,
"Complete genome sequence of an aerobic hyper-thermophilic
DNA Res. 6:33-101(1999).

-I- CATALYTIC ACTIVITY: DELOTP + H(2)0 = DUTP + NH(3).
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InterPro; IPR001322; dCTP_deaminse.
InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase; 1.
Pr050m; PD004900; dCTP_deaminse; 1.
Pydrolase; Complete proteome.
SEQUENCE 181 AA; 19894 MW; D8B6CBDC1722EFE9 CRC64;
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                                           Deckert G., Warren P.V., Gasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium Aquifex
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"Nucleotide sequence and genome organization of bacteriophage S13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfan: PF00692; durease; l.-
ProDom; PD004900; dcTP-deaminse; l.
Hydrolase; Complete proteome
SEQUENCE 180 AA; 20544 MW; B2710421A2FA48D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                   MALUE 392:353-358(1998).
-!- CATALYTIC ACTIVITY: DCTP + H(2)O - DUTP + NH(3).
-!- SIMILARITY: BELONGS TO THE DCTP DEAMINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssDNA viruses; Microviridae; Microvirus.
NCBI_TaxID=10844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-705-1988 (Rel. 08, Created)
01-705-1988 (Rel. 08, Last sequence update)
01-707-1996 (Rel. 34, Last annotation update)
MINOR SPIKE PROTEIN (H PROTEIN) (PILOT PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000747; AAC07499.1; -. InterPro; IPR003232; dCTP_deaminse. InterPro; IPR001428; dUTPase.
MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14428; AAA32592.1; -. PIR; JS0459; JS0459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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P07933;
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Joens A., Mettenleiter T.C.;
"Identification and characterization of pseudorables virus dUTPase.";
J. Virol. 70:1242-1245(1995).
                                                                                                                                                                                                                                                                                                                 Trepanier L.A., Cribb A.E., Spielberg S.P., Ray K.;
"Deficiency of cytosolic arylamine N-acetylation in the domestic cat and wild felids caused by the presence of a single NATI-like gene.", Pharmacogenetics 8:169-179(1998).
-i- FUNCTION: PARTICIPATES IN THE DETOXIFICATION OF A PLETHORA OF HYDRAZINE AND ARYLAMINE DRUGS.
-i- CATALXTIC ACTIVITY: ACETYL-COA + ARYLAMINE = COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                               Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE (EC 2.3.1.5) (ARYLAMINE ACETYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUT_PRVKA STANDARD; PRT; 268 AA.
Q90030; Q85226;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DEOXYGRIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30138 MW; AD31B8745E79F2C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%; Score 6; DB 1;
100.0%; Pred. No. 11;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudorabies virus (strain Kaplan) (PRV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001447; Acetyltransf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD002783; Acetyltransf2; 1.
                                                                                                                                                                                                                                                                                                MEDLINE=99145352; PubMed=10022754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 196-268 FROM N.A.
MEDLINE=95363968; PubMed=7637001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DUTPASE) (DUTP PYROPHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00797; Acetyltransf2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF030398; AAC18940.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-ACETYLARYLAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 IVDAGF 116
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SEQUENCE
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                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase, Nuclease; Endonuclease; Restriction system; Helicase, SEQUENCE 984 AA; 112970 MW; 8649BlAB5E9456BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TYPE III RESTRICTION-MODIFICATION SYSTEM STYLTI ENZYME RES (EC 3.1.21.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 984;
                                                                                                         Length 328,
                                                                                                                                                           0; Indels
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                        EEABE8053765177F CRC64;
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                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                       984 AA.
                                                                                                                            100.0%; Pred. No. 1.2
1ve 0; Mismatches
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100.0%; Pred. No. 3;
live 0; Mismatches
                                                                                                      Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                        328 AA; 34405 MW;
                                                                                                         50.0%;
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                      Query Match 50.0
Best Local Similarity 100.
Matches 7; Conservative
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REBASE; 1788; StyltI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         143 IVDAGFE 149
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315 VDAGFEG 321
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                                                                                                                                                                                                             3 IVDAGFE 9
Coat protein
SEQUENCE 3:
                                                                                                                                                                                                                                                                                                                                                                                                       T3RE_SALTY
P40815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella.
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ARYL_FELCA ID ARYL_FI AC 062696 DT 15-JUL

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MEDLINE-88227946; PubMed-2897360;
Ohsako S., Ohtoml M., Sakamoto Y., Uyemura K., Deguchi T.;
Ohtoml M. Arylamine N-acetyltransferase from chicken liver II. Cloning of cDNA and expression in Chinese hamster ovary cells.";
J. Blol. Chem. 265:734-7538(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1999 (Rel. 13, Last annotation update)
ARYLAMINE N-ACETYLITRANSFERASE, LIVER ISOZYME (EC 2.3.1.5) (ARYLAMINE ACETYLASE)
Gallus gallus (Chicken)
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
MEDIATE-8827945; bubMed-2897359;
MEDIATE-8827945; bubMed-2897359;

"Arylamine N-acetyltransferase from chicken liver. I. Monoclonal antibodies. immunoaffinity purification, and amino acid sequences.";

J. Blol. Chem. 263:7528-7538(1988).

-:-CATALYTIC ACTIVITY: ACETYL-COA + ARYLAMINE = COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-ACETYLARYLAMINE.
-!- SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                         ó,
                                                                                                                                                                                                                                                                                                                                  Length 268;
                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                               Interpro: IPR001428; dUTPase.
Pfam. PF00692; dUTPase; 1.
Hydrolase; Nucleotide metabolism.
SEQUENCE 268 AA; 28617 WW; 79D7CFA999204776 CRC64;
                                                                                                                                                                                                                                                                                                                                42.9%; Score 6; DB 1;
100.0%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 287 AA.
                                                                                                                                                                                                                              EMBL; U38547; AAB02855.1; -. EMBL; X87246; CAA60688.1; -. HSSP; P16088; IDUT.
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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P12275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 2.3.1.5) (ARYLAMINE ACETYLASE).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata: Euteleostomi,
Erchosauria; Aves; Neognathae, Galliformes; Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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STRAIN-WHITE LEGHORN; TISSUE-Pineal gland;
MEDLINE-90060108; Dubmed-2583181;
Obtomn M., Sasaki M., Deguchi T.;
Two arylamine N-acetyltransferases from chicken pineal gland;
identified by cDNa cloning.";
Eur. 7. Blochem. 185:253-261(1989).
- 1. CATALYTIC ACTIVITY; ACETYL-COA + ARYLAMINE = COA +
N-ACETYLANYLAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
U-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE, PINEAL GLAND ISOZYME NAT-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%; Score 6; DB 1; Length 287; 100.0%; Pred. No. 12; tive. 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      PlK; ACBLO; ACBLO; ACBLO; ACBLO; ACBLO; INTERPO; IRRO01447; ACETYLTANSf2.

Probom: PD002783; ACETYLTANSf2; 1.

Transferase; ACYLTANSferase; Multigene family.

ACT_SITE 68

BY SIMILARITY.

SEQUENCE 287 AA; 32915 MW; 6E2919AD2979E210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      First Succession Accession First Property Control of Succession Figure 1. Acetyltransf2.

Probom: PD002783: Acetyltransf2: 1.

Probom: PD002783: Acetyltransf2: Acetyl
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PIR, A28168; A28168.
PIR; A28167; A28167.
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Best Local Similarity 100.(
Matches 6; Conservative
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Best Local Similarity
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P13913;
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                                                                                       ARYLANDAN STANDARD; PRT; 290 AA.
P18440; O15300; O15159;
O1-NOV-1990 (Rel. 16, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE 1 (EC 2.3.1.5) (ARYLAMIDE ACETYLTRANSFERASE, MONOMORPHIC) (MNAT) (N-ACETYLTRANSFERASE, MONOMORPHIC) (MNAT) (N-ACETYLTRANSFERASE 1)
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ebisawa T., Deguchi T.;
"Structure and restriction fragment length polymorphism of genes for
human liver arylamine N-acetyltransferases.";
Blochem. Blophys. Res. Commun. 177:1252-1257(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Butcher N.J., Ilett K.F., Minchin R.F.; "Functional polymorphism of the human arylamine N-acetyltransferase type 1 gene caused by C190T and G560A mutations."; Pharmacogenetics 8:67-72(1998).
                                                                                                                                                                                                                                                                    Blum M., Grant D.M., McBride W., Heim M., Meyer U.A.; "Human arylamine N-acetyltransferase genes: isolation, chromosomal localization, and functional expression."; how cell Biol. 9:193-203(1990).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (NAT1*11).
SEQUENCE FROM N.A. (NAT1*11).
Vatsis K.P., Neber W.W.
Structural heterogeneity of Caucasian N-acetyltransferase at the
                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
MEDLINE-90170975; PubMed=1968463;
Ohsako S., Deguchi T.;
"Cloning and expression of cDNAs for polymorphic and monomorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS OF ARG-64.
MEDLINE-97234849; PubMed-9173883;
Delomenie C., Goodfellow G.H., Krishnamoorthy R., Grant D.M.,
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANTS NAT1*14 AND NAT1*17 MEDLINE=98172173; Pubmed=9511183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 233:584-591(1997).
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0
 Mismatches
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                                                                                                                                                                                                                                                           MEDLINE-90253613; PubMed-2340091;
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6; Conservative
                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                   TISSUE=Leukocyte;
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                                        120 IVDAGF 125
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                    3 IVDAGF
                                                                                 ARY1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- POLYMORPHISM: N-ACETYLATION POLYMORPHISM IS DETERMINED BY A LOW OR HIGH NAT ACTIVITY IN LIVER, IT HAS BEEN IMPLICATED IN THE ACTION AND TOXICITY OF AMINE-CONTAINING DRUGS. SLOW ACETYLATION GENOTYPES HAVE BEEN ASSOCIATED WITH SIGHIFICANT LUNG CANCER RISK. CANDIDATE RISK PACTOR FOR SUSCEPTIBILITY TO NEURAL TUBE DEFECTS. THE NATI+10 ALLELE HAS BEEN ASSOCIATED WITH INCREASED RISK OF COLON AND URINARY BLADDER CANCERS AND WITH HIGHER LEVELS OF N-ACETYLTRANSFERASE ACTIVITY AND DNA ADDUCTS IN AROWATIC AMINE TUMOR TARGET ORGANS SUCH AS COLON AND URINARY BLADDER.
-- MISCELLANGOUS: NATH WAS HISTORICALLY CONSIDERED TO BE MONOMORPHIC IN NATURE BUT REPORTS OF ALLELIC VARIATIONS AT THE NATI LOCUS SUGGEST THAT IT IS A POLYMORPHICALLY EXPRESSED ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINAL MAGGERICS 8:269-281(1998).
-1- FUNCTION: PARTICIPATES IN THE DETOXIFICATION OF A PLETHORA OF HYDRAZINE AND AFFLAMINE DRUGS. CATALYZES THE N- OR O-ACETYLATION OF VARIOUS ARYLAMINE AND HETEROCYCLIC AMINE SUBSTRATES AND IS ABLE TO BIOACTIVATE SEVERAL KNOWN CARCINOGENS.
-1- CATALYTIC ACTIVITY: ACETYL-COA + ARYLAMINE = COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin H.J., Probst-Hensch N.M., Hughes N.C., Sakamoto G.T., Louie A.D., Kau I.H., Lin B.K., Lee D.B., Lin J., Frankl H.D., Lee E.R., Hardy S., Grant D.M., Haile R.W.;
"Variants of N-acetyltransferase NAT1 and a case-control study of
"Study of the role of the highly conserved residues Arg9 and Arg64 in the catalytic function of human N-acetyltransferases NAT1 and NAT2 by site-directed mutagenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.
-!- CAUTION: THE ALLELIC VARIATION ILE-149 DESIGNATED AS NAT1*17 IS
PART OF THE NAT1*11 ALLELIC VARIATION AS REPORTED BY THE
NOMENCLATURE COMMITEE.
-!- DATABASE: NAME-NAT; NOTE-NAT alleles;
WWW-"http://www.louisville.edu/medschool/pharmacology/NAT.html".
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R -> W (IN NAT1*17; A SLOW ACETYLATOR; HAS DEFECTIVE ENZYME ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                               "Identification and characterization of variant alleles of human
                                                                                                                                                                                                                                                                                                     Hughes N.C., Janezic S.A., McQueen K.L., Jewett M.A., Castranio
Bell D.A., Grant D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Acyltransferase; Multigene family; Polymorphism.
ACT_SITE 68 68 BY SIMILARITY.
VARIANT 64 64 R -> W (IN NAT1*17; A SLOW ACETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS NAT1*17; NAT1*21; NAT1*22; NAT1*24 AND NAT1*25.
MEDLINE-98347194; PubMed-9682272;
                                                                                                                                                                                                                                                                                                                                                                                                                                        acetyltransferase NAT1 with defective function using p-aminosalicylate as an in-vivo and in-vitro probe.";
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Pfam; PF00797; Acetyltransf2; 1.
ProDom; PD002783; Acetyltransf2; 1.
                                                                                                                                                                                                                                                            MEDLINE=98172172; PubMed=9511182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colorectal adenomas.";
Pharmacogenetics 8:269-281(1998)
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EMBL; AF008204; AAB84384.1; -.
                                                                                                                                  Biochem. J. 323:207-215(1997)
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PIR; B35729; B35729.
MIM; 108345; -.
                                                                                                                                                                                                                             VARIANT NAT1*14
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 40, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE 2 (EC 2.3.1.5) (ARYLAMIDE ACETYLASE 2)
(ARYLAMINE N-ACETYLTRANSFERASE, POLYMORPHIC) (PNAT) (N-ACETYLTRANSFERASE)
ACETYLTRANSFERASE TYPE 2.) (NAT-2) (AT-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Heart;
MEDLINE-84193006; PubMed-8144033;
MEDLINE-94193006; DubMed-8144033;
Ferguson R.J., Doll M.A., Baumstark B.R., Hein D.W.;
Ferguson R.J., and M.A., Baumstark B.R., Hein D.W.;
Forlymorphic arylamine N.acetyltransferase encoding gene (NAT2) from homozygous rapid and slow acetylator congenic Syrian hamsters.";
Gene 140:247-248(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-94362736; PubMed=7915937;
Magata K., Ozawa S., Miyata M., Shimada M., Yamazoe Y., Kato R.;
Nagata K., Ozawa S., Miyata M., Shimada M., Yamazoe Y., Kato R.;
Magata K., Ozawa S., Miyata M., Shimary structure and molecular basis of polymorphic appearance of an acetyltransferase (AT-II)* in hamsters.";
Pharmacogenetics 4:91-100(1994)
-!- FUNCTION: PARTICIPATES IN THE DETOXIFICATION OF A PLETHORA OF HYDRAZING AND ARYLAMINE DRUGS
-!- CATALYTIC ACTIVITY: ACETYL-COA + ARYLAMINE = COA +
N-ACETYLARYLAMINE
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Liver;
TISSUB-Liver;
PUBDLINE-94332979; PubMed-8055637;
Land S.J., Jones R.F., King C.M.;
Land S.J., Jones R.F., King C.M.;
Land S.J., Jones R.F., Ring C.M.;
Land S.J., Jones R.F., Ring C.M.;
Falcohemical and genetic analysis of two acetyltransferases from hamster tissues that can metabolize aromatic amine derivatives.";
Carcinogenesis 15:1585-1595(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster).
Wakaryota: Metazoa: Chordeta: Cranata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sclurojanthi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                              EMBL; D10108; BAA00989.1; -.
EMBL; X53765; CAA37785.1; -.
EMBL; S11220; X1220.
InterPro; IPR001447; Acetyltransf2.
InterPro; IPR001447; Acetyltransf2.
Pfam; PP00797; Acetyltransf2; 1.
Probom; PD00783; Acetyltransf2; 1.
Transferase; Acyltransferase; Multigene family.
AcT_SITE 68 68 F SIMILARITY.
CONFLICT 285 285 N -> H (IN REF. 2).
SEQUENCE 290 AA; 33780 MW; 31175E83651EE693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6; DB 1;
Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%; Sccilarity 100.0%; Pr
Conservative 0;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARY 2_MESAU
P50293;
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/FTId=VAR_004606.

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Y= T (IN NATI*5).

V-> I (IN NATI*11; CATALYZES THE

N-ACETYLATION OF AROMATIC AMINES AND THE
O-ACETYLATION OF ARIES OF THEIR N-HYDROXYLATED METABOLITES AT RATES UP TO

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Sasaki Y., Obsako S., Deguchi T.;
Sasaki Y., Obsako S., Deguchi T.;
Wolecular and genetic analyses of arylamine N-acetyltransferase
polymorphism of rabbit liver."
J. Blol. Chem. 268:13243-13250(1991).
N-ACETYLARVIAMINE.
N-ACETYLARVIAMINE.
I- SUBCELLULAR LOCATION: CYTOPLASMIC.
I- SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.
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01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE 1 (EC 2.3.1.5) (ARYLAMIDE ACETYLTRANSFERASE, MONOMORPHIC) (MNAT) (N-ACETYLTRANSFERASE, MONOMORPHIC) (MNAT) (N-MAT) OR AACI.
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C015F7F3D4830107 CRC64;
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STRAIN-NEW ZEALAND WHITE; TISSUE-Liver;
STRAIN-NEW ZEALAND WHITE; TISSUE-Liver;
Blum M. Helm M. Meyer U.A.;
"Nucleotide sequence of rabbit NaTI encoding monomorphic arylamine acetyltransferase.",
Nucleic Acids Res. 18:5287-5287(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Walkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Pred. No. 12;
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Conservative 0; Mismatches
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290 AA;
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SEQUENCE FROM N.A.
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Blum M., Heim M., Meyer U.A.;
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifixed and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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POLYMORPHISM: THERE ARE TWO FORMS OF NAT2: A RAPID ISOFORM AND A
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANYLAMINE N-ACETYLITRANSFERASE 2 (EC 2.3.1.5) (ARYLAMIDE ACETYLASE 2)
(N-ACETYLITRANSFERASE TYPE 2) (NAT-2).
                                                          SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=91342604; PubMed=1875909;
MEDLINE=91342604; PubMed=1875909;
Martell K.J., Vatsis K.P., Weber W.W.;
Molecular genetic basis of rapid and slow acetylation in mice.";
Mol. Pharmacol. 40:218-227(1991).
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STRAIN=BALB/C; TISSUE-Liver;
MEDLINE=94379961; PubMed=7545952;
Kelly S.L., Sim E.;
Kelly S.L., Sim E.;
Raylamine N-acetyltransferase in Balb/c mice: identification of novel mouse isoenzyme by cloning and expression in vitro.";
Biochem. J. 302:347-353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pfam; PF00797; Acetyltransf2; 1.
ProDom; PD002783; Acetyltransf2; 1.
Transferase; Acyltransferase; Multigene family; Polymorphism.
ACT_SITE 68 68 BY SIMILARITY.
VARIANT 243 290 MISSING (IN SLOW ISOFORM).
SEQUENCE 290 AA; 33832 MW; 54C10F5F6990F6FD CRC64;
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Hein D.W., Doll M.A.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-92382565; PubMed=1513324
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100.0%;
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P50295;
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"Cloned mouse N-acetyltransferases: enzymatic properties of expressed Nat-1 and Nat-2 gene products.";
Mol. Pharmacol. 42:265-272(1992).
-!- FUNCTION: PARTICIPATES IN THE DETOXIFICATION OF A PLETHORA OF HYDRAZINE AND ARYEMENED SUGGRAFES FOR NAT-2. LESS ACTIVITY WITH ANISIDINE AND BARELY DETECRABLE WITH SM2.
-!- CAPALYTIC ACTIVITY: ACETYL-COA + ARYLAMINE = COA +
                                                                                                                                                                                                                                                      N-ACETYLARYLAMINE.
-- SUBCELLULAR LOCATION: CYTOPLASMIC.
-- POLYMORPHISM: THERE ARE TWO FORMS OF NAT2: A RAPID/STABLE ISOFORM (ASN-99) AND A SLOW/UNSTABLE ISOFORM (ILE-99).
-- SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.
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20-AUG-2001 (Rel. 40, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE 2 (EC 2.3.1.5) (ARYLAMIDE ACETYLASE 2)
ARYLAMINE N-ACETYLTRANSFERASE, POLYMORPHIC) (PNAT) (N-ACETYLASE 2)
ACETYLTRANSFERASE TYPE 2) (NAT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Probom; PD002783; Acetyltransf2; 1.
Transferase; Acyltransferase; Multigene family; Polymorphism.
ACT_SITE 68
BY SIMILARITY.

ACT_STE 68
N -> I (IN NAT2*9; SLOW/UNSTABLE
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Nucleotide sequence of a full-length cDNA for arylamine N-
acetyltransferse from rabbit liver.";
Nucleic Acids Res. 17:3589-3589(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 290;
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Pred. No. 12;
0; Mismatches
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MEDLINE-89263801; PubMed-2726493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001447; Acetyltransf2.
Pfam; PF00797; Acetyltransf2; 1.
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100.0%; Pre
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SEQUENCE FROM N.A.
MEDLINE-90384846; PUDMed-2402461;
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Best Local Similarity
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Search completed: January 31, 2002, 13:39:21
Job time: 81 sec
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                                                                                                                                  I. SUBCELCULAR LOCATION: CYTOPLASMIC.

I. SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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10-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE 2 (EC 2.3.1.5) (ARYLAMIDE ACETYLASE
NAT2 OR AAC2.
                                        SEQUENCE FROM N.A.

ISSUE-Liver;
MEDLINE-1302353; PubMed=2071601;
Sasaki Y., Ohsako S., Deguchi T.;
Sasaki Y., Ohsako S., Deguchi T.;
Molecular and genetic analyses of arylamine N-acetyltransferase
polymorphism of rabbit liver.";
J. Biol. Chem. 266:13243-13250(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SETRAILWESTAR; TISSUE-Pineal gland;
MEDLINE-95188895; Pubmed-788293;
Ebisawa T., Sasaki P., Deguchi T.;
"Complementary DNAs for two arylamine N-acetyltransferases with identical 5' non-coding regions from rat pineal gland.";
Eur. J. Blochem. 228:129-137(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
of rabbit NAT2 encoding polymorphic liver
                                                                                                                                                                                                                                             Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                12.9%; Score 6; DB 1
100.0%; Pred. No. 12;
ive 0; Mismatches
"Nucleotide sequence of rabbit NAT2 en
arylamine N-acetyltransferase (NAT).";
Nucleic Acids Res. 18:5295-5295(1990).
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STRAIN-WAY/ANCELERS, TISSUE-Heart;
MEDLINE-96034572; Pubmed-8528272;
Doll M.A., Hein D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                              N-ACETYLARYLAMINE.
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P50298;
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NR EMBL; U03418; AAA70161.1; -..

DR EMBL; U01348; AAA50161.1; -..

DR EMBL; U17261, AAA56702.1; -..

DR InterPro; IPRO0147, Acetyltransf2.

DR Pfan; PF00797; Acetyltransf2; 1.

Probom; P5002783; Acetyltransf2; 1.

DR Pfan; PF00797; Acetyltransf2; 1.

Probom; P500797; Acetyltransf2; 1.

DR Pfan; PF00797; Acetyltransf2; 1.

DR Pfan; Acetyltransf2; 1.

Acetyltransf2; 1.

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DR Pfan; Acetyltransf2; 1.

DR Pfan; Ace
                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
JONES R.F., Gott B., Land S.J., Park J., King C.M.;
JONES R.F., Gott B., Land S.J., Park J., King C.M.;
Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: PARTICIPATES IN THE DETOXIFICATION OF A PLETHORA OF
HYDRAZINE AND ARYLAMINE DRUGS. ACETYLATES ONLY ARYLAMINES.

-I- CATALYTIC ACTIVITY: ACETYL—COA + ARYLAMINE = COA +
N-ACETYLARIAMINE
-I- SUBCELLULAR LOCATION: CYTOPLASMIC.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC.

-I- POLXMORPHISM: THERE ARE TWO FORMS OF NAT2: A RAPID ISOFORM
(NAT2*21A) AND A SLOW ISOFORM (NAT2*21B).

-I- SIMILARITY: BELONGS TO THE ARYLAMINE N-ACETYLTRANSFERASE FAMILY.
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expression of NAT1 and NAT2 encoding genes lator inbred rats.";
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Pred. No. 12;
0; Mismatches
                                                                from rapid and slow acetylator inl
Pharmacogenetics 5:247-251(1995).
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Best Local Similarity 100.
Matches 6; Conservative
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GenCore	(c) 1993
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OM protein - protein search, using sw model

January 31, 2002, 13:20:11; Search time 78.64 Seconds (without alignments) 13:561 Million cell updates/sec Run on:

US-08-957-709-74 14 1 AGWIDAGFKGKITL 14 Title: Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

219241 seqs, 76174552 residues Searched:

0

Word size

219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ø	Description	dCTP deaminase (EC	thioredoxin reduct	hypothetical prote		Ω,	hypothetical prote	_	_	_	hypothetical prote	probable aldehyde	histone deacetylas	prephenate dehydro	photosystem II oxy	threonine synthase	nucleotide-binding	iron utilization p	probable periplasm	cellobiose/cellotr	hypothetical prote	hypothetical prote		protein disulfide-			hypothetical prote	probable flavoprot	probable malate sy	hypothetical prote
SUMMARIES	<u> </u>	F64353	D35156	QQBYPT	T26053	G81178	B81926	B64334	I64006	T17241	S74064	S72569	T48401	B70451	S04132	H70338	E64048	T10888	D81345	T46602	D81809	T18793	A30007	ISRTSS	ISMSSS	A38362	T47409	m	T44752	m
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DNA topoisomerase	probable tail comp	transcription fact	guanine nucleotide	hypothetical prote	gamma crystallin I	gamma-thionin SI-a	gamma-purothionin	purothionin gamma	hordothionin gamma	gamma-zeathionin 1	gamma-thionin SI-a	alpha-amylase inhi	gene T1 protein -	transcription regu
T18085	USBFL D85584	A46423	T14096	н86127	A60894	S69146	S11529	S11530	S13849	A58319	S69144	S13963	160384	139925
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1061	1138	1160	1849	2104	19	47	47	47	47	47	47	48	23	92
42.9	42.9	42.9	42.9	42.9	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7
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30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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dCTP deaminase (EC 3.5.4.13) MJ0430 [similarity] - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: F64353

Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A;Reference number: A64300; MUID:96337999

A; Accession: F64353
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-204 <BUL>
A; Cross-references: GB:U67494; GB:L77117; NID:g1591120; PIDN:AAB98415.1; PID:g1591133
C; Genetics:

A,Map position: REV386963-386349 C,Superfamily: dCTP deaminase C,Keywords: hydrolase

ö Gaps .; 0 Length 204; Indels Score 14; DB 2; I Pred. No. 1.2e-07; ; Mismatches 0; 0; 100.0%; Conservative Query Match Best Local Similarity Matches 14; Conserv

1 AGWIDAGFKGKITL 14 ò

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thioredoxin reductase (NaDPH) (EC 1.6.4.5) - Eubacterium acidaminophilum N;Alternate names: dlhydrolipoamide dehydrogenase [misidentification] C;Species: Bubacterium acidaminophilum C;Species: Dubacterium acidaminophilum C;Date: 06·Nov-1998 #sequence_revision 06·Nov-1998 #text_change 04·Feb-2000 C;Accession: S38988; D35156 R;Luebbers, M.; Andreesen, J.R. Bur. J. Biochem. 217, 791-798, 1993 A;Fitle: Components of glycine reductase from Eubacterium acidaminophilum. Cloning, 3A;Reference number: S38988; MUID:94039119

A; Accession: S38988

A; Molecule type: DNA
A; Residues: 1-315 < LU04500; NID:92708733
A; Cross-references: GB:LU04500; NID:92708733
B; Dietrichs, D.; Meyer, M.; Schmidt, B.; Andreesen, J.R.
J. Bacteriol. 172, 2088-2085, 1990
A; Title: Purification of NADPH-dependent electron-transferring flavoproteins and N-te
A; Reference number: A35156; MUID:90202731

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Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Species: Neisseria meningitidis (C; Date: 05-May-2000 #text_change 02-Feb-2001 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C; Accession: B81926 (C
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C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                            C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C. Sims, M.
Submitted to the EMBL Data Library, June 1995
A. Recession: 72603
A. Accession: 72603
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Caesareferences: EMBL: Z49969; PIDN: CAA90270.1; GSPDB:GN00020; CESP:W01C9.2
A. Experimental source: clone W01C9
C. Genetics:
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A;Map position: 3
A:Introns: 30/1; 64/1; 100/3; 124/3; 229/3; 272/3; 536/2
                                                                                                                                        Caenorhabditis elegans
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Pred. No. 4.5;
0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pi
Matches 7; Conservative 0;
                                                                                                                                        hypothetical protein W01C9.2
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ONDERFY

Hypothetical protein YER152c - yeast (Saccharomyces cerevisiae)

C.Species: Saccharomyces cerevisiae

C.Species: Saccharomyces

C.Species: Saccharomyces

R.Dietrich, F.S.

A.Description: The Sequence of S. Cerevisiae cosmids 8229, 9115, 9132, 9981, and lambda

A.Reference number: S50430

A.Reciones: Efference S. Emil: U18917; NID: 9603377; PIDN: AAB64679.1; PID: 9603392; GSPDB: GNOOC

R.Ohmen, J.D.: Burke, K.A.; McEwen, J.E.

A.Reference number: A35328; MUID: 90258894

A.Reference number: A35328; MUID: 90258894

A.Reference number: A35328; MUID: 90258894

A.Recession: G30328

A.Residues: 1.230 cOHMA

A.Residues: 1.230 cOHMA

A.Residues: 1.230 cOHMA

A.Residues: 1.230 cOHMA

A.Residues: 1.250 cOHMA

A.Residues
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A; Accession: D35156
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Start codon: GTG
A; Start codon: GTG
A; Start codon: GTG
A; Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
C; Complex: homodimer; each chain has a tightly associated but noncovalently bound FAD
C; Stuperfamily: thioredoxin reductase: thioredoxin reductase homology
C; Reywords: FAD; flavoprotein; homodimer; NADE; oxidoreductase; redox-active disulfide
F; 1-309/Domain: thioredoxin reductase homology cTRXB>
F; G-34/Region: beta-alpha-beta FAD nucleotide-binding fold
F; 146-173/Region: beta-alpha-beta NADP nucleotide-binding fold
F; 136-173/Region: beta-alpha-beta NADP nucleotide-binding fold
F; 134-137/Disulfide bonds: redox-active #status predicted
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A:Map position: 58
C:Superfamily: yeast hypothetical protein YER152c
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252 FKGKITL 258
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Thu Jan 31 13:32:42 2002

A; Accession: B81926

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84093.1; PID:g737953
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein MJ0273 - Methanococcus jannaschii C.Species: Methanococcus jannaschii C.Species: Methanococcus jannaschii C.Species: Methanococcus jannaschii C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #sequence_revision 13-Sep-1996 #sequence_revision 13-Sep-1996 #sep-1996 #sequence_revision 5.1.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, F. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Senience 273, 1058-1073, 1996
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Reference number: A64300; MUID:96337999
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A;Molecule type: DNA
Asesidues: 1-103 <BUL>
A;Cross-references: GB:U67482; GB:L77117; NID:g2826267; PIDN:AAB98261.1; PID:g1590998;
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Conservative 0; Mismatches
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Pred. No.
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A; Residues: 1-183 <TIGR>
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| 50 AGFKGK 55
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GWIDAG 84
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DB 1; Length 183;

42.9%; Score 6;

Query Match

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A;Molecule type: DNA
A;Residues: 1-233 <SRNS
A;Cross-references: EMBL:Y08256; NID:g1707679; PID:g1707763
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
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R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome A; Reference number: S73076; MUID:97055432
A;Accession: S74064
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C; Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MT
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                                                                                                                                                                                                                                 hypothetical protein DKF2p434L057.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S72569
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A;Reference number: 218722
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A;Experimental source: adult testis; clone DKFZp434L057
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73 AGFKGK 78
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2 KGKITL 7
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164 GFKGKI
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A. Wolecule type: mRNA
A. Residues: 1-329 < WAL>
A. Molecule type: mRNA
A. Residues: 1-329 < WAL>
A. Cross-references: EMBL:X15350; NID:g20620; PID:g20621
A. Accession: A30457
A. Molecule type: protein
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A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Title: Partial amino acid sequences of the proteins of pea and spinach photosystem
A. Molecule type: protein
A. Accession: S03269
A. Molecule type: protein
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                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: 1-31 A;Molecule type: A;Cross-references: GB-AE000754; NID:g2984047; PIDN:AAC07589.1; PID:g2984048; GB-AE00 A;Experimental source: strain VF5 C;Genetics: A;Gene type A;Gene: type C;Superfamily: cyclohexadienyl dehydrogenase
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Affilie: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. Affilie: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. Afference number: A70300; MUID:98196666

Affactus: preliminary; nucleic acid sequence not shown; translation not shown Affactus: preliminary; nucleic acid sequence hown; translation not shown Affactuse type: DNA
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278 KGKITL 283
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| 53 GFKGKI 58
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Riwilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, Ulton, L.; Gardener, A.; Green, P.; Hawkins, T.; Hillier, L.; Jar, M.; Johnston, L.; Jon submitted to the EMBL Data Library, Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. submitted to the EMBL Data Library, February 1995
Ainthors: Showninkeen, R.; Smaldon, N.; Smith, A.; Sonnhammer, E.; Staden, R.; Sulston, J proat, J.; Wohldman, P.
A.; Description: The C. elegans genome project: Contiguous nucleotide sequence of over two A; Reference number: S7256
A; Reference number: S7256
A; Residues: 1-287 < VML>
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A; Residues: 2073; 69/2; 195/3; 261/3
A; Note: C35010 (6
C; Superfamily: aldehyde reductase
C; Reywords: oxidoreductase
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T48401

histone deacetylase-like protein - Arabidopsis thaliana

histonate names: protein F17C15.160

C. Species: Arabidopsis thaliana (mouse-ear cress)

C. Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C. Accession: T48401

R. Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, I submitted to the Protein Sequence Database, March 2000

A; Reference number: 224492

A; Accession: T48401

A; Retains: preliminary

A; Molecule type: DNA

A; Residues: 1-296 ABV>

A; Residues: 1-296 ABV>

A; Consorreferences: EMBL:Al162506

A; Experimental source: cultivar Columbia; BAC clone F17C15
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A;Introns: 5/1, 28/3; 93/3; 116/3; 164/3; 195/3; 227/1
A;Note: F17C15.160
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A; Residues: 1-352 <AQF>
A; Cross-references: GB:AE000689; NID:g2983082; PIDN:AAC06690.1; PID:g2983084; GB:AE00065
A; Cross-references: GB:AE000689; NID:g2983082; PIDN:AAC06690.1; PID:g2983084; GB:AE00065
C; Genetics:
A; Gene: thrC2
C; Function:
A; Gene: thrC2
A; Gene: thrC3
A; Gene: thrC3
A; Gene: thrC3
A; Gene: thrC3
C; Superfain: catalyzes hydrolyzation of O-phospho-L-homoserine to L-threonine and orth A; Pathway: threonine biosynthesis
A; Note: pyridoxal phosphate cofactor
C; Superfamily: threonine dehydratase
C; Superfamily: threonine dehydratase
C; Superfamily: threonine dehydratase
C; Superfamily: threonine biosynth
F; 63/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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A;Molecule type: DNA A;Residues: 1-1197 <TOH> A;Note: sequence extracted from NCBI backbone (NCBIN:129069, NCBIP:129070)

A; Accession: A48350

A.Map position: 0.375-0.405 C;Superfamily: herpesvirus DNA-binding protein C;Keywords: DNA binding; zinc finger

C; Genetics:

ribose-5-phosphate ribosephosphate is hypothetical prote

E85947

unknown protein,

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collagen alpha 1(VI) chain precursor - mouse
(S.Species: Mus musculus (house mouse)
(S.Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
(S.Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
(S.Accession: 334839; S31405; S33603; S31403; S32003
R:Bonaldo, P.; Piccolo, S.; Marvulli, D.; Volpin, D.; Marigo, V.; Bressan, G.M.
Matrix 13, 223-233, 1993
A.Title: Mutine alpha-1(VI) collagen chain. Complete amino acid sequence and identifi
A.Reference number: S34839; MUID:93316904
A.Nolecule type: MRNA
A.Residues: 1-1025 GBON>
A.Residues: 1-1025 GBON>
R.Bonaldo, P.; Piccolo, S.; Marvulli, D.; Volpin, D.; Bressan, G.M.
A.Reference number: S31403
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(Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 18-Feb-2000

(C) Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 18-Feb-2000

(C) Accession: T04135

(A) Title: A novel suppressor of cell death in plants encoded by the Lls1 gene of maize A: Title: A novel suppressor of cell death in plants encoded by the Lls1 gene of maize A: Title: A novel suppressor of cell death in plants encoded by the Lls1 gene of maize A: Title: A novel suppressor of cell death in plants encoded by the Lls1 gene of maize A: Title: A novel suppressor of cell death in gB/EMBL/DDBJ

A: Reference number: Z15232; MUID:97248483

A: Reference number: Z1532; MUID:97348918910; PIDN:AAC49677.1; PID:91935911

A: Title: A novel suppressor of cell death in the Lls1 gene of maize A: Title: A novel suppressor of cell death in the Lls1 gene of maize A: State and S1 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 and S2 an
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A; Residues: 1-31 <- CONA
A; Residues: 1-31 <- CONA
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A; Cross-references: EMBL:X66406; NID:951055; PIDN:CAA47033.1; PID:951056
B; Zhang, R.Z.; Pan, T.C.; Timpl, R.; Chu, M.L.
Biochem, J. 291, 787-792, 1993
A; Title: Cloning and sequence analysis of cDNAs encoding the alpha-1, alpha-2 and alpha, Recession: S32603; MUID:93256888
A; Reference number: S32603; MUID:93256888
A; Accession: S32603; MUID:93256888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: COLGA1
C; Superfamily: collagen alpha 1(VI) chain; von Willebrand factor type A repeat homolo
C; Superfamily: collagen alpha 1(VI) extracellular matrix; glycoprotein; heterotrim
C; Reywords: cell binding; coiled coil; extracellular matrix; glycoprotein; heterotrim
F;1-19/Domain: signal sequence #status predicted <STG>
F;20-1025/Product: collagen alpha 1(VI) chain #status predicted <MAT>
F;34-212/Domain: von Willebrand factor type A repeat homology <WAI>
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A; Residues: 442-673, 'TL', 676-708, 'A', 710-942, 944-959, 'R', 961-1025 <ZHA>
A; Cross-references: EMBL:218271; NID:97955; PIDN:CAA79152.1; PID:957956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 29; Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 DPGYEG 10
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30 GRPEY
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E8326
hypothetical protein PA3054 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 955-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathotha; Reference number: A82950; MUID:20437337
A; Reference number: A82950; MUID:20437337
A; Residues: DNA
A; Residues: DNA
A; Residues: Cidanosa
A; Cross-references: GB:AE004730; GB:AE004091; NID:999949154; PIDN:AAG06442.1; GSPDB:GN001
C; Genetics:
C; Genetics:
A; Gene: PA3054
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To 29427
Probable exonuclease - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Decies: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
C;Accession: T29427
R;Parkhill, J; Barrell, B.G; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1998
A;Reference number: 220619
A;Reference number: 220619
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-259 < PAR>
A;Molecule type: DNA
A;Residues: 1-259 < PAR>
A;Residues: 1-259 < PAR>
A;Rossidues: BMBL:AL031155; PIDN:CAA20072.1
C;Genetics:
A;Note: SC3A7.09
C;Superfamily: exodeoxyribonuclease III
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                                                                                                                                  Length 1197;
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                                                                                                                                  Score 7; DB 1;
Pred. No. 2.3;
0; Mismatches
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50.0%; Soc
Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
    F;499-512/Region: zinc finger
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504 PGYEGR 509
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RESULT S34839

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Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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hypothetical protein SCE19A.13c - Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C; Accession: T36136
R; Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable regulatory protein - Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: J4-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999 C;Accession: T03008 R;Figueroa-Bossi, N.; Bossi, L. Submitted to the EMBL Data Library, June 1998 A;Reference number: Z14818 A;Reference number: Z14818
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                     Gaps
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A;Molecule type: DNA
A;Residues: 1-136 <FIG>
      DB 2;
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100.0%; Pred. No. 69;
tive 0; Mismatches
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                                                               62;
      Score 5; DB 2; Pred. No. 62; 0; Mismatches
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35.7%;
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Best Local Similarity
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A; Residues: 1-140 <KAN>
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R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A: Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.D.; P.; Krieger, J.E.; Kurmae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.; Madeira, H.W.; Martins, E.R.; Kitajima, J.D.; Mricoca, E.C.; Miyaki, C.Y.; F.G.; Muthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Olliveira, M.N.; de Olliveira, M.C.; Ge Olliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvain, T.Suhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A; Contents: annotation
                                                                                                     immediate-early-5 protein - human herpesvirus 1
C;Species: human herpesvirus 1
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A;Residues: 1-13,'T',15-88 <MUR>
A;Cross-references: GB:L00036; GB:L00037; GB:M12354; GB:M12355; GB:M12506; GB:M30738; GE
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A;Residues: 1-119 <SIM>
A;Cross-references: GB:AE003916; GB:AE003849; NID:99105626; PIDN:AAF83550.1; GSPDB:GN001
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A; Residues: 1-88 < MATD:
A; Residues: 1-89 < MATD:
A; Residues: 1-89 < MATD:
B; Murchle, M.J.; McGeoch, D.J.
J. Gen. Virol. 62, 1-15, 1982
A; Teference number: A92789; MUID: 83032477
A; Accession: A92789; MUID: 83032477
A; Mccession: A92789; MUID: A92789; MUID: 83032477
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C;Superfamily: Escherichia coli ribosomal protein L20
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C;Superfamily: herpesvirus immediate-early protein
C;Keywords: early protein
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Search completed: January 31, 2002, 13:20:14
Job time: 115 sec
                                                                 Query Match 35.7%;
Best Local Similarity 100.0%;
Matches 5; Conservative (
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74 DPGYE 78
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151014
MHC class I protein - Nerodia sipedon (fragment)
C:Species: Nerodia sipedon
C:Species: Nerodia sipedon
C:Species: 04-sep-1997 #sequence_revision 07-Nov-1997 #text_change 23-Jul-1999
C:Accession: 151014
R:Grossberger, D.: Parham, P.
Immunogenetics 36, 166-174, 1992
A:Title: Reptillan class I major histocompatibility complex genes reveal conserved eleme A:Reference number: 150012; MUID:92307752
A:Reference number: 150012; MUID:92307752
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-147 <GRO>
A:Cross-references: GB:M81099; NID:9213382; PIDN:AA49389.1; PID:g213383
A:Gross-references: GB:M81099; NID:g213382; PIDN:AA49389.1; PID:g213383
A:Gene: SCI
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Cross-references: GB:X16622; GB:X15821; NID:g62634; PIDN:CAA34619.1; PID:g62635
A; Cross-references: GB:X16622; GB:X15821; NID:g62634; PIDN:CAA34619.1; PID:g62635
A; Cross-references: GB:X16622; GB:X16821; NID:g62634; PIDN:CAA34619.1; PID:g62635
C; Superfamilly: oxytocin-neurophysin
C; Reywords: amidated carboxyl end: neuropeptide
F; 21.29/Froduct: lostocin 1 #status predicted <ISO>
F; 33-148/Froduct: neurophysin #status predicted <NEU>
F; 31-26/Disulfide bonds: #status predicted
F; 29/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
1506019
1506019
1506019
N;Contains: lsotocin; neurophysin
N;Contains: lsotocin; neurophysin
N;Contains: lsotocin; neurophysin
C;Specias; Catostomus commersoni (white sucker)
C;Specias; Catostomus commersoni (white sucker)
C;Accession: S06019
R;Figueroca, J; Worley, S.D.; Helerhorst, J.; Krentler, C.; Lederis, K.; Richter, D.
EMBO J. 8, 2873-2877, 1989
A;Title: Two isotocin genes are present in the white sucker Catostomus commersoni both A;Reference number: S06018; MUID:90059870
A;Reference number of mompared with conceptual translation
A;Residues: 1-148 <FIG>
A; Reference number: 221598
A; Accassion: 136136
A; Accassion: 136136
A; Accassion: 136136
A; Actauts: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-140 <-SEE>
A; Residues: 1-140 <-SEE>
A; Cross-references: EMBL;AL096852; PIDN:CAB50994.1; GSPDB:GN00070; SCOEDB:SCE19A.13c
A; Experimental source: strain A3(2)
C; Genefics:
C; Genefics: SCOEDB:SCE19A.13c
C; Superfamily: Streptomyces coelicolor hypothetical protein SCE19A.13c
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                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.7%; Score 5; DB 2; Best Local Similarity 100.0%; Pred. No. 74; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 EGRPE 13
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34 EGRPE 38
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Accession: Adding the compared with conceptual translation A; Note: sequence extracted from NUBS.

A. Status: Accession: Adding the compared with conceptual translation A; Note: sequence compared with conceptual translation A; Note: sequence compared with conceptual translation A; Status: Protein interaction cloning in yeast: identification of mammalian proteins the conceptual translation A; Status: preliminary; not compared with conceptual translation A; Status: preliminary; not compared with conceptual translation A; Status: preliminary conceptual translation A; Status: accession: 1-149 ccHE>
A; Residues: 1-149 ccHE>
A; Note: sequence extracted from NCBI backbone (NCBIP:108531)
                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Aar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03501
E;VICEA, C; Paces, V,; Maltesev, N; Paces, V; Haselkorn, R; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1
A;Reference number: Z14955; MUID:97404404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-149 <VLC>
A;Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16154.1; PID:g3128302
C;Genetics:
                                                                Gaps
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   Length 148;
                                                         0; Indels
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Score 5; DB 2;
Pred. No. 75;
0; Mismatches
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C;Superfamily: hypothetical protein HI1355
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US-08-824-405-6
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Sequence 24, Appl
Sequence 3, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 17, Appli
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4.837 Million cell updates/sec
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Sequence 23
Sequence 24
                                                                                                         ; Search time 65.13 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-110-910A-2
US-09-110-910A-4
US-08-023-980B-29
US-08-466-953A-24
US-08-314-596-3
US-08-314-596-9
US-08-314-596-9
US-08-314-596-23
US-08-314-596-23
US-08-314-596-23
US-08-320-982-4
US-08-320-982-9
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-09-021-715-16
                                                                                                                                                                                                                                                                                  212252 seqs, 22503292 residues
                                                                                                         January 31, 2002, 13:15:14
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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1 AGVVDRDYTGEVKV 14
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                       Perfect score:
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                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stree
CTTY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 14; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.5e-07; Matches 14; Conservative 0; Mismatches 0;
                                                         US-08-993-674A-39
US-08-30-862B-11
US-08-21-95-27
US-08-284-391B-27
US-09-21-95-27
PCT-US92-0176S-27
PCT-US95-00454-27
US-08-908-332-9
US-08-908-332-1
US-08-908-332-2
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ladner, Robert D.
APPLICANT: Ladner, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPase, Its Isoforms, and TITLE OF INVENTION: Diagnostic and Other Uses NUMBER OF SEQUENCES: 20
             PCT-US94-04361-40
US-08-557-309B-39
US-08-834-306-39
                                                                                                                                                                                                                   US-08-961-083-208
US-09-188-930-189
US-09-188-930-331
                                                                                                                                                                                                                                                                   US-08-530-862B-9
                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BLOOM, Allon
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 350163-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08824405
Patent No. 5962246
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 147 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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TOPOLOGY: linear
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Length 333;
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Patent No. 6025175

GENERAL INPORMATION:
APPLICANT BURNHAM, MARTIN K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: By Lenort Price & Rhoads
CITY: Lawrenceville
STREET: USA
COUNTRY: USA

ZIP: 08543
                                               MEDION TYPE: DISKETE COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/896,083 FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: SPING APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION: NAME: BLOOM, Allen REGISTRATION NUMBER: 29,135 REFERENCE/POCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-2314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DOS
SOFTWARE: FASTENCE FOR WINGOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,910A
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: 08/896,083
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   red. No. 33;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-896-083-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
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ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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74 GVVDRD 79
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US-09-110-910A-2
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Fatent No. 5840508:
Fatent No. 5840508:
APPLICANT: Burnhan, Martin K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: 0
TREET: 997 Lenox Diive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NY
COUNTRY: USA
                                                                                                                                              Sequence 2. Application US/08896083
Patent No. 5840560
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPEDINDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPENATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
FILING APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6; DB Pred. No. 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bloom, Allen
REGISTRATION NUMBER:
REFERENCE/POCKET NUMBER:
TELECHMUNICATION INFORMATION:
TELECHMUNE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: 1. LENGTH: 333 amino acids TYPE: amino acid STRANDEDNESS: single 1. TOPOLOGY: linear US-08-896-083-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100
Matches 6; Conservative
                     1 AGVVDRDYTGEVKV 14
                                      81 AGVVDRDYTGEVKV 94
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74 GVVDRD 79
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US-08-896-083-2
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US-08-896-083-4
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Sequence 29, Application US/08023980B Patent No. 5843641
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 5; Conserv
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ZIP: 02109-1024
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STREET: 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,910A
                                                                                                                                                                                    Pred. No. 33;
Mismatches
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                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09110910A
Patent No. 6025175
GENERAL INFORMATION:
APPLICANT: Burnham, Martin K.
TITLE OF INVENTION: NOVEL GLUCOSE KINASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%; Score 6;
100.0%; Pred. No
tive 0; Mismat
                                                                                                                                                                     Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/896,083
                                                                                                                                                                 Query Match 42.9%; Scc
Best Local Similarity 100.0%; Pi
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                             EQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
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TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                   linear
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Best Local Similarity
Matches 6; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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74 GVVDRD 79
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74 GWDRD 79
                                                                                                                                                                                                                                  2 GVVDRD 7
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                                                                                                 ; TOPOLOGY:
US-09-110-910A-2
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RESULT

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APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
APPLICANT: ROSEN, DANIEL R.
APPLICANT: ROSEN, DANIEL R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08486953A Patent No. 5849290 GENERAL INFORMATION:
                                                                                                                                                                                                ADDRESSEE: Clark & Elbing LLP STREET: 585 Commercial Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Clark & Elbing LLP
176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/POCKET UNMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/723-4123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
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                                                                                                                                                                                                                                             Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 55; Matches 5; Conservative 0; Mismatches
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US-08-314-596-9
Sequence 9, Application US/08314596
Patent No. 5668292
GENERAL INFORMATION:
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: STRANDEDNESS: single; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-314-596-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jinear
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STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: peptide
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195-08-1314-596-3

1 Sequence 3. Application US/08314596

1 Patent No. 566829

2 Sequence 3. Application US/08314596

3 Fatent No. 566829

3 Fatent No. 566829

3 Fatent No. 566829

3 Fatent No. 566829

3 FAPLICANT: VAN DE LOO, FRANT FATTY ACYL HYDROXYLASES TO TITLE OF INVENTION: USE OF PLANT FATTY ACIDS AND DERIVATIVES IN PLANTS

3 TITLE OF INVENTION: PRODUC HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

4 CORRESPONDENCE ADDRESS:

5 CORRESPONDENCE ADDRESS:

6 CORRESPONDENCE ADDRESS:

7 TITLE OF USHANN DARBY & CUSHMAN L.L.P.

8 STATE:

8 STATE:

8 COUNTRY: U.S.A.

8 CONDITER READABLE FORM:

9 CONDITER READABLE FORM:

9 COMPUTER READABLE FORM:

9 MEDIUM TYPE: Floppy disk

9 COMPUTER READABLE FORM:
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       COMPUTER: IBM PC compatible
OPERATING SYSTEM:
OPERATION SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,953A
FILLNG DATE: 07-JUN 1995
CLASSIFICATION TA4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,052
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
RECISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 45;
Best Local Similarity 0; Mismatches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids:
TYPE: Amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-953A-24
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APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,596
FILING DATE: 26-SEP-1994
ATYORNEY/AGEN"
ANYONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 55; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL. N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206905/1220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-300
TELEFAX: 202-822-0944
                               16,773
RR: 206905/1220
                                                                                                                                                                                                                                                                                                                                                Score 5; 1
Pred. No.
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100.0%; Pre
0; 7
                NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 2065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                             TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-314-596-17
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Best Local Similarity
                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 VDRDY 23
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US-08-314-596-23
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APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
                           TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXXLASES TO TITLE OF INVENTION: PRODUCE HYDROXXLATED FATTY ACIDS AND DERIVATIVES IN PLANTS NUMBER OF SEQUENCES: 48
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                                                                                                                                                                         STATE: MEDITION OF STATE: COUNTRY: U.S.A.

ZIP: 20005
COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,596
FILING DATE: 26-SEP-1994
CLASSIFICATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206905/1220
TELEFONNE: 202-861-3000
TELEFAN: 202-861-3000
TELEFAN: 202-861-3000
TELEFAN: 202-861-3000
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/314,596
FILING DATE: 26-SEP-1994
CLASSIFICATION: 435
                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P. STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 17, Application US/08314596; Patent No. 5668292; GENERAL INFORMATION:
SOMERVILLE, CHRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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20005
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| 19 VDRDY 23
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APPLICANT:
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| Sequence 4, Application US/08320982
| Sequence 4, Application US/08320982
| Patent No. 2801026
| Sequence 4, Application US/08320982
| Sequence 4, Application US/08320982
| Sequence 5 801026 | PRANT
| TITLE OF INVENTION: USE OF PLANT FATTY ACIDS AND DERIVATIVES IN PLANTS
| TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
| TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
| CORRESPONDENCE ADDRESS: A8 | CORRESPONDENCE ADDRESSE: CUSHWAN DARBY & CUSHWAN L.L.P. CITY: WASHINGTON OF AVENUE, N.W. CITY: WASHINGTON OF A COUNTRY EADAbale FORM: CONTYTER READAbale FORM: CONTYTER READAbale FORM: CONTYTER EADAbale FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBW PC COMPATION REPEATION PATA: BAPLICATION DATE: US-08 | PATENTA PAPLICATION DATE: US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US-08 | US
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPUTE:
SOTTWARE: PARCHIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,982
FILING DATE: 11-CCT-1994
CLASSIFICATION NUMBER: US/08/314,596
FILING DATE: 26-5EP-1994
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 206905/1220
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202-861-300
TELEPRAX: 202-861-300
TELEPRAX: 202-861-300
TELEPRAXION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
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Best Local Similarity 100.0%; Pred. No. 55;
Best Local Similarity 0.0 Wismatches
5; Conservative 0; Mismatches
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-320-982-3
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19 VDRDY 23
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US-08-320-982-4
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JERURAL INFORMATION:
Sequence 24, Application US/08314596

Patent No. 566392

JERURAL INFORMATION:
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACYL HYDROXYLASES TO
THERE OF SOURMESS:
ADDRESSES:
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US-08-320-922-3
US-08-320-922-3
Sequence 3, Application US/08320982
Sequence 3, Application US/08320982
Sequence 3, Application US/08320982
Sequence 3, Application US/08320982
SEQUENCE 3, APPLICANT: SOMERVILE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
NUMBER OF SEQUENCES: 48
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
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0; Indels
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Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
; LENTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-320-982-4
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Search completed: January 31, 2002, 13:15:15 Job time: 96 sec

4 VDRDY 8 |||||| 19 VDRDY 23

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Q9sdz8 arabidopsis
9xvh8 caenorhabdi
Q9sis5 arabidopsis
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Viruses; dSDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
NCBL_TaxID-28321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moyer R.W.;
"Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
Analysis and Comparison with Other Poxviruses.";
Virology 274:120-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
MOyer R.W.;
Moyer R.W.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF250284; AAG02708.1; -
Interpro; IPRO1428; dUTPase.
Fram, PP00692; dUTPase; 1.
ProDom; PD000946; dUTPase; 1.
SEQUENCE 143 AA; 16181 MW; E0F84E9CF0673214 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20396580; PubMed=10936094;
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
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09dhc9
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Last annotation update)
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              Q9XVH8
Q9SIS5
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0900K5
0900K4
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Q51188
Q49485
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082572
09Y7X2
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Q9YXL5
Q9YXL4
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09YJM8
09IGR4
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09DHC9
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Q23173
Q9GYK9
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                                                                                                         058587
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Best Local Similarity 100.
Matches 14; Conservative
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 77 AGVIDEDYRGNVGV 90
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 09EN44
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15.633 Million cell updates/sec
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                                                                                                       January 31, 2002, 13:37:50 ; Search time 130.99 Seconds
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                                                                                                                                                                                                                                                                                                                                          473505
               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             473505 seqs, 146272329 residues
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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090J44
090CU90
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sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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14
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Maximum DB seq length: 2000000000
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Match Length
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Word size :

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01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 5031412106RIK PROTEIN.
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                                                                      01-A0G-1998 (TrEMBLrel. 07, Created)
01-A0G-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last an
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DUTPASE.
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kan L., Varanasi U., Zhu Y., Qi C., Reddy J.K.;

Mouse ddTPase cloning and genomic structural analysis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF091101, AAF74514 1;
InterPro; IPR001428; dUTPase.
Promom; PD0009946; dUTPase; 1.

SEQUENCE 162 AA; 17414 MW; 88DF490EA9B890AD CRC64;
                                                                                                                                                                                                                                                                             STRAIN-01701;
FIGURE H. J., COLTONE R.;
Submitted (VAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF056304; AAD03407.1; -.
HSSP; P06968; 1EUW.
InterPro; IPF001428; duTPase.
Pfam; PF006945; duTPase.
ProDom; PD000946; duTPase; 1.
ProDom; PD009046; duTPase; 1.
SEQUENCE 160 AA: 17175 MW; 4C9B13EFAEB0D0A3 CRC64;
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Q9CQ43;
01-JUN-2001 (TrEMBLrel. 17, Created)
                                     PRT;
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Best Local Similarity 100.
Matches 14; Conservative
                                       PRELIMINARY;
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81 AGVIDEDYRGNVGV 94
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STATAN-CSTBL/64): TISSUB-EMBRYO, AND SPLEEN;

Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Fuku M., Nishi K., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Saburner M., Batalov S., Casavant T.,

Kadota K., Matsudi F., Sizuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Robifelli D., Bojunga N., Caninici P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Rozuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

K. Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STAIR—STAIR—STRINE;

MEDIJINE=21085660; PLOMEd=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishli Y.,

Arakawa T., Haza A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalow S., Casawant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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PRELIMINARY; PRT; 204 AA.
09CU90;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
131340009RIK PROYEIN (FRAGMBNT).
513340009RIK PROYEIN (FRAGMBNT).
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmuslia; Referazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musinae; Musculusiculus).
Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_maxID=10090;
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"Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
EMBL; AK011407; BAB22551.1; ---
EMBL; AK001076; BAB22551.1; ---
EMBL; AK001076; BAB22551.1; ---
EMBL; AK001076; BAB22551.1; ---
EMBL; AK001076; BAB22551.1; ---
InterPro; IPR001428; dUTPase.

ProDom; PP00692; dUTPase; 1.

ProDom; PD000946; dUTPase; 1.

PRODOM; PD000946; dUTPase; 1.
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us-08-957-709-80.rspt

Pred. No. 0.0039;

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Best Local Similarity
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrimi L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima N., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshalla M., Rodriguez Y., Kawaji H., Kohtsuki S.,
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MEDLINE=98229462; PubMed=9568042;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
"The genomic sequence analysis of the left and right species-specific
terminal region of a cowpox virus strain reveals unique sequences and
a cluster of intact ORFs for immunomodulatory and host range
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cowpox virus (CPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                     Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                        Length 204;
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                                                                                                                                                                                                                                                                                                            A5907170BF71B37B CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 14; DB 11;
100.0%; Pred. No. 4.2e-07;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                            204 AA; 21513 MW;
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Pfam; PF00692; dUTPase; 1.
ProDom; PD000946; dUTPase; 1.
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Virology 243:432-460(1998).
EMBL; X94355; CAA64116.1; -.
EMBL; Y11842; CAA72545.1; -.
                                                                                                                                                                                                                                                             Pfam; PF00692; dUTPase; 1
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Best Local Similarity 100.
Matches 14; Conservative
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NCBI_TaxID=10243;
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71.4%; Score 10; DB 12; Length 147;

Query Match

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Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Avipoxvirus.
                                                                                                                                                                                                                                                            Vaccinia virus (strain Tian Tan).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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Jin O., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
Jin O., Hou Y.D., Yuan J.S., Ma X.J.;
Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
Complete genomic sequence of vaccinia virus (Tian Tan strain).";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF095689; AAF33892.1;
InterPro; IPR001428; dUTPase.
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Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF198100; AAF44382.1;
InterPro; IPR001428; dUTPase.
Pfam; PF00692; dUTPase:
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J. Virol. 74:3815-3831(2000).
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 Indels
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Pfam; PF00692; dUTPase; 1.
ProDom; PD000946; dUTPase; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTNW-2001 (TrEMBLrel. 17, Last annotation update)
0RF FPV038 DUTP PYROPHOSPHATASE VACCINIA F2L HOMOLOG.
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Last annotation update)
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Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
10; Conservative
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                                2 GVIDEDYRGN 11
                                                    82 GVIDEDYRGN 91
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MEDLINE-84165064; PubMed-6223741;

MEDLINE-84. Macaulay C., Block W., Mueller T., McFadden G.;

"Tumorigenic poxviruses: construction of the composite physical map of the Shope fibroma virus genome.";

J. Virol. 50:408-416(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88322873; PubMed-2842947;
MEDLINE-88322873; PubMed-2842947;
Upton C., Macen J.L., Maranchuk R.A., DeLange A.M., McFadden G.;
"Tumorigenic poxylruses: fine analysis of the recombination junctions
in malignant rabbit fibroma virus, a recombinant between Shope fibroma
virus and myxoma virus.";
virology 166:229-239(1988).
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                                                                                                                                                                                                                                                 Shope fibroma virus (strain Kasza) (SFV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MEDLINE-91021027; PubMed-2219722;
Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
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MEDLINE-Z0032074; PubMed-10562495;
MEDLINE-Z0032074; PubMed-10562495;
Willer D.O., McFadden G., Evans D.H.;
"The complete genome sequence of shope (Rabbit) fibroma virus.";
Virology 264:319-343(1999).
EMBL: AFI70722; AAFI7896.1; -.
HSSP: P16088; IDUT.
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 Length 145;
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Last sequence update)
Last annotation update)
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Pred. No. 4.5;
 57.1%; Score 8; DB 12;
100.0%; Pred. No. 0.43;
iive 0; Mismatches
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ProDom; PD000946; dUTPase; 1.
SEDITENCE 143 AA; 15425 MW;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
GP012L.
Query Match 57.1
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
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NCBI_TaxID=10272;
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FREININARY: PRT; 188 AA.

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FREININARY: PRT; 188 AA.

DT 01-AMY-2000 (TREMBLEG-1 13) Last sequence update)

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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                           Length 1060;
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1060 AA; 110185 MW; 2E58DBC17B19B368 CRC64;
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RROULL D., FOURTHER P.E., ROUX V.;
RROULL D., FOURTHER P.E., ROUX V.;
SUDMILTED (DEC.) (1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 083448; AAG35184.1; -
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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1060 AA; 110255 MW; 3DD48C98A231E76D CRC64;
1060 AA; 110162 MW; 2844797B5B7B112E CRC64;
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Raoult D., Fournier P.E., Roux V.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 083453; Aac35189.1; -.
InterPro; IRR003858; TompA_rOmpB.
Pfam; PF02708; rompA_rOmpB; 1.
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32;
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100.0%; Pred. No. 32;
Live 0; Mismatches
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Best Local Similarity 100...
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STRAIN-SEVEN MALISH;
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Best Local Similarity
Matches 7; Conserv
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
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Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_maxID-781.
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                                                                                                                                                                    0; Indels
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STRAIN-INDIAN TICK TYPHUS;
STRAIN-LO., FOURTIER P.E., ROUX V.;
SUDMITTEE (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U83440; AAC35176.1; -.
InterPro; IPR003858; rOmpA_rOmpB.
Pfan; PF02708; rOmpA_rOmpB; 1.
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U83443; AAC35179.1; -.
PTATPRO; IPROU3858; rOmpA_rOmpB.
PF02708; rOmpA_rOmpB; 1.
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                 Pfam; PF00692; dUTPase; 1.
ProDom; PD000946; dUTPase; 1.
SEQUENCE 188 AA; 19958 WW; C2C74EE89711B9F1 CRC64;
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100.0%; Pred. No. 32;
tive 0; Mismatches
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100.0%; Pred. No. 5.9
iive 0; Mismatches
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InterPro; IPR001428; dUTPase.
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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| 671 AGVIDED 677
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STRAIN=73:

STRAIN=73:

Albrecht J.-C., Fleckenstein B.;

Albrecht J.-C., Fleckenstein B.;

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL; APO83424; AAC95540.1:

R InterPro; IPR002475; BGL2_family.

Pfam; PF00452; BCL2_family.

R PR051TE; PS50602; BGL2_FAMILY; 1.

PR051TE; PS50602; BGL1_FAMILY; 1.

SEQUENCE 174 AA; 19492 MW; E4E476717CAB59DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.9%; Score 6; DB 12; Length 174; Best Local Similarity 100.0%; Pred. No. 58; Matches 6; Conservative 0; Mismatches 0; Indels
Length 1060;
                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9YTQO PRELIMINARY; PRT; 174 AA.
O9YTQO;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
05F 16.
Ateline herpesvirus 3.
Viruses; dsDAM viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
Query Match 50.0%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 32; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                          671 AGVIDED 677
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Search completed: January 31, 2002, 13:37:52 Job time: 177 sec

104 IDEDYR 109

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:20:19 ; Search time 78.64 Seconds (without alignments).
13.561 Million cell updates/sec

US-08-957-709-80 14 1 AGVIDEDYRGNVGV 14 score:

Perfect sc Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

219241

Post-processing: Listing first 45 summaries

PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pirl:*
pir2:*
pir3:*

		di			SUMMARIES		
Result No.	Score	Query Match	Length	DB		Description	
7	14	100.0	141	5	A46256	dUTP pyrophosphata	nata
7	14	100.0	164	7	G02777		ata
æ	14	100.0	205	7	T10819		lata
4	10	71.4	144	Н	PRVZWR	retroviral protein	Lein
2	10	71.4	147	Н	PRVZ7F	probable durp	pyro
9	10	71.4	147	~	F36839		vari
7	10	71.4	147	7	H72153	٠	vari
80	10	71.4	147	7	T28464	Н	prote
6	7	50.0		٣	JC7565	н	soye
10	7	50.0	1003	7	833760	myosin IE heavy ch	ch.
11	9	•	174	7	T42929	hypothetical prote	rote
12	9		178	7	S26429	probable durp	pyro
13	9	ά.	218		A43522		ambr
14	9		239	7	C70684	probable PE protei	otei
15	9	42.9	259	7	D84343	TRK potassium upta	upta
16	9		271	7	A55517	dapB protein - Myc	Myc
17	9	42.9	289	7	D69825	qlucose 1-dehydroq	lrod
18	9		304	7	C84430	probable purple ac	ac,
19	9	42.9	339	7	T25315	, hypothetical p	prote
20	9	42.9	351	~	D84430	probable purple ac	ac
21	9		394	7	E71136	threonine synthase	ase
22	9		455	7	C83494	probable 2-isoprop	orco
23	9	42.9	484	7	T26190		prote
24	9	42.9	585	7	T28884		prote
25	9	42.9	589	7	T35784	н	ed
56	9	•	603	7	T05416	probable phosphogl	logi
27	9	42.9	624	7	T52296	phosphoglycerate	e d
28	9	42.9	695	~	T40451	n-terminal acet	acetylt
58	9	42.9	760	~	A45174	eye cell developme	omdo

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G02777
dUTP pyrophosphatase (EC 3.6.1.23) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999

75 AGVIDEDYRGNVGV 88

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RESULT

hypothetical prote	hypothetical prote	alaninetRNA liga	. probable transcrip	hypothetical prote	hypothetical prote	apolipoprotein(a)	photosystem I 9K c	incFVI protein - E	hypothetical prote	Al9L protein - var	hypothetical prote	A20L protein - var	major coat protein	coat protein B of	protein gp16 - Org
T40527	A96592	B84977	T50252	829068	T24146	T18518	S14316	S21511	T14687	B36850	T28561	A72166	S15143	C83556	T10397
7	~	7	7	7	7	7	7	7	7	7	7	.01	7	7	7
819	849	878	1268	1391	1696	2869	13	24	74	97	97	16	82	82	103
42.9	42.9	42.9	42.9	42.9	42.9	42.9	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7	35.7
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

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C; Species: Homo saplens (man)
C; Date: 08-Nov-1993 #sequence_revision 25-Aug-1995 #text_change 22-Jun-1999
C; Date: 08-Nov-1993 #sequence_revision 25-Aug-1995 #text_change 22-Jun-1999
C; Accession: A46256; A47548
R; McIntosh, E.M.; Ager, D.D.; Gadsden, M.H.; Haynes, R.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 8020-8024, 1992
A; Title: Human dUTP pyrophosphatase: cDNA sequence and potential biological importanc
A; Accession: A46256; MUID:92390380
                                                                                                                                                                                                                                                                                                                                                                        A.Residues: 1-141 <MCI>
A.Residues: 1-141 <MCI>
A.Residues: 1-141 <MCI>
A.Residues: 1-141 <MCI>
A.Crossreferences: GB.M89913; NID:g181843; PIDN:AAA58444.1; PID:g181844
A.Crossreferences modified after extraction from NBI backbone
B.McIntosh, B.M.; Ager, D.D.; Gadsden, M.H.; Haynes, R.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 4328, 1993
A.Reference number: A83861
A.Contents: annotation; erratum
R.Strahler, J.R.; Zhu, X.; Hora, N.; Wang, Y.K.; Andrews, P.C.; Roseman, N.A.; Neel, Proc. Natl. Acad. Sci. U.S.A. 90, 4991-4995, 1993
A.Title: Maturation stage and proliferation-dependent expression of dUTPase in human A.Reference number: A47548; MuID:93281681
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A, Molecule type: mRNA
A, Residues: 1-141 <STR>
A, Cross-references: GB:L11877; NID:g292876; PIDN:AAA36801.1; PID:g292877
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100.0%; Pred. No. 3.1e-08;
tive 0; Mismatches 0;
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A;Map postlicin: 15415-15421.1
C;Superfamily: retroviral proteinase
C;Keywords: hydrolase; phosphoprotein
dUTP pyrophosphatase (EC 3.6.1.23) - human N,Alternate names: dUTPase
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Query Match 71.4%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 10; Conservative 0; Mismatches
         A;Molecule type: DNA
A;Residues: 1-144 <-ROOS>
A;Cross-references: EMBL:M34368
C;Superfamily: retroviral proteinase
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PRIVAR

retroviral proteinase-like protein - vaccinia virus (strain WR)

N.Alternate names: F2L protein
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: J1-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Jun-1999
C.Accession: A32907; H16213; A31310
R.Slabaugh, M.B.; Roseman, N.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 4152-4155, 1989
A.Title: Retroviral protease-like gene in the vaccinia virus genome.
A.Reference number: A32907; MUD:89264577
A.Molecule Type: DNA
A.Residues: 1-144 < SLA>
A.Cocssion: A32907; MUD:9335616; PIDN:AA448238.1; PID:9335617
R.Reseman, N.A.: Slabaugh, M.B.
Virology 178, 410-418, 1990
A.Title: The vaccinia virus HindIII F fragment: nucleotide sequence of the left 6.2 kb.
A.Reference number: A36213; MUD:91020979
A.Rocession: H36213
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C;Accession: G02777
R;Cohen, D:, McIntoSh, E.M.; Pearlman, R.E.
submitted to the EMBL Data Library, July 1996
A;Reference number: H01715
A;Accession: G0277
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1.164 <CCOH>
A;Residues: 1.164 <CCOH>
A;Cross-references: EMBL:U62891; NID:g1421817; PIDN:AAC51123.1; PID:g1421818
C;GenetLos:
A;Genet GDB:DUT
A;Cross-references: GDB:135164; OMIM:601266
A;Genet GDB:17; retroviral proteinase
C;Reywords: hydrolase
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GUTP pyrophastase (EC 3.6.1.23) - rat
GUTP pyrophosphatase (EC 3.6.1.23) - rat
GUTP pyrophosphatase (EC 3.6.1.23) - rat
Cypecies: Rattus norvegicus (Norway rat)
C; Date: 16-Ju1-1999 #sequence_revision 16-Ju1-1999 #text_change 11-Jan-2000
C; Accession: T10819
R; Chu, R.Y.; Lin, Y.L.; Rao, M.S.; Reddy, J.K.
submitted to the EMBL Data Library, September 1998
R; Chu, R.Y.; Lin, Y.L.; Rao, M.S.; Reddy, J.K.
submitted to the EMBL Data Library, September 1998
A; Recence number: 21173
A; Accession: T10819
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-205 cCHUJ
A; Residues: 1-205 cCHUJ
A; Cross-references: EMBL:U64030; NID:93550953; PID:93550954
C; Superfamily: retroviral proteinase
C; Keywords: hydrolase
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A; Accession: 642506
A; Rolecule type: DAB
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Residues: 1-147 < CADS
A; Experimental source: strain Copenhagen
B; Cobeli, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E. Vicology 179; 247-266, 1990
A; Title: The complete DNA sequence of vaccinia virus.
A; Contents: annotation; possible protein-coding frames
A; Contents: annotation; possible protein-coding frames
A; Contents: annotation; possible protein-coding frames
A; Note: neither amino acid nor nucleotide sequence is given
B; Antoine, G.; Scheilinger, F.; Falkner, F.G.; Dorner, F.
S; Note: neither amino acid nor nucleotide sequence is given
B; Antoine, G.; Scheilinger, F.; Falkner, F.G.; Dorner, F.
A; Note: neither amino acid connected sequence of the Modified Vaccinia Ankara (MVA) st
A; Reference number: Z20877
A; Accession: T30780
A; Accession: T30780
A; Accession: T30780
A; Residues: 1-147 < ANT>
A; Residues: 1-147 < ANT>
A; Residues: 1-147 < ANT>
A; Experimental source: strain Ankara
C; Genetics:
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Alvariety: strain Ankara and Copenhagen

Ciprocession: 442506; 130780

Rigobel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E. Virology 179, 517-563, 1990

Alritle: Appendix to "The complete DNA sequence of vaccinia virus".

Alritle: Appendix to "Alvasoin Grand Alvasoin Alvasoin Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Grand Alvasoin Gr
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C6L protein - variola virus (strain India-1967)
C6L protein - variola virus
C5Species: variola virus
C;Species: variola virus
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: F36839
Siblinov, V.M.
Submitted to GenBank, November 1992
A;Reference number: A36859
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Length 144;
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C;Superfamily: retroviral proteinase
C;Keywords: hydrolase; nucleotide metabolism; proteinase
DB 1; LE
0.00062;
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0.00063;
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C;Accession: S33760
R;Urrutia, R.A.; Jung, G.; Hammer III, J.A.
Bjochim. Biophys. Acta 1173, 225-229, 1993
A;Title: The Dictyostelium myosin IE heavy chain gene encodes a truncated isoform tha A;Reference number: S33760; MUID:93277957
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C;Superfamily: brush border myosin heavy chain I; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop
F;11-678/Domain: myosin motor domain homology .KMMOT>
F;101-108/Region: nucleotide-binding motif A (P-loop)
                                                                   nucleoside-triphosphatase (BC 3.6.1.15) - fruit fly (Drosophila melanogaster) N;Alternate names: deoxyuridine-triphosphatase; duTPase C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                             C) Accession: JC7565

R) Fiser, A: Vertessy, B.G.
Biochem. Biophys. Res. Commun. 279, 534-542, 2000

A) Title: Altered subunit communication in subfamilies of trimeric dUTPases. A) A) Ascession: JC7565

A) Reference number: JC7565, MUID: 20568712

A) Recession: JC7565

A) Residues: 1-188 <FIS>
C) Comment: This ensyme is essential in preventing uracil incorporation into I WP precursor for dTTP biosynthesis.
C) Reywords: hydrolase
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G;Species: ateline herpesvirus 3
A,Variety: strain 73
A,Variety: strain 73
G;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
G;Accession: T42929
R;Albrecht, J.C.; Fleckenstein, B.
R;Abbrecht, J.C.; Fleckenstein, B.
Submitted to the EMBL Data Library, August 1998
A;Description: Primary structure of the herpesvirus ateles genome.
A;Reference number: 222274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Dictyostelium discoideum
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S337ci
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1003 <URN>
A;Cross references: EMBL:L06805; NID:g167767; PIDN:AAA33201.1; PID:g167768
C;Genetics:
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100.0%; Pred. No. 5.9;
tive 0; Mismatches
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Best Local Similarity 100.v
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Matches 7; Conserv
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594 AGVIDED 600
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98 DEDYRGN 104
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E2L protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: H72153
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C6L - variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28464
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993
A;Reference number: Z20488; MUID:94088747
A;Reference number: Z20488; MUID:94088747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-147 <MAS>
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A;Reference number: A72150
A;Accession: H72153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <SHC>
A;Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54626.1; PID:95830587
A;Experimental source: strain Garcia-1966
C;Genetics:
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                  A;Molecule type: DNA_A;Residues: 1-147 <BLI>A;Residues: 1-147 <BLI>A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA48967.1; PID:g297207 C;Superfamily: retroviral proteinase
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                                                                                                                                                     71.4%; Scc. 100.0%; Pred. No. ... 0; Mismatches
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C,Superfamily: retroviral proteinase
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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82 GVIDEDYRGN 91
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82 GVIDEDYRGN 91
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Cybecessian Mycobacterium tuberculosis

Cybecessian: To-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

CyAccession: C70684

RyCole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A;Reference number: A70500; MUD:9829587

A;Accession: C70684

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-23 CCOL.

A;Cross-references: GB:281368; GB:All23456; NID:93261656; PIDN:CAB03719.1; PID:e27963

A;Gross-references: Strain H37Rv
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B4343
TRK potassium uptake system protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: D84343
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja. Jung, K.H.; Alam, M.; Freitas, T.
C;Anthors: Hou, S.; Daniels, T.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Accession: D84343
A;Accession: D84343
A;Accession: D84343
A;Residues: 1-259 <ATO>
A;Residues: 1-259 <ATO>
A;Gene: LtxA6
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                                            Length 218;
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                                                 Score 6; DB ]; Pred. No. 18; 0; Mismatches
                                                 Query Match 42.9%;
Best Local Similarity 100.0%;
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152 DYRGNV 157
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A44522
234 integral membrane protein - fluke (Schistosoma mansoni)
N; Alternate names: Sm23
C; Species: Sofistosoma mansoni
C; Species: Sofistosoma mansoni
C; Date: 28-Oct-1992 sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C; Accession: A4352 sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C; Accession: A4352 sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C; Accession: A4352 munuogenic M-r 23,000 integral membrane protein of Schistosoma mansoni worm
A; Reference number: A4352; MUD:90217533
A; Residues: 1-218 <AWIA
A; Residues: 1-218 <AWIA
A; Residues: 1-218 <AWIA
A; Residues: 1-218 <AWIA
A; Residues: 1-218 <AWIA
A; Note: observations of molecular weight suggest this protein is at most lightly glycosy
C; Superfamily: CD9 antigen
C; Keywords: glycoprotein; transmembrane predicted <CWIA
F; 1-13/Domain: intracellular #status predicted <CWIA
F; 1-13/Domain: transmembrane #status predicted <CWIA
F; 184-206/Domain: transmembrane #status predicted <CWIA
F; 184-206/Domain: transmembrane #status predicted <CWIA
F; 184-206/Domain: intracellular #status predicted <CWIA
F; 184-206/Domain: intracellular #status predicted <CWIA
F; 184-206/Domain: intracellular #status predicted <CWIA
F; 184-206/Domain: intracellular #status predicted <CWIA
F; 207-218/Domain: intrace
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A; Accession: T42929
S; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-174 ASLB>
A; Residues: 1-174 ASLB>
A; Crost-references: EMBL:AF083424; PIDN:AAC95540.1
A; Experimental; source: Strain 73
                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 15; Matches 6; Conservative 0; Mismatches
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Sequence 1 Sequence 1 Sequence 1

Sequence 1 Sequence 1 Sequence 3

Perfect score:

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sednence:

Scoring table:

Word size :

Searched:

Database:

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Query Match . 100.0%; Score 14; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 4.2e-08; Matches 14; Conservative 0; Mismatches 0; Indels
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
           US-09-549-111-11
US-09-549-111-11
US-09-5106-11
US-08-315-695-18
US-08-8123-120-6
US-08-612-788-30
US-09-066-028-30
US-08-486-099-114
US-08-486-099-114
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ladner, Robert D.
APPLICANT: Ladner, Frank
APPLICANT: Larank
TITLE OF INVENTION: dUTPase, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 US-08-471-913A-114
US-08-485-264A-114
                                                                                                                                                        US-08-484-223B-114
US-08-919-597-114
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US-08-485-551A-114
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DAVE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08824405
Patent No. 5962246
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1997
V: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TOPOLOGY: linear
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ZIP: 19103-2793
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 Sequence 12, Appl
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Sequence 2, Appli
                                                                                            January 31, 2002, 13:15:15; Search time 65.13 Seconds (without alignments) 4.837 Million cell updates/sec
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Sequence 8
Sequence 8
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.: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

.: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

.: /cgn2_6/ptodata/2/iaa/PcTUS.COMB.pep:*

.: /cgn2_6/ptodata/2/iaa/PcTUS.COMB.pep:*

.: /cgn2_6/ptodata/2/iaa/PcTUS.COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-824 405-2
US-08-824 405-2
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PCT-US95-02455-2
US-08-195-152-2
US-08-105-223-286
US-08-612-788-18
US-08-676-3-288-4
US-08-763-528A-4
US-08-763-528A-4
US-08-77-3-3-112
US-08-47-031-12
US-08-47-031-15
US-08-47-031-15
US-08-47-031-15
US-08-473-034-12
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US-08-473-034-12
US-08-973-611-15
US-08-973-611-15
US-08-973-611-15
US-08-973-611-15
US-08-973-611-15
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                          212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                           Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                      1 AGVIDEDYRGNVGV 14
                                                                                                                                                     US-08-957-709-80
14
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Maximum DB seq length: 2000000000
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Match Length
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78
78
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Score

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Gaps

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CORRESONDENCE ADDRESSE
ADDRESSE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COMPUTE: 19103-2793
COMPUTER RADBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER IBM COMPATIBLE
COMPUTER READBLE
COMPUTER: 19003-2793
COMPUTER SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
FILING DATE: 26-MAR-1997
FILING DATE: 26-MAR-1997
FILING DATE: 36-MAR-1997
FILING DATE: APPLICATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Sequence 13, Application US/08824405

Patent No. 5962246

GENERAL INFORMATION: Robert D.

APPLICANT: Ladner, Frank

APPLICANT: Ladner, Frank

APPLICANT: Ladner, Salvatore J.

TITLE OF INVENTION: Disgnostic and Other Uses

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSE: Dechert, Price & Rhoads

STREET: Philadelphia

CITY: Philadelphia

STATE: PASA

COUNTRY: USA

ZIP: 19103-2793

MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6e-08;
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COMPOTER: IBM Compatible
COMPAGE: FastSEG for Windows Version 2.0
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,405
FILING DATE: 26-MR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 14; DE Best Local Similarity 100.0%; Pred. No. 6.6 Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 AGVIDEDYRGNVGV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGVIDEDYRGNVGV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-824-405-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-824-405-4
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                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LAGIOET D.
APPLICANT: LAGIOET D.
APPLICANT: LAGIOET D.
APPLICANT: LAGIOET CARAGONIA, STARK
APPLICANT: LYNCH, Frank
APPLICANT: CARAGONIA, SALVACOTE J.
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
CORRESPEDINDE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STREET: Dechert, Price & Rhoads
STREET: Dechert, Price & Rhoads
STRATE: Philadelphia
STRATE: Philadelphia
STRATE: Dechert, Price & Rhoads
LIP: 19103-2793
COMPUTEN: USA
ZIP: 19103-2793
COMPUTEN: BADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTEN: FRSTEM: DOS
SOFTWARE: FRSTEM: DOS
SOFTWARE: FRSTEM: DOS
SOFTWARE: FRSTEM: DOS
SOFTWARE: FRSTEM: US/08/824,405
FILING DATE: 26-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 29,135
RECISTRATION NUMBER: 29,135
RECISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 350163-101
TELEPHONE: 609/520-3214
TELEPHONE: 609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ladner, Robert D.
APPLICANT: Lynch, Frank
APPLICANT: Caradonna, Salvatore J.
TITLE OF INVENTION: dUTPase, Its Isoforms, and
TITLE OF INVENTION: Diagnostic and Other Uses
NUMBER OF SEQUENCES: 20
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                                                                                                                                                                            Sequence 2, Application US/08824405; Patent No. 5962246
GENERAL INFORMATION:
APPLICANT: Ladner Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08824405
Patent No. 5962246
GENERAL INFORMATION:
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-824-405-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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                                               80 AGVIDEDYRGNVGV 93
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US-08-824-405-2
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US-08-824-405-4
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100.0%; Pred. No. 16;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
PCT-US95-02455-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08195152
Patent No. 5679541
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.99
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                          LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                               INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                             HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
CREANELLE:
IMMEDIATE SOURCE:
POSTITON IN GENOME:
CHROMOSOME/SEGMENT:
                  FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: BCG
STRAIN:
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19 AGVIDE 24
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VOLUME:
PAGES:
                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jacobs et al
TITLE OF INVENTION: GENE FOR MYCOBACTERIAL
TITLE OF INVENTION: DIAMINOPIMELIC ACID
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amster, Rothstein & Ebenstein
STREET: 90 Park Avenue
CITY: New York
COUWTR: U.S.A.
ZIP: 10016
COMPTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: George, Kenneth P.
REGISTRATION NUMBER: 30,259
REPERCE/DOCKET NUMBER: 96700/358
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELESA: (212) 286-084 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02455
FILING DATE: Not Yet Assigned
CLASSIFICATION:
PRIOR APPLICATION DATA: none
APPLICATION NUMBER: none
FILING DATE: none
ATTORNEY/AGENT INFORMATION:
                                             NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 350163-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609/520-3214
TELEFRAX: 609/520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 inch 1.44 Mb
MEDIUM TYPE: storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dapB protein
               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                        Query Match 71.4
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
APPLICATION NUMBER:
                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-824-405-13
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79 GVIDEDYRGN 88
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HYPOTHETICAL:
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PCT-US95-02455-2
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RESULT 7

RESULT 7

Sequence 286 Application US/08905223

Sequence 286 Application US/08905223

Sequence 286 Application US/08905223

SPECENT NOT Edwards, Jean-Baptiste D. APPLICANT: Edwards, Jean-Baptiste D. APPLICANT: Lacroix, Bruno

TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS

NUMBER OF SEQUENCES: 503

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANObbe, Martens, Olson & Bear

STREET: Sol West Broadway

CITY: San Diego

STRATE: California

COUNTRY: USA

MEDIUM TYPE: Floppy Disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: Word

COMPUTER: Word

APPLICATION NUMBER: US/08/905,223
REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPANE: (415) 781-1989
TELEFAX: 910 277299
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMCTH: 760 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: sig_peptide
LOCATION: -31...1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: SCORE 8.2
OTHER INFORMATION: Seq LECLLYLAESSG/LR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATORNEY CARES

ATTORNEY AGENT INFORMATION:
NAME: 1Sraelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 235-6176
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
TISSUE TYPE: Brain
                                                                                                                                                                                                  . TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-195-152-2
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616 YRGNVG 621
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GENERAL INFORMATION:
APPLICANT: Co'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: San, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: 600194
CONNTY: U.S.
CONNTY: U.S.
CONNTY: U.S.
CONNTY: U.S.
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Ouery Match 35.7%; Score 5; DB 4; Best Local Similarity 100.0%; Pred. No. 38; Matches 5; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-612-788-18
Sequence 18, Application US/08612788
Sequence 18, Application US/08612788
Setent No. 5837682
GENERAL INFORMATION:
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US-08-763-528A-4
; Sequence 4, Application US/08763528A
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORGINAL SOURCE:
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
CLONE: K3
US-08-612-788-18
                                                                                                                                                                                       35 GNVGV 39
                                                                                                                                            10 GNVGV 14
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|9 YRGNV 13
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Sequence 12, Application US/08487031
Patent No. 5977306
GENERAL INFORMATION: Robert B.
APPLICANT: Grieve, Marcia
APPLICANT: Frank, Glenn R.
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/487,031
06-JUN-1995
                  COMPUTER READABLE FORM:
BEDIOW TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPDERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
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100.0%;
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
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Matches 5; Conserv
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CITY: Denver
STATE: Colorad
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9 YRGNV 13
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                GENERAL INFORMATION:
APPLICANT: Cao, Yihai
APPLICANT: FOLKman, M. Judah
TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: FOlkman, M. Judah
APPLICANT: Gro, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVERTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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; OTHER INFORMATION: /note= "Kringle 3 - Figure 3"
US-08-763-528A-4
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/763,528A
FILIND DATE: 12-DEC-1996
CLASSIFICATION: 530
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                                                                                                                                                         E: Jones & Askew, LLP
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION UNDRER: 36,714
REFERENCE/DOCKET NUMBER: 0594(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3709
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
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Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                  Georgia
                                                                                                                                                                                       CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
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Patent No. 5854221
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US-09-066-028-18
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USSQUENCE 20, Application US/08487031
Sequence 20, Application US/08487031
Fatent No. 5977306
GENERAL INCPRAZION:
FRAPLICANT: Erank, Glen R.
APPLICANT: Erank, Glen R.
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVELE PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVELE PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVELE PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVELE PARASITIC HELMINTH P39
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TITLE OF INVENTION: NOVELE PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVELE PARASITIC HELMINTH P39
TITLE OF INVENTION OF STATES
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
COUNTRY: U.S.A
STATE: Colorado
COUNTRY: U.S.A
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Delicht IN Release #1.0, Version #1.25
CURSENT APPLICATION NUMBER: U.S.A
SOFTWARE: PAGAPICATION NUMBER: U.S.A
TELLING DATE: OG-JUN-1995
CLASSIFICATION NUMBER: 23,459
REFERENCE/DOCKET NUMBER: 23,450
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-084473-034-20
US-084473-034-20
Sequence 20, Application US/08473034
Patent No. 6114142
REBERAL INFORMATION:
APPLICANT: FIRTK, Gleve, Marcia
APPLICANT: Tripp, Cynthia A.:
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVEL PARASITIC ADDITIONS OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSION OF SUCCESSI
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68 DEDYR 72
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                                                             5 DEDYR 9
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US-08-487-031-20
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APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Hika-Grieve, Marcia
APPLICANT: Hika-Grieve, Marcia
APPLICANT: Hika-Grieve, Marcia
APPLICANT: Hika-Grieve, Marcia
APPLICANT: Hika-Grieve, Marcia
APPLICANT: Hika-Grieve, Marcia
APPLICANT: Tripp, Cynthia Novel PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
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TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Elba PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-195
CLASSIFICATION NUMBER: US/08/473,034
ATTORNEY/AGENT INFORMATION:
REGISTRICE/POCKET UNBER: 37 459
REFERENCE/POCKET UNBER: 37 459
REPERENCE/POCKET UNBER: 37 459
RELEFAX: (303) 863-9700
FELEFAX: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.7%; Score 5; DB 2; Best Local Similarity 100.0%; Fred. No. 80; Matches 5; Conservative 0; Mismatches
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Pred. No. 80;
0; Mismatches
                                    ATTORNEY AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37 459
REFERENCE/DOCKET NUMBER: 2618-34-
TELECOMMUNICATION INFORMATION:
TELEFEAK: (303) 863-923
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acids
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Best Local Similarity 100.0%; P.
Matches 5; Conservative 0;
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CLASSIFICATION:
ATTORNEY/AGENT IN
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68 DEDYR 72
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Search completed: January 31, 2002, 13:15:16 Job time: 97 sec
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Best Local Similarity 100.
Matches 5; Conservative
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; MOLECULE TYPE: protein
US-08-487-031-15
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79 DEDYR 83
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APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Mixa Grieve, Marcia
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PRASITIC HELMINTH P39
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF NUMBER OF SEQUENCES: 33
AUGHESPONDENCE ADDRESS:
ADDRESSEE: Sharidan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 105;
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,034
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: VERSEX Carol Talkington
REGISTRATION NUMBER: 37.459
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COUNTRY: U.S.A
ZIP: 80203
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPGRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,031
FLING DATE: 06-JUN-1995
CLASSIFICATION: 424
1700 Lincoln St., Suite 3500
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NAME: Verser, Carol Talkington
RECISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%; Score 5;
100.0%; Pred. N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 105 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-034-20
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Best Local Similarity
Matches 5; Conserv
                                                                          STATE: Colorado COUNTRY: U.S.A
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STATE: Colora
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69 DEDYR 73
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                                                                                                                                                             35.7%; Score 5; DB 2;
100.0%; Pred. No. 87;
tive 0; Mismatches
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
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Human

Peptide #8303 ero Peptide #12231 enc Arabidopsis thalia Peptide #7210 enco Human kringle 3. Peptide #7210 enco Peptide #10173 enc Human plasminogen Peptide #2272 enco Peptide #2286 enco Arabidopsis thalia Arabidopsis thalia

Title: Perfect score: Sequence:

protein

Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Word size Searched:

Database :

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Polymerase enhancing factor; PEF; dUTPase; PCR; amplification; sequencing; replication; human.
                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                   AAG15616
AAG15615
AAW29490
                                                                                                                                                          AAM32103
AAG12512
AAG14512
AAY13002
AAM31809
AAM38194
AAG50020
AAM38194
AAM38194
AAM36136
AAM36136
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AAG40018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human dUTPase uridine-binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW72856 standard; Peptide; 14 AA
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                                                                                                 97US-0957709.
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Hogrefe H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9842860-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-1998;
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 RESULT
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Human dUTPase prot
                                                                 Search time 140.03 Seconds (without alignments) 7.406 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human dUTPase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                 /SIDSZ/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                              522463 seqs, 74073290 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                  January 31, 2002, 13:18:14
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AAR70144
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AAW30281
AAB58469
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                                                protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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141
164
164
252
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227
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Polymerase enhancing factor proteins, extracts and complexes -improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

Score

Result Š 444 444 60 60 60 60

Length 141;

100.0%; Score 14; DB 16; 100.0%; Pred. No. 6.1e-08;

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Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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                          This is the uridine-binding motif of human dUTPase. Sequences are provided (see AAW72849-57) of the uridine-binding motifs of the dUTPases and dCTP deaminases of Pyrococcus furiosus (see also AAW72847), Methanococcus jannaschli, Desulfurolobus ambivalens, Escherichia coli, yeast, human and herpesvitus; a consensus (see AAW72848) is also provided. A claimed method of enhancing a coperase reaction comprises performing the reaction in the presence of one or more of the following: a polymerase enhancing factor (PEF), a dUTPase, a protein that turns-over dUTP and a protein having one or more of the sequences provided in AAW72848-57. Rits are provided in AAW72848-57. Rits are provided for replicating sequencing or for site-directed mutagenesis, for nucleic acids, for site-directed mutagenesis, for nucleic acid nucleic acid protein (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human dUTPase (given in AAQ83219) was cloned into pUC19 and recombinants used to transform E. coli BW 286. A transformant selected for growth at 39 deg was cultured overnight. Recombinant human dUTPase was purified and shown to be identical in sequence to the natural protomeric peptide (AAR70144).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pure native human deoxyuridine tri:phosphate nucleotido:hydrolase - used to identify inhibitors, potentially useful as antimicrobial and anticancer agents
                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                         100.0%; Score 14; DB 19; Length 14; 100.0%; Pred. No. 7.3e-09; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deoxyuridine-triphosphate-nucleotidohydrolase; dUTPase;
antimicrobial; anticancer; cytostatic; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALLX ) ALLELIX BIOPHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR70144 standard; Protein; 141 AA.
Claim 71; Page 47; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig.1; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Climie S, Vandenberg E;
                                                                                                                                                                                                                                                                                                                                                                                            1 AGVIDEDYRGNVGV 14
                                                                                                                                                                                                                                                                                                                                                                                                           Human dUTPase protomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-115928/16.
N-PSDB; AAQ83219.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                             14 AA;
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                                                                                                                                                                                                                                                                               Sequence
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141 AA;

Sequence

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This polypeptide comprises the nuclear form, designated DUT-N, of muran deoxyuridine triphosphate nucleotidohydrolase (durpase). Its amino acid sequence was deduced from a T-cell cDNA clone (see AAT90987).

AAT90987). A single gene codes for 2 isoforms of human dUTPase, the nuclear form (DUT-N) and a cytoplasmic form (DUT-N, see AAM30281).

Which is targeted to the mitochondria. The isoforms arise by the use of alternative 5' exons which then join in a common sequence. The DUT-N isoform is produced at low or undetectable levels during non-proliferative periods of the cell cycle, and can be used as a marker for cellular proliferation. It is phosphorylated by plydcc2 at a Ser residue within the consensus sequence for cyclin-dependent kinase phosphorylation. Measuring the amount of dUTPase in a cell can be used to determine its proliferative status (or changes in this status), particularly in nutrient-deprived or neoplastic cells anticancer agents (A) on cells, or monitoring the effect of (claimed). Agents that inhibit dUTPase are potential and antifungal agents.

The dUTPase can also be used to raise antibodies for assaying the erzyme and for drug screening.
   Gaps
                                                                                                                                                                                                                                                                               dUTPase; DUT-N; human; cell proliferation; inhibitor; cytostatic;
antiviral; antibacterial; antifungal; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding two isoform(s) of human dUTPase - used in assays for assessing status of cell proliferation, effect of anticancer agents and progress of treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal peptide unique to DUT-N"
Mismatches
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                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                  AAW30280 standard; Protein; 164 AA.
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                                                                                                                                                                                                                                                 Human dUTPase (nuclear form).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US04886.
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96US-0014748.
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                                                    11111111111111111175 agvidedyrgnvgv 88
                                1 AGVIDEDYRGNVGV 14
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N-PSDB; AAT90987.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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29-MAR-1996;
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises the mitochrondrial form, designated DUT-M, of human deoxyuridine triphosphate nucleotidohydrolase (dUTPase). Its amino acid sequence was deduced from a fibroblast cDNA clone (see AAT90989). A single gene codes for 2 isoforms of human dUTPase, the nuclear form (DUT-M, see AAW30280) and the cytoplasmic form (DUT-M) which is targeted to the mitochondria. The isoforms arise by the use of alternative 5' exons which then
                                                                                                                                                                                                                                                                   dUTPase; DUT-M; human; cell proliferation; inhibitor; cytostatic;
antiviral; antibacterial; antifungal; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding two isoform(s) of human dUTPase - used in assays for assessing status of cell proliferation, effect of anticancer agents and progress of treatment
                                                                                                                                                                                                                                                                                                                                      70..93 /note= "DUT-M unique sequence 5' to common Glu residue of DUT-M and DUT-N"
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                                              Length 164;
                                                                  0; Indels
                                           100.0%; Score 14; DB 18; 100.0%; Pred. No. 7e-08;
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lynch F;
                                                                                                                                                                        AAW30281 standard; Protein; 252 AA
                                                                                                                                                                                                                                               Human dUTPase (mitochondrial form)
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96US-0014748.
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                                           Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                     98 agvidedyrgnvgv 111
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          164 AA;
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          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal activity. The invention antinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynuclocide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
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to raise antibodies for assaying the enzyme and for drug screening
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                                                                                                                                                                          Score 14; DB 18; Length 252;
Pred. No. 1e-07;
Mismatches 0; Indels
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Best Local Similarity 100.
Matches 14; Conservative
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                           Length 63;
                            Score 9; DB 21; Length 63; Pred. No. 0.0063; Pred. No. 0. 1ndels
                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 55105.
                                                                                                                                           AAG44032 standard; Protein; 219 AA.
                            Query Match
Best Local Similarity 100.0%; Pr
Matches 9; Conservative 0;
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05-MAR-1999;
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 Sequence
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                            DYRGNV '2
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100.0%; Pred. No. 32;
ive 0; Mismatches
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                Gene involved in the synthesis of di:amino:pimelic acid in mycobacteria - and methods for inhibiting its expression to treat mycobacterial infection
                                                                                                                                                 A BGC dapB gene (see AAT04154) was isolated that encoded a bifunctional enzyme (AAR79946) capable of catalyzing the dihydrodipicolinate-reductase and diaminopimelate-dehydrogenase reactions involved in diaminopimelic acid (DAP) biosynthesis. Prodn. of mycobacterial DapB will allow the screening of DapB-inhibitory (antimycobacterial) cpds.
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Pred. No. 39;
Mismatches 0; Indele
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                                                                                                                    Disclosure; Page 29-29; 48pp; English
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N-PSDB; AAT04154.
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19-APR-1999;
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Desulfurolobus amb	Polypeptide encode	Arabidopsis apopto	Human ORFX ORF8 po	Partial 36 kD anti	S. epidermidis ope	Soybean vestitone	Soybean vestitone	Soybean apoptosis	BARÎ gene product.	Barrier protein.
	ID	AAW72852	AAR51078	AAB20302	AAB40244	AAR05583	AAG81528	AAY05529	AAY97832	AAB20313	AAP70143	AAR13383
	9B	19	14	22	21	11	22	20	21	22	œ	12
	ength 1	14	173	488	121	159	174	327	327	543	585	587
ФP	Query Match Length DB ID	100.0	100.0	50.0	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9
	Score	14	14	7	9	9	9	9	9	9	9	9
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BAR1 barrier prote Arabidopsis RAN1 c Arabidopsis ran1-1 Arabidopsis ran1-1 Peptide epitope of Entry vector pEWTR Human secreted pro Rieske motif in DN Homo sapiens liver Liver neoplastic d 12 kD M.tuberculos Mycobacterium 12 k	se illos if a if a inti inti inti inti inti inti inti int	Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o GDP-D-mannose dehy Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o Chlamydial major o
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## ALIGNMENTS

RESULT

Desulfurolobus ambivalens dCTP deaminase uridine-binding motif. Polymerase enhancing factor; PEF; dCTP deaminase; PCR; amplification. AAW72852 standard; Peptide; 14 AA. 97US-0957709. 97US-0822774. 98WO-US05497 (first entry) Desulfurolobus ambivalens Hogrefe H; (STRA-) STRATAGENE. WO9842860-A1 20-MAR-1998; 24-OCT-1997; 21-MAR-1997; 01-MAR-1999 01-0CT-1998 Hansen CJ, AAW72852; AAW72852 

Polymerase enhancing factor proteins, extracts and complexes -improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

WPI; 1998-542284/46.

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                                                                                                       This is the uridine-binding motif of the dCTP deaminase of Desulfuciobus ambivalens. Sequences are provided (see AAW72849-57) of the uridine-binding motifs of dUTPases and dCTP deaminases of Pyrococcus furiosus (see AAW72847), Methanococcus jannaschii, Desulfuciobus ambivalens, Escherichia coli, yeast, human and herpesvirus; a consensus (see AAW72848) is also provided. A claimed herpesvirus; a consensus (see AAW72848) is also provided. A claimed method of enhancing a nucleic acid polymerase reaction comprises performing the reaction in the presence of one or more of the following: a polymerase enhancing factor (PEF), a dTPPase, a Collowing: a polymerase enhancing factor (PEF), a dTPPase, a ctivity comprises one or more of sequences given in AAW72848-57. C Kits are provided for replicating nucleic acids, for site-directed mutagenesis, for nucleic acid sequencing or for amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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100.0%; Pred. No. 3.3e-08;
1ve 0; Mismatches 0;
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Claim 71; Page 47; 161pp; English
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N-PSDB; AAQ62300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding plant apoptosis inducing factor for engineering male sterility, altering plant architecture, manipulating stress response, and influencing growth of cells and tissues in culture
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a monodehydroascorbate reductase like apoptosas inducing factor (AIF) of Arabidopsis thaliana candsberg erecta. The sequence is predicted from the full-length CDNA (see AAF30431) of a clone isolated from a fertilised carpel CDNA library. It shows 51.7% amino acid identify to previously known monodehydroascorbate-reductase-like AIFs of Gryza sativa and Brassica juncea. The invention relates to isolated nucleic acids encoding plant AIFs. These are used in sense or antisense constructs to alter levels of AIFs in plant cells, and hence to alter apoptosis and eventually to control cell tissue culture growth, facilitate studies of programmed cell death in plants, increase the efficiency of gene transfer, help provide more stable transformations, engineer male sterility, alter plant architecture or manipulate stress response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis inducing factor; AIF; monodehydroascorbate reductase; male sterility; stress response; tissue culture; plant.
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      Length 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis apoptosis inducing factor-like protein.
100.0%; Score 14; DB 14;
100.0%; Pred. No. 2.8e-07;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.1
Best Acthes 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                              AAB20302 standard; Protein; 488 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                    Conservative
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N-PSDB; AAF30431.
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   Ouery Match
Best Local Similarity
Matches 14; Conserv
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267 fegglti 273
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coagulation; to inhibit thrombosis; and as a contraceptive.

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; antidabetic; hypotensive; dermatolojytic; coagulant; vasotropic; antidabetic; hypotensive; dermatolojytic; coagulant; vasotropic; antithabetic; hypotensive; dermatolojytic]; antithidabetic; hypotensive; dermatolojytic]; antithidabetic; hypotensive; antithidabetic; proteins antiviral; antithing; antithenatic; antithidabetic; hypotensive; dermatolojytic]; antithidabetic; proteins antithidabetic; proteins antithidabetic; proteins and nucleic acids may be used for determining the presence of or predisposition to, or preventing or treating tractions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, astania, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirhemmatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinaria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                    Human ORFX ORF8 polypeptide sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 431-432; 5507pp; English.
                                           AAB40244 standard; Protein; 121 AA
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05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                     (first entry)
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N-PSDB; AAC74453.
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RESULT
AAB40244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of eliciting an antibody which recognises an epitope of an M. hyo antigen. The recombinant proteins can be used in a vaccine for protection against Mycoplasma phoumonia, partic in swine, or in an assay for detection of antibodies to M. hyo. See also AAQ03629-Q03634, AAQ04959-Q04963 and AAQ02474.
                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Mycoplasma hyopneumoniae antigens - used in vaccines against mycoplasma pneumonia and in assays for detection or determination of antibody.
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                                                  Length 121;
                                                                                                                                                                                                                                                                  Recombinant Mycoplasma hyopneumoniae antigens; mycoplasma pneumonia; vaccine; antibody; ds.
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                                                                                                                                                                                                                                            Partial 36 kD antigen of Mycoplasma hyopneumonia.
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Pred. No. 37;
0; Mismatches
                                                 42.9%; Score 6; DB 2
100.0%; Pred. No. 30;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrews WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG81528 standard; Protein; 174 AA.
                                                                                                                                                                           AAR05583 standard; protein; 159 AA.
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100.0%; Pre
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                                                              Similarity 100.6; Conservative
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Best Local Similarity
                    121 AA;
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                                                    Query Match
Best Local S
Matches 6
                     Sequence
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AAG81528

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The present sequence is soybean vestitone reductase, encoded by
the cDNA insert (see AAX25131) of an EST clone, ser pk0016.cg,
solated from a soybean root cDNA ilbrary following a BLASTX
search. The sequence shows similarity to Medicago sativa vestitone
reductase. The invention relates to isolated nucleic acids
ancoding soybean enzymes that catalyse steps in the blosynthesis of
sofiavones, i.e. chalcone isomerase (see AAX05527), isofiavone
calcutase (see AAX05528) and vestitone reductase. The invention also
reductase (see AAX05528) and vestitone reductase or antisense or antisense or substantial portion of the enzymes, in sense or antisense orientation,
where expression of the enzymes, in sense or antisense orientation,
where expression of the chimeric gene results in production of altered
levels of the enzyme in a transformed host cell. The method is
used to alter isoflavone levels in plants and seeds, particularly
of food plants. High accumulation of isoflavones may have flavour
controgenic tumor-suppressing, antihypercholestere and
hypolipidemic activities. Since the specified enzymes are involved
late in isoflavone synthesis, they are unlikely to interfere with
cother parts of the phenylpropanoid pathway (leading to lignin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean; vestitone reductase; root elongation zone; EST;
expressed sequence tag; isoflavone biosynthesis;
phenylpropanoid biosynthetic pathway; transgenic plant; antihaemolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid encoding enzymes for isoflavone biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean vestitone reductase, encoded by cDNA clone sre.pk0016.c8
                 Vestitone reductase; soybean; isoflavone; transgenic plant;
antihaenclytic; hypocholesterolemic; hypolipidemic; oestrogenic;
antitumour; antifungal.
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42.9%; Score 6; DB 20; Length 327;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-244040/20.
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                                                                                                                                                                   WO9914351-A1.
                                                                                                                                                                                                                                                                                                            17-SEP-1997;
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                                                                                                                     Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                             Fader GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II) and (II) and AGG81120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used to production of vectors containing them which are used to produce hosts cells which express the perpeptides. The polypeptides (II) via final/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their reatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH5509 represent specifically claimed S. epidermidis genomic DNA AH5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to AAH5509 represent invention specification of the present specification, no the present invention specifically claims of the present specification, however the sequence listing of the present specification, however the sequence listing only goes up to SEO ID NO:4465 to 4472, no sequences are present for SEO ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                        S. epidermidis open reading frame protein sequence {\rm SEQ}~{\rm ID}~{\rm NO}{:}150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                   Staphylococcus epidermidis SR1 strain; infection; diagnosis; . vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.9%; Score 6; DB 22; Length 174;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 84; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05529 standard; Protein; 327 AA.
                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000; 2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1999; 99US-0164258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soybean vestitone reductase
                                                                                                                                                                                                              Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-1999 (first entry)
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-316495/33.
N-PSDB; AAH52378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200134809-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VDAGFE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimmerly WJ;
                                          03-SEP-2001
                                                                                                                                                                                                                                                                                                         17-MAY-2001.
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Gaps

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Sequence

ò QQ AAY05529;

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WO200119994-A2.
             Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP70143
  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                    This sequence represents soybean vestitone reductase, encoded by CDNA clone sre.pk0016.08. This CDNA was identified in a soybean root clone store CDNA in the first expressed sequence and clone CDNA in the first expressed sequence can go come CDNA in the first expressed sequence tag (EST) identified for soybean chalcone isomerase. Vestitone reductase can component enzymes of the phenylpropanoid biosynthetic pathway which is responsible for the biosynthesis of isoflavones from phenylalanine in leguminous plants. The isoflavones found in soybeans are thought to provide several health benefits to humans. Soybean isoflavones chave antihaemolytic, antifungal, oestrogenic, tumour suppressing, hypolipidaemic and serum cholesterol-lowering effects. However, certain isoflavones, such as isoflavone, flavone, anthocyanins and flavanois adversely affect the flavour of certain soy food products. The nucleic cacids of the invention (AAA38424-AA8426) may be used to generate transgenic plants in which expression of chalcone isomerase, isoflavone cacids and/or vestitone reductase is altered. The sequences are also same or other plant species, synthesising DNA primers and probes for mapping the genes and for immunological screening of CDNA expression callbraries. The nucleic acid sequences can be used to mainpulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                New polynucleotide encoding chalcone isomerase for altering the levels of plant isoflavone biosynthetic enzyme in a host cell and for producing transgenic plants and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis inducing factor; AIF; monodehydroascorbate reductase; male sterility; stress response; tissue culture; plant; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoflavone content without affecting other portions of the phenylpropanoid pathway associated with lignin biosynthesis.
 oestrogenic; tumour suppressor; hypolipidaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 327; 0. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean apoptosis inducing factor-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 6; DB 2
100.0%; Pred. No. 68;
tive 0; Mismatches
                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20313 standard; Protein; 543 AA.
                                                                                                                                                                                                                                                                                                   Example 2; Fig 4; 25pp; English.
                                                                                                            98US-0154874.
                                                                                                                                   97US-0931668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
          hypocholesterolaemic
                                                                                                                                                                                                            WPI; 2000-338516/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AA;
                                                                                                                                                                                                                         N-PSDB; AAA38426
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300 vdagfe 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VDAGFE 9
                                                                                                            17-SEP-1998;
                                                                                                                                   17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-2001
                                                           US6054636-A.
                                    Glycine max.
                                                                                                                                                                                   Fader GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB20313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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14.7

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New polynucleotide encoding plant apoptosis inducing factor for engineering male sterility, altering plant architecture, manipulating stress response, and influencing growth of cells and tissues in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a monodehydroascorbate reductase like apoptosis inducing factor (AIF) of soybean, as predicted from a full-length CDNA (see AAF30442). It shows 52.6% amino acid identity to known monodehydroascorbate-reductase-like AIFs of Oryza sativa and Brassica juncea. The invention relates to isolated nucleic acids encoding plant AIFs. Such nucleic acids, used in plant cells, and hence to alter levels of AIFs in plant cells, and hence to alter apoptosis and eventually to control cell tissue culture growth, facilitate studies of programmed cell death in plants, increase the efficiency of gene transfer, help provide more stable transformations, engineer male sterility, alter plant architecture and manipulate stress response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 6; DB 22; Length 543 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308..0
/label-potential glycosylation site
366..0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366...v
/label=potential glycosylation site
                                                                                                                                                                                                                  Mazithulela G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0
/label_potential glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1(i); Page 71-72; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..24
/label=signal peptide
                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70143 standard; protein; 585 AA.
                                                                                                                                                                                                                  Cahoon RE, Klein TM,
                                                                                                         99US-0153737.
                                                      11-SEP-2000; 2000WO-US24859.
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Best Local Similarity الاست
المراقبة وفي Conservative
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                                                                                                                                                                                                                                                                      WPI; 2001-244804/25.
N-PSDB; AAF30442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAR1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 feggit 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 FEGQLT 13
                                                                                                         13-SEP-1999;
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22-MAR-2001
                                                                                                                                                                                                                  Butler KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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us-08-957-709-76.rag

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1 PTIVDA 6
                                                              14-NOV-1988;
02-OCT-1987;
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08-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9118988-A.
                           06-AUG-1991
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             AAR20109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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Matches
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   οy
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                                                                                                                                                                                                                                                                           The BARI gene product is expressed as a fusion polypeptide/protein in S.cerevisiae, esp. with insulin or proinsulin. The fusion protein pref. also comprises a KEX 2 processing site. The presence of the BARI sequence means that the fusion protein is secreted into the culture medium or periplasmic space, facilitating its purificn.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        New DNA fragment contg. yeast BAR I gene and foreign structural gene - under control of promoter, esp. for producing insulin which is secreted from the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heterlogous protein; expression; secretion; urokinase; insulin; EGF; TGF; PDGF.
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0
                                                                                                                                                                                                                                                                                                                                                        Length 585;
                                                                                                                                                                                                                                                                                                                                                                          0; Indels
398..0
/label=potential glycosylation site
468..0
/label=potential glycosylation site
503..0
                                        7] Alabel-potential glycosylation site 551...0
/label-potential glycosylation site
                                                                                                                                                                                                                                                                                                                                                        Query Match 42.9%; Score 6; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+02,
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                           Disclosure; Fig. 1A-C; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..24
/label= sig_peptide
25..587
/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13383 standard; Protein; 587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 503 /label- ASN, GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label- ASN, GLN
                                                                                                                 86EP-0114769
                                                                                                                                 86WO-US02198
85US-0791305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                              WPI; 1987-124280/18.
                                                                                                                                                            (MACK/) MACKAY V L.
                                                                                                                                                                                                                                                                                                                               585 AA;
                                                                                                                                                                                                         P-PSDB; AAP70143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                     |||||||
| 246 ptivda 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrier protein
                                                                                                                                                                                                                                                                                                                                                                                           1 PTIVDA 6
                                                                                                                                  20-OCT-1986;
25-OCT-1985;
                                                                                               06-MAY-1987
                                                                              EP220689-A.
                                                                                                                                                                              Mackay VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13383;
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                  Region
                                   Region
                                                     Region
  Region
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Asn468 and/or Asn503 may be replaced by Gln to prevent glycosylation. A hybrid secretory peptide comprising the signal sequence and amino acids 391-526 or 423-526 directs the secretion of heterlogous proteins or polypeptides. e.g. urokinase, insulin, platelet-derived growth factor, epidermal growth factor or transforming growth factor see also AAQ13195-7.
                                                                                                                                                                                                                              DNA constructs for secretion of foreign proteins - using signal sequence and portion of BAR1 C-terminal domain to direct secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 6; DB 12; Le ilarity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..24
/note= "signal peptide"
25..587
/note= "mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR20109 standard; Protein; 587
                                                                                                                Yip CL;
88US-0270933.
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90US-0534933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1992 (first entry)
                                                                     (ZYMO-) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO-) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
                                                                                                                Welch SK, Mackay VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAR1 barrier protease.
                                                                                                                                                           WPI; 1991-252061/34.
N-PSDB; AAQ13195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587 AA;
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Gaps

.; 0

Length 1001; Indels

DB 21; ໄປຣາເລີ ທີ່ 1.8e+02; 0;

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New isolated plant copper transporter genes, useful for modulating e.g. germination, sex determination, flower or leaf senescence, fruit ripening, pathogen resistance or response to stress
with other copper transporters, including an N-terminal metal binding motifs, a phosphatase domain, a transduction domain, a phosphorylation domain, and an ATP binding domain. The invention relates to the ranl gene and to antegonist responsive mutants controlling copper transport in the plant. It also relates to the manipulation of ranl and its protein product to modulate the ethylene response in plants, thereby permitting the regulation and controlled alteration of plant growth and developmental processes, including germination, cell elongation, flower and leaf senescence, abcsission, fruit ripening, insect, herbicide and pathogen resistance, and response to stress (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutein ran1-1. The mutein has an amino acid substitution of Ile for Thr497 of the wild-type protein (see AAX58677). RAN1 is a copper transporter and early-acting regulator of the ethylene gas signalling pathway. Thr497 is in the phosphatase domain and is conserved in all copper transporters. The ran1-1 protein accumulates to the same level as RAN1 but has reduced copper transporting activity. The invention relates to the RAN1 gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the Arabidopsis thaliana RANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copper transporter; ranl-1; responsive-to-antagonist1; ethylene signalling pathway; ATPase; copper transport; transgenic plant; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "replaces wild-type Thr"
                                                                                                                                                                                                                                                                                                                 Score 6; DB 21; Pred. No. 1.86 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY58717 standard; Protein; 1001 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis ran1-1 mutant protein.
                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 30; Page -; 78pp; English.
                                                                                                                                                                                                                                                                                                                   42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
'-hag 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-171318/15.
N-PSDB; AAZ58168.
                                                                                                                                                                                                                                                    1001 AA;
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|193 dagfeg 198
                                                                                                                                                                                                                                                                                                                                                                                                  5 DAGFEG 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000
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                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY58717;
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ID AAY5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                    The amino acid sequence is that of barrier protease (BP) from S. cerevisiae. BP compsns. may be used in a variety of industrial processes, partic. those calling for the cleavage of leucine-lysine or leucine-arginine bonds under acidic conditions or at high temp. BP may also be used in the prodn. and isolation of proteins made by genetic engineering methods, e.g. to cleave fusion proteins at Leu-Arg bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana ecotype Columbia (Col-0) as predicted from the exons of RANI cONA (see AAE27895). RANI is a copper transporting P-type ATPase that acts as an early acting regulator in the ethylene gas signalling pathway. Its shares structural features
                                                                                                         Pure barrier protease – useful in industrial processes where leucine-lysine or leucine-arginine cleavage is required at low pH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copper transporter; RAN1; responsive-to-antagonist1; ethylene signalling pathway; ATPase; copper transport; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 6; DB 1
100.0%; Pred. No. 1.1
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY58677 standard; Protein; 1001 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker JR, Hirayama T, Kieber JJ;
                                                                                                                                                                                        Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 5; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US16591.
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Best Local Similarity الاست
احد 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                          WPI; 1992-007471/01
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                                                                                                                                                                                                                                                                                                                                                                                                587 AA;
                                                                N-PSDB; AAQ20266
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                                                                                                                                                  or high temp.
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      Mackay VL;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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RESULT 13

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New isolated plant copper transporter genes, useful for modulating e.g. germination, sex determination, flower or leaf senescence, fruit ripening, pathogen resistance or response to stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of the Arabidopsis thaliana RANI mutein rani-2. The mutein has an amino acid substitution of Glu for Gly173 of the wild-type protein (see AAY5867). RANI is a copper transporter and early-acting regulator of the chiylene gas signalling pathway. The rani-2 protein accumulates to the same level as RANI but has reduced copper transporting activity. The invention relates to the RANI gene and to antegonist responsive mutants controlling copper transport in the plant. It also relates
to antagonist responsive mutants controlling copper transport in probability of RANI and its protein product to madulate the manipulation of RANI and its protein product to modulate the ethylene response in plants, thereby permitting the regulation and controlled alteration of plant growth and developmental processes, including germination, ripening, insect, herbicide and pathogen resistance, and response to stress (claimed).

The present sequence is not shown in the specification but is derived from the Arabidopsis RANI gene sequence given in figure 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.9%; Score 6; DB 21; Length 1001; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copper transporter; ranl-2; responsive-to-antagonistl; ethylene signalling pathway, AfPase; copper transport; transgenic plant; mutant; mutain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "replaces wild-type Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY58718 standard; Protein; 1001 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis ranl-2 mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecker JR, Hirayama T, Kieber JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 31; Page -; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US16591.
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                                                                                                                                                                                                                                                                                                                                                                                                             1001 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ58168
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193 dagfeg 198
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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XX AAYS8718

XX AAYS

XX AAYS

XX AAYS

XX AAYS

XX ACDP

XX COPP

XX ACDP

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CC to the manipulation of RAN1 and its protein product to modulate the replace of explainer response in plants, thereby permitting the regulation and controlled alteration of plant growth and developmental processes.

CC controlled alteration, cell elongation, flower and leaf senescence, abosission, fruit ripening, insect, herbicide and pathogen

CC resistance, and response to stress (claimed).

CC resistance, and response to stress (claimed).

CC resistance and response to stress (claimed).

CC resistance and response to stress (claimed).

CC resistance and response to stress (claimed).

CC resistance and response to stress (claimed).

CC resistance and response to stress (claimed).

CC resistance and response to stress (claimed).

XX SQ sequence 1001 AA;

COLETY Match

Best Local Similarity 100.0%; Pred. No. 1.80+02; Length 1001;

Best Local Similarity 100.0%; Pred. No. 1.80+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COLETY Match 193 dagfeg 198

Search completed: January 31, 2002, 13:18:11
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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using sw model OM protein - protein search, Search time 78.64 Seconds (without alignments) 13.561 Million cell updates/sec January 31, 2002, 13:20:15; Run on:

US-08-957-709-77 14

1 AHRIDPGWSGCIVL Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

0 Word size :

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote probable transcrip cell fusion protei hypothetical prote flak protein - vib hypothetical prote notch protean homo translation initia hypothetical prote ferredoxin precurs hypothetical prote hypothetical prote hypothetical prote hypothetical alvek hemoglobin alpha-T calcium-binding pr Jag-related prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote dCTP deaminase (EC 2'-deoxycytidine 5 dCTP deaminase (EC dCTP deaminase (EC probable membrane Description SUMMARIES A42940 C85833 C85833 C84942 C84942 C84942 C84942 C84942 C84942 C84942 C84942 C84942 C84942 C84942 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C849443 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C849443 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C84943 C849443 C84943 E75544 T35766 T47962 E85806 S76965 T46836 H75504 % Query Match Length DB 141 300 340 407 488 733 980 2555 78 83 Score Result Š

RESULT 2
C85833
2'-deoxyytidine 5'-triphosphate deaminase [imported] - Escherichia coli (strain O157
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: C85833
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

hypothetical prote probable DNA glyco hypothetical prote phenylacetaldehyde hypothetical prote probable transposa translation elonga hypothetical prote probable aldo-keto hypothetical prote probable transposo probable transposo	probable ribosomal probable membrane hypothetical prote hypothetical prote hypothetical prote
G72406 G70865 F84902 B82645 H64018 B85787 C70643 F39901 D836493	T34943 E71095 T41002 164240 D82987
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258 279 279 2294 2299 3306 313	314 320 321 323 323
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0.42843940 0.42843940	44444 114843

## ALIGNMENTS

RESULT 1  Add 2940  GOTP deaminase (EC 3.5.4.13) dcd [validated] - Escherichia coli  Add 2940  GOTP deaminase (EC 3.5.4.13) dcd [validated] - Escherichia coli  Add 2940  GOTP deaminase (EC 3.5.4.13) dcd [validated] - Escherichia coli  GOTP deaminase (EC 3.5.4.13) dcd [validated] - Escherichia coli  G. Accession: Add 2040; H64372  E. Mactariol. 174. 5647-5637, 1923  A. Reference number: Add 2940; MUID: 92380341  A. Reference conders: Add 2940; MUID: 92380341  A. Reference conders: Add 2940; MUID: 92380341  A. Reference conders: Add 2940; MUID: 92380341  A. Status: preliminary  A. Accession: Add 2940  A. Rose, D. J.; Mau, B.; Shao, Y.  A. Rose, D. J.; Mau, B.; Shao, Y.  A. Rose, D. J.; Mau, B.; Shao, Y.  A. A. Reference conders: Gother acid sequence of Escherichia coli K-12.  A. Reference number: Add 720; MUID: 97426617  A. Reference number: Add 720; MUID: 97426617  A. Residues: 1143 - 4847  A. Residues: 1143 - 4847  A. Residues: 1143 - 4847  A. Reference number: Add 720; MUID: 97426617  A. Reference number: Add 720; MUI
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Length 206;

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A;Gene: dcd; BU108
C;Keywords: hydrolase
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A64050
dCTP deaminase (EC 3.5.4.13) HI0133 [similarity] - Haemophilus influenzae (strain Rd KWZ
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Fuhrmann, J.L.; Geoglagen, N.S.M.
C, M.; Erandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoglagen, N.S.M.
A;Reference number: A64000; MUID:95350630
A;Accession: A64000; MUID:95350630
A;Accession: A64000
A;Accessio
lller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A.Reference number: A85480; MUID:21074935; PMID:11206551
A.Accession: C85833
A.Accession: C85833
A.Accession: C85833
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-193 < STO>
A.Residues: 1-193 < STO>
A.Residues: 1-193 < STO>
A.Residues: 1-193 < STO>
A.Residues: 1-194 < STO>
A.Residues: 1-194 < STO>
A.Residues: 1-194 < STO>
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A.Residues: 1-194 < STO-104 < STO-
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GM442

M.Alternate names: deoxycytidine triphosphate deaminase
G.Specias: Buchnera sp. (strain APS)
N.Alternate names: deoxycytidine triphosphate deaminase
G.Specias: Buchnera sp.
G.Specias: Buchnera sp.
G.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
G.Accession: C84942
R.Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A.Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A.Recession: C84942
A.Accession: C84942
A.Steus: pre-liminary
A.Accession: C84942
A.Steus: pre-liminary
A.Fesidues: 1-206 CSTO>
A.Accessive control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a control of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 100.0%; Score 14; DB 2; L Similarity 100.0%; Pred. No. 1.5e-09; 4; Conservative 0; Mismatches 0;
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Matches 14;
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RESULT 6
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Hobbable transcription regulator PA2076 [imported] - Pseudomonas aeruginosa (strain P C; Species: Pseudomonas aeruginosa aeruginosa (strain P C; Species: Pseudomonas aeruginosa (strain P C; Species: Pseudomonas aeruginosa aeruginosa (strain P C; Species: Pseudomonas aeruginosa (strain P C; Species: Pseudomonas aeruginosa 31-Dec-2000 (states) (strain P C; Stover, C. K.; Pham, X. Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
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Nature 406, 959-964, 
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C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C;Date: 13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C;Date: 13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C;Date: 13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C;Date: 13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C;Date: 13-Peb-1998 #sequence 78. July # M. S.; Tuthgraphers, S.; Tuthgraphers, S.; Tuthgraphers, S.; Tuthgraphers, S.; Pujii, C.; Cotton, M.D.; Horst, K.; Roberts, R.; Hatch, B. Naturbors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrella burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Ressidues: 1-141 < KLE>
A;Residues: 1-141 < KLE>
A;Resperimental source: strain B31
C;Superfamily: Borrella burgdorferi hypothetical protein BB0085
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Ouery Match 57.1%; Score 8; DB 2; I Best Local Similarity 100.0%, Pred. No. 0.019; Matches 8; Conservative 0; Mismatches (
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Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches
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58 SGCIVL 63
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R;Stewart, B.J.; McCarter, L.L.
Mol. Microbiol. 20, 137-149, 1996
A;Title: Vibrio parahaemolyticus FlaJ, a homologue of FliS, is required for productio
A;Reference number: S71027; MUID:97014377
A;Accession: S71029
                                                                                                                                                                                                                                                                                      C;Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo F;137-358/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S56277
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces A;Reference number: S56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D50617; NID:g836685; PID:d1009902; PID:g836777; MIPS:YFR022w
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A;Molecule type: DNA
A;Residues: 1-980 cMIL>
A;Cross-references: EMBL:Z68317; PIDN:CAA92690.2; GSPDB:GN00020; CESP:T01H3.2
                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-488 «STES-
A;Cross-references: EMBL:U12816; NID:g6806922; PIDN:AAC27806.1; PID:g1254206
A;Experimental source: strain BB22
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C;Species: Caenorhabditis elegans
C;Species: La-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T24336
R;Burton, J
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19876
A;Reference number: Z19876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable membrane protein YFR022w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 15-Sep-2000
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C;Keywords: transmembrane protein
F;382-398/Domain: transmembrane #status predicted <TMM>
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100.0%; Pred. No. 12;
tive 0; Mismatches
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. 8.7;
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100.0%; Pred. No. 8.7
Live 0; Mismatches
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Best Local Similarity 100...
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Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-733 <MUR>
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43 SGCIVL 48
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K.; Apodaca,
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E,Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pypothetical protein 21487 [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: D85643
R;Perna, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: perliminary
                                                                                                 cell fusion protein precursor - human herpesvirus 3
C;Species: human herpesvirus 3, varicella-zoster virus
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C;Accession: E27212
R;Davison, A.J.; Scott, J.E.
J;Gen. Virol. 67, 7759-1816, 1986
A;Fitle: The complete DNA sequence of varicella-zoster virus.
A;Reference number: A27345; MUID:86306657
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C;Species: Vibrio parahaemolyticus
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S71029
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                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-340 <DAV>
A;Cross references: EMBL:X04370; NID:g59989; PIDN:CAA27888.1; PID:g59994
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <CFP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: herpesvirus cell fusion protein
C;Superfamily: herpesvirus cell fusion protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-340/Product: cell fusion protein #status predicted
F;115-137/Domain: transmembrane #status predicted <TM1>
F;220-238/Domain: transmembrane #status predicted <TM1>
F;251-269/Domain: transmembrane #status predicted <TM4>
F;307-322/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 6; DB 1;
100.0%; Pred. No. 6.6;
tive 0; Mismatches
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100.0%; Pred. No. 7.5
tive 0; Mismatches
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Matches 6; Conserv
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A; Residues: 1-407 <STO>
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RESULT **S71029** 

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ferredoxin precursor - Psalteriomonas lanterna
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T35979
R;Seeger, W. T.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, January 1999
A;Reference number: 221551
A;Reference number: 221551
A;Reference number: 221551
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A; Accession: S01562
A; Molecule type: DNA
A; Residues: 1-78 <FUK>
A; Residues: 1-78 <FUK>
C; Genetics: EMBL: X04465; NID: g11640; PIDN: CAA28120.1; PID: g11709
C; Genetics: A; Gene: infa
A; Gene: infa
A; Genome: chloroplast
C; Superfamily: translation initiation factor IF-1
C; Keywords: chloroplast; protein biosynthesis
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches
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31 AHRID 35
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A40043

notch protein homolog TAN-1 precursor - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Accession: A40043
R; Ellisen, L.W., Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, Cell 166, 649-661, 1991
A; Fillie: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal A; Recession: A40043; MuID:91347367
A; Recession: A40043; MuID:91347367
A; Residues: Press. Preliminary; nucleic acid sequence not shown; not compared with conceptual tra A; Molecule type: MRNA
A; Residues: 1-2555 cELL>
A; Cross-references: GB:M7380
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology cEGF>
F; 494-525/Domain: EGF homology cEGF>
F; 149-1180/Domain: EGF homology cEGF>
F; 1187-1218/Domain: ankyrin repeat homology cAN3>
F; 1207-1259/Domain: ankyrin repeat homology cAN3>
F; 1207-2056/Domain: ankyrin repeat homology cAN3>
F; 2027-2059/Domain: ankyrin repeat homology cAN3>
F; 2027-2056/Domain: ankyrin repeat homology cAN3>
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A05008
translation initiation factor IF-1 - liverwort (Marchantia polymorpha) chloroplast
C;Species: chloroplast Marchantia polymorpha
C;Species: a0-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C;Accession: A05008; S01562
S;Ohyama, K.
Submitted to the EMBL Data Library, October 1986
A;Reference number: A00150
A;Reference number: A00150
A;Reference number: A00150
A;Reference number: A00108
A;Molecule type: DNA
A;Residues: L'78 COHYA
A;Residues: R'78              A:Introns: 25/1; 83/3; 242/1; 314/3; 357/3; 399/3; 437/3; 487/2; 561/3; 603/3; 636/3; C:Superfamily: Caenorhabditis elegans hypothetical protein T01H3.2
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Search completed: January 31, 2002, 13:20:16 Job time: 117 sec

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Holt G., Nelborner M., Henderson S.N.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxten B.P., Bhandari D., Bolshakov S.,
RA Abril J.F., Busam D.A., Bernan B.P., Bhandari D., Bolshakov S.,
RA Becson K.Y. Benos P.V., Bernan B.P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Gabriella N., Ralush R.A., Helman T.J., Hernandez J.R., Houck J.,
RA Fosler C., Gabriellan A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Fosler C., Gabriellan A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Houck J.
RA Hostin D., Houston K.A., Helman T.J., Mei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Helman T.J., Mei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Helman T.J., Mei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Q9VBC3
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Q22088 caenorhabdi
Q9r172 rattus norv
Q9zbi2 streptomyce
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Ogi239 pseudomonas
Ogkxb5 escherichia
Ogxil2 bacteriopha
O56708 vibrio para
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09h935 homo sapien
09rph3 burkholderi
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Q9mca0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                       473505 seqs, 146272329 residues
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sp_fungi:*
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Q9asi3 oryza sativ Q9cxz2 mus musculu Q9cvp6 mus musculu Q9ta01 lampetra f1 Q9rxri deinococus O69066 oseudomonas	Q95212 streptomyce Q95212 streptomyce Q96369 mus musculu Q96369 homo sapten Q63404 rattus norv Q88461 stealth vir Q95502 orvza sativ	088116 rhodobacter 09ji13 rattus norv 09ji05 mus musculu 09jhk0 mus musculu P74757 synechocyst 065234 african swi	V97449 cautobacter Q9a8k0 cautobacter Q9ln66 arabidopsis Q53138 rhodococcus Q9rww5 deinococcus Q9wy34 thermotoga
10 Q9ASI3 11 Q9CXZ2 11 Q9CVP6 8 Q9TA01 2 Q9RXR1 2 O69066	2 095212 10 09M368 11 09D559 4 09ULQ9 11 063404 12 088461 10 09FSN2	О щ (	2 Q9NRW5 2 Q9ARKU 10 Q9LN66 2 Q53138 2 Q9WY34 2 Q9WY34
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## ALIGNMENTS

Eukaryota; Metazoa; Arthropoda; Trācheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[1] SEQUENCE FROM N.A.

Drosophila melanogaster (Fruit fly).

Last sequence update) Last annotation update)

01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, CG14244 PROTEIN.

Created)

81 AA.

PRT;

PRELIMINARY;

Q9VBC3

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RESULT 4
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AC 09KXB5;
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DT 01-0CT-:
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P.,
Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
Shue B.C., Siden Kiamos I., Simpson M., Strong R., Smith T.,
A Shirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
X. Jeng X.H., Zaveri J.S., Zhan X., Zhang G., Zhao Q., Zhang X.,
A Short S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Short S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Jeng X.H., Zaveri J.S., Zhan X., Zhang G., Zhao Q., Zhang X.,
A Glubs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The Genome sequence of Drosophila melanogaster.";
B. EMBL: AEO03757; AAF56691;
B. EMBL: AEO03757; AF56691;
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Haemonchus contortus.
Haemonchus contortus.
Bikaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae, Haemonchus.
NCHI_TaxID-6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

GREDINE-20183859; PubMed-10717307;

Greenhalph C.J., Loukas A., Donald D., Nikolaou S., Newton S.E.;

A. family of galectins from haemonchus contortus.";

Mol. Biochem. Parasitol. 107:117-121(2000).

EMBL, AF105967; AAF63404.1;

InterPro. IFR001079; Gal-bind_lectin.

Pfam; PF00337; Gal-bind_lectin.

PROSTIE: PS00337; Gal-bind_lectin.

PROSTIE: PS003309; Gal-APTIN; 2.

SEQUENCE 291 AA; 33094 MW; DEAF6FF1808BF8BC CRC64;
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9185 MW; AF1E54DECDEC8CE1 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 17, Last annotation update)
GALECTIN.
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091239; 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR.
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Stover C.K., Pham X. O'T., Furin A.L., Mizoguchi S.D., Warrener P., R. Hickey M. J., Brithmam F.S. L., Hidragle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; T. Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."

In Nature 406.959-964 (2000).

REMBL, ABOO4635, AAG05464.1; -

- SIMLARIYTY TO THE LYSR FAMILX OF TRANSCRIPTIONAL REGULATORS.

REMBL, ABOO4635, AAG05464.1; -

REMBL, SROOMS9, HTHLLYSR.

PRINTS, PROROUS9, HTHLLYSR.

PRINTS, PROROUS9, HTHLYSR.

PROSTUES, SOGO044, HTHLLYSR.

PROMPTE, PROCHEOMS DNA-binding Transcription regulation.

SEQUENCE 300 AA, 32458 MW; 21A99BFBF848BEGC CRC64;
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EMBL, APO0422: BAA94169.1;

EMBL, APO04422: BAA94169.1;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBL_TaxID-83334;
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Pseudomonas aerúginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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SEQUENCE 422 AA; 45496 MW; 146BB1299BE985B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          097XB5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 45.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.9%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches
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100.0%; Pred. No. 17;
:ive 0; Mismatches
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MEDLINE=20198780; PubMed=10734605;
                                                                                                                                                                                       STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
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Best Local Similarity 100.
Matches 6; Conservative
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                                                               Pseudomonas.
NCBI_TaxID=287;
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RESULT 09XJL2

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MEDLINE-21173698; PubMed=11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
                           Vibrio parahaemolyticus, ";
J. Bacteriol. 177:155-1609(1995).
-!- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
McCarter L.L.; "Genetic and molecular characterization of the polar flagellum of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                      PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
PROSITE; PS50045; SIGMA54_INTERACT_4; 1.
ATP-binding; DNA-binding; Flagella; Transcription regulation.
SEQUENCE 488 AA; 54330 MW; 25D560C091A4A028 CRC64;
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SEQUENCE 889 AA; 95775 MW; 75FCBD7A726A01A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TONB-DEFENDENT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL: AE005717; AAX22433.1; -.
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100.0%; Pred. No. 31;
ive 0; Mismatches
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100.0%; Pred. No. 19;
Live 0; Mismatches
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                                                                                                        EMBL; AF069392; AAC27806.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR002197; HTH_Fis.
InterPro; IPR002078; Si954_interact.
Pfam; PF00158; Sigma54; 1.
SMART; SM00382; AAA; 1.
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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441 DPGWSG 446
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48 WSGCIV 53
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Q22088;
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MEDLINE-99419919; Pubmed-10492170;
Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES-Phage 933W;
MEDLINE-99173898; PubMed=10074068;
MEDLINE-99173898; PubMed = 1.07. Blattner F.R.;
Sequence of Shiga toxin 2 phage 933W from Escherichia coli 0157:H7:
Shiga toxin as a phage late-gene product.";
J. Bacteriol. 181:1767-1778(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsushiro A.;
"Sequence analysis of Stx2-Converting phage VT2-Sa shows a great
"Sequence analysis of Stx2-Converting phage VT2-Sa shows a great
dyvergence in early regulation and replication regions.";
DNA Res. 6:235-240(1999).
EMBL; AF125520; AAD25468.1;
EMBL; AP000363; BAA84345.1;
                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA phages.
NCBL_TaxID=10730, 97081;
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SPECIES-Phage 933W;
Plunkett G. III;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 422 AA; 45496 MW; 146BB1299BE985B0 CRC64;
                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 45.5 KDA PROTEIN.
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Last annotation update)
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100.0%; Pred. No. 17;
ative 0; Mismatches
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                                                                          PRELIMINARY;
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                                                                                                                                                                                                          Bacterlophage 933W, and
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SPECIES-Phage VT2-Sa;
                                                                                                                                                                                                                          Bacteriophage VT2-Sa.
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Best Local Similarity
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01-JUN-2001
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Q56708;
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SEQUENCE FROM N.A.

SETALINE-37(2):

MEDLINE-97000351; PubMed=8843436;

Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

Rinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL035161; CAA22740.1;

Hypothetical protein.

NON_TER B3

SEQUENCE 83 AA; 9361 MW; F13F85AEB0A19DE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC9C7.28.
Streptomyces coelicolor.
Bacteria; Firmicoutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
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Busaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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                                                                                                                                    DB 11; Length 2319;
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       Indels
   EGF-like domain; Glycoprotein; Hydroxylation.
SEQUENCE 2319 AA; 244298 MW; 243ECA02D7C3283D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2);
Seeger K.J., Harris D.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q92B12, PRELIMINARY; PRT; 83 AA. 092B12, 00.2B12, 01.AMX-1999 (TrEMBLrel. 10, Created) 01.AMX-1999 (TrEMBLrel. 10, Last sequence update) 01.AMX-1999 (TrEMBLrel. 10, Last annotation update) HYPOTHER TOTAL 9.4 KDA PROTEIN (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
5730493B19RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.7%; Score 5; DB 2; Best Local Similarity 100.0%; Pred. No. 68; Matches 5; Conservative 0; Mismatches
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                                                                                                                                    Query Match
42.9%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches
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723 DPGWSG 728
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31 AHRID 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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Q9CYF9
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09R172;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
NOTOH 3 PROTEIN
Rattus norvegicus (Rat)
Rattus norvegicus (Rat)
Rattus Lutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C.elegans: A platform for investigating biology."; science 282:2012-2018(1998). EMBL; Z68317; CAR92690.2; -. SEQUENCE 980 AA; 111805 MW; BB69ACEAAD78D69C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A. Haritunians T., Boulter J., Weinmaster G., Schanen N.C.; Rattus norvegicus mRNA for Notch 3 "; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AFI648618, AAD46653.2; -- HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                           Burton J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0101H3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
42.9%; Score 6; DB 5;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches
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Interpro: IPR00110; Asx_hydroxyl.
Interpro: IPR000551; BGF-11ke.
Interpro: IPR001881; EGF_2.
Interpro: IPR001881; EGF_Ca.
Interpro: IPR001488; EGF_II.
Interpro: IPR001498; IRR014088; IRR014088; IRR014089; IRR014089; IRR014089; IRR0140890; IRV014089; IRV0140890; IRV014
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MEDLINE-99069613; Pubmed-9851916;
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Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, BAC CLONE: T21E2.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryopta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudlcotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus. NCBL_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 5:55-76(1998).
EMBL. AP000002; BAA29651.1; -
HYPOTHETICAL protein; Complete proteome,
SEQUENCE 128 AA; 14457 MW; A17BEA3BB59FFEDF CRC64;
                                                                                                                                                                      01-AGG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) HYPOTHETICAL 14.5 KDA PROTEIN PH0562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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0; Mismatches
                                                                                                                                                         07, Created)
                                                                                                                        PRT;
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DNA Res. 7:217-221(2000).
EMBL; AP002061; BAB02644.1;
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Matches 5; Conservative
                                                                                                                        PRELIMINARY;
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                                                                                                                                                         01-AUG-1998 (TrEMBLrel.
                                                                                                                                                                                                                                               Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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PubMed-10907853;
10 GCIVL 14
                               8 GCIVL 12
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Q9LH77
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                                                                                    RESULT
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STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J.D., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Last annotation update)
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100.0%; Pred. No. 86;
live 0; Mismatches
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100.0%; Pred. No. 87;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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              STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
EMBL, AK017723; BAB30895.1; -.
MGD; MGI:1917880; 5730493B19R1k.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
EMBL; AE004155; AAF93853.1;
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Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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VC0688

Q9KU41

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RESULT 12
098K41
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AC 098K41
DT 01-0CT
DT 01-0CT
DT 01-0CT
DE HYPOTH
DE YOUGH
ON VCO688
OS VLDF10
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RN | I]
RP SEQUEN
RX STEALN
RA Heidel
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136 AA; 15692 MW; 61916EF1FF6E3316 CRC64;

SEQUENCE

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SEQUENCE FROM N.A.

STRAIN-NIPPOWBARE; TISSUE-GREEN SHOOT;

Stahl U., Lee M., Sjoedahl A., Acher D., Cellini F., Ek B.,

Iannacone R., MacKenzle D.A., Semeraro L., Tramontano E., Stymne S.;

Iannacone R., MacKenzle D.A., Semeraro L., Tramontano E., Stymne S.;

"Plant low molecular weight phospholipose A2s (PLA2s) are structurally related to the animal secretory PLA2s and are present as a family of submitted (ARF-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ238116; CA840841.1; -.

HSSP; P14418; 1BK9.

InterPro; IPR001211; PLP_A2.

PROSITE; PS00118; PA2_HIS; 1.

Signal; Hydrolase.
                                                                                                                                    Gaps
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OINOV-1999 (TIEMBLIEL 12, Created)
OINOV-1999 (TIEMBLIEL 12, Last sequence update)
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
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OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
OINOV-1999 (TIEMBLIEL 17, Last sequence 3.1.1.4).
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Ouery Match 35.7%; Score 5; DB 10; Length 136; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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52 GWSGC 56
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89 AHRID 93
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Search completed: January 31, 2002, 13:37:47 Job time: 172 sec

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Sequence 17, Appl
Sequence 20, Appl
Sequence 1, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 10, Appli
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-185-432-17

US-08-185-432-17

US-08-18-20

US-08-400-208B-1

US-08-400-208B-1

US-08-479-939-9

US-08-483-432-9

US-08-959-212-10

US-08-997-362-55

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Sequence 75, Appl Sequence 75, Appl Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 24, Appl Sequence 18, Appl Sequence 72, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli	olated PEF Proteins, ifying Same	4; 0; Gaps 0;
273 3 US-08-873-970-75 274 US-09-095-855-75 284 1 US-09-095-855-75 284 3 US-08-411-777-10 284 3 US-09-057-088-10 285 3 US-08-651-136C-20 294 3 US-08-651-136C-24 298 3 US-08-651-136C-4 298 3 US-08-651-136C-4 305-08-651-136C-4 305-08-651-136C-4 305-08-651-136C-4 305-08-651-136C-4 305-08-08-09-013-2 305-1 US-08-081-328-2 305-1 US-08-081-328-2 305-1 US-08-081-328-2 305-1 US-08-233-64A-2 305-2 US-08-33-64A-2 305-2 US-08-33-64A-2 305-2 US-08-33-64A-2 305-2 US-08-33-64A-2 305-2 US-08-340-1 305-2 US-08-340-1	ALIGNMENTS  lication US/08822774  TION: GGREFE, Holly SWTION: Extracts, PEF Protein Complexes, Isolated NWTION: Extracts, N.W. Sulte 700  SATION DATA: ISOLOGO STREET, N.W. Sulte 700  Indication Per Protein Pe	00.0%; Score 14; DB 4; Length 1 00.0%; Pred. No. 1.1e-09; ve. 0; Mismatches 0; Indels
28 330 331 331 331 331 331 331 331 331 331	1	Query Match Best Local Similarity 1 Matches 14; Conservati 1 AHRIDPGWSGCIVL 14
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APPLICANT: Arravanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STRATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                      CORRELATION DATA:
COMPALIANT GYSTEM: PC-DOS/MS-DOS
CSOFTWARE: Patentin Release #1.0, Version #1.25
CSOFTWARE: Patentin Release #1.0, Version #1.25
CSOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-UN-1993
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 7326-015
REGISTRATION NUMBER: 7326-015
TELEPHONE: 212 790-9909
TELEPHONE: 212 790-9909
TELEPHONE: 212 780-8909
TELECTH: 2556 anino acids
TYPE: amino acid
STRANDBNESS: aliqle
TYPE: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: Unknown
TOPOLOGY: Unknown
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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GENERAL INCOMATION:

APPLICANT: Busseau, Isabelle
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Musseau, Isabelle
APPLICANT: Musseau, Isabelle
APPLICANT: Musseau, Muspert J.
APPLICANT: Musseau, Musper Berner, Muspe
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TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                           ; Sequence 17, Application US/08185432
; Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
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; MOLECULE TYPE: protein
US-08-185-432-17
     1 AHRIDPGWSGCIVL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-08-083-590A-20
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Gaps

Length 2556; 0; Indels

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ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor CITY: New York
                    ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 32;
                                                                                                             ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION NOMBER: US/05/301/520
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: DCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INPORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0298
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 5; D
Pred. No.
                                                                                New York : United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.7%; Scc...
100.0%; Pre
0; 7
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; Patent No. 5686593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 amino acids
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWSGC 11
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                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-479-939-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Artificial Sequence:oligopeptide; OTHER INFORMATION: useful in immunogenic compositions
US-09-400-208B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences, TITLE OF INVENTION: Compositions and Diagnostic Methods FILE REFERENCE: 77-96B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Brzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
                                                                                                                                                                                                                                       Length 2556;
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/400,208B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 08/951,984
PRIOR FILING DATE: 1997-10-15
PRIOR PELING DATE: 1997-10-16
PRIOR FILING DATE: 1996-10-16
PRIOR APPLICATION NUMBER: US 60/028,482
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09400208B Patent No. 6271011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08361920
Patent No. 5457046
GENERAL INFORMATION:
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                       Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                               ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Henk, Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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742 DPGWSG 747
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16 RIDPG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-400-208B-1
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US-08-361-920-9
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LENGTH: 20
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RESULT 9
US-00-959-212-10
Sequence 10, Application US/08959212
Fatent No. 6060274
GENERAL INFORMATION:
APPLICANT: Blornvad, Mads
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Brensenen, Per
ITILE OF INVENTION: Extracellular Expression Of Cellulose
ITILE OF INVENTION: Binding Domains (CBD) Using Bacillus
FILE REFERENCE: 4987-200-US
CURRENT APPLICATION NUMBER: US/08/959,212
CURRENT FILING DATE: 1996-10-28
EARLIER APPLICATION NUMBER: 1192/96
EARLIER APPLICATION NUMBER: 1426/96
EARLIER FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRACESQ for Windows Version 3.0
FENDING THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM FOR THE PROBLEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 18; Matches 5; Conservative 0; Mismatches
                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE: 05-OCT-1992
APPLICATION NUMBER: US 07/340,860
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 09-MAY-1990
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 09-MAY-1991
APPLICATION NUMBER: DCT/DK91/00124
FILING DATE: 08-MAY-1991
APPLICATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELEPHONE: 212-867-029
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
TUBENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Humicola insolens
; STRAIN: DSM 1800
US-08-483-432-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 32 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDENNES: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHERICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Humicola insolens US-08-959-212-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 GWSGC 11
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| 8 GWSGC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,939
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/361,920
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1991
PRIOR APPLICATION NUMBER: DK 1158/90
FILING DATE: 109-MAY-1991
ATTORNEY/AGENT INFORMATION:
FILING DAME: LAMBILIS, Ellas J.
APPLICATION NUMBER: 33/728
FILING DAME: 100-MAY-1991
ATTORNEY/AGENT INFORMATION:
FILING DAME: 13-867-0123
TELEDAMONE: 212-867-0123
TELEDAMONE: 212-867-0129
TELEDAMONE: 212-867-0129
TELEDAMONE: 212-867-0129
TELEDAMONE: 212-867-0129
TELEDAMONE: 110-02-016
SEQUENTY: 32 amino acid
STRANDEDNESS: single
TOPOLOGY: 110-02-01
ORIGINAL SOUNCE:
ORGANISM: Humicola insolens
STRAIN: BWA 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 18; Matches 5; Conservative 0; Mismatches
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APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Visser, Elizabeth
APPLICANT: Scott, Linda
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
  TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                                                                                                                                                              FILLING CALE.
CLASSITION CALE.
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                                                             ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/08873970 Patent No. 6001361 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-997-362-55
                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Best Local Similarity
Matches 5; Conserv
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                                                                                   STREET: 2601 E
                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-873-970-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                        APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Scott, Linda
Prestidge, Ross
VENTION: COMPOUNDS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                             Sequence 55, Application US/08997080 Patent No. 5968524 GENERAL INFORMATION:
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US-08-997-362-55
Sequence 55, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Hiyama, Jun
APPLICANT: Hiyama, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTR.
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: DOSPETIBLE
DOS
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Hiyama, Jun
Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7
Best Local Similarity 100
Matches 5; Conservative
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APPLICANT: Skinner,
APPLICANT: Scott, Li
APPLICANT: Prestidge
TITLE OF INVENTION:
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CLASSIFICATION:
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| 117 AHRID 121
               GWSGC 11
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US-08-997-080-55
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RESULT 14
US-08-705-347A-55
is Sequence 55, Application US/08705347A
is Sequence 55, Application US/08705347A
is General Invormation
is Applicant Tan, Paul
APPLICANT Tan, Paul
APPLICANT Wisser, Elizabeth
APPLICANT Scott, Linda
TITLE OF INVENTION: DIAGNOSIS OF WICOBACTERIAL INFECTIONS
INVERSE SEQUENCES: 55
INVERSE ADPRESSE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
INTER: WA
COUNTY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 145;
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STATE: "...
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/705,347A
FILIKH DATE: 28-AUG-1996
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: Sleath, Janet.
RESTERRENCE/DOCKET NUMBER: 11000.1002
REGISTRATION NUMBER: 37,007
REGISTRATION NUMBER: 37,007
REGISTRATION NUMBER: 37,007
REGISTRATION NUMBER: 11000.1002
TELEPHONE: 206.269.0565
INFORMATION CAPION INFORMATION:
TELEPHONE: 206.269.0565
INFORMATION CAPION OF SECUENCE CLASSIFICES:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.7%; Score 5; DB 4 Best Local Similarity 100.0%; Pred. No. 59; Matches 5; Conservative 0; Mismatches
                                                                11000.1002c3
   NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEPAX: 206-269-0565
                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AHRID S
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US-09-09-68-55
Sequence 55 Application US/09095855
Patent No. 6160093
Patent No. 6160093
Patent No. 6160093
Patent No. 6160093
Patent No. 6160093
Patent No. 6160093
PAPLICANT: Viner, Margot
APPLICANT: Viner, Margot
APPLICANT: Prestide, Rass
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
CORRESPONDENCE ADDRES: 206
CORRESPONDENCE ADDRES: 206
CORRESPONDENCE ADDRES: 206
CORRESPONDENCE ADDRES: 206
COUNTY: USA
STATE: WA
STATE: WA
STATE: WA
STATE: WA
COUNTY: USA
STATE: WA
STATE
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                 11000.1002C1
                                                                                                                                           FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-40G-1996
ATTORNEY/AGENT INFORMATION:
NAME: 31-8ath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1
TELEPHONE: 206-269-0565
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INPORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS: LENGTH: '145 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-873-970-55
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US-08-766-605-3

i Sequence 3, Application US/08766605

patent No. 576320

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HOLMAN APOPTOSIS-RELATED CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 317 Palo Alto
CONTRY: US
CONTRY: US
ZIP: 94304
COMPUTER: EASTEM COMPATIER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EASTEM Version 1.5
CURRENT APPLICATION DATA::
PRIOR APPLICATION DATA::
PRIOR APPLICATION DATA::
PRIOR APPLICATION DATA::
PILING DATE: Filed Herewith
PRIOR APPLICATION DATA::
PILING DATE:
FILING DATE:
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100.0%; Pred. No. 59;
tive 0; Mismatches
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APPLICALLAL.

ATTORNEY/AGENTE:
NAME: Billing, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0174 US
REPERBENCE/DOCKET NUMBER: PF-0174 US
TELEPHONE: 415-855-0555
IRECREALS: 415-845-4466
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
ITYPE: amino acid
STRANDEDNESS: Single
"ODD 1007 STRANDEDNESS: Single
"ODD 1007 STRANDEDNESS: Single
"ODD 1007 STRANDEDNESS: Single
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MOLECULE TYPE: peptide
MMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1213520
US-08-766-605-3
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Best Local Similarity 100.
Matches 5; Conservative
Best Local Similarity 100.
Matches 5; Conservative
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| 154 GCIVL 158
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Search completed: January 31, 2002, 13:15:14 Job time: 95 sec This Page Blank (uspto)

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secreted pro secreted pro secreted pro

Human

AAE01617 AAG03260 AAG03790 AAB34611 AAW51350

AAY29194 AAG23792

Human

Human protein sequ Mycobacterium vacc M. vaccae antigen Arabidopsis thalia

AAW35378 AAB95281 AAW60119 AAY14865 AAG23791 AAW60970 AAB63225

Streptococcus pneu Gene 44 human secr Human protein sequ

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C glutamicum prote
S cerevisiae apopt
Human protein kina
Human complementar
Pasteurella multoc
Carbohydrate bindi
Peptide encoded by
3-Deoxy-D-arbino-h
Taxus cuspidata RT
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Human secreted pro
C glutamicum prote
S cerevisiae apopt
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| SIDSZ/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                 January 31, 2002, 13:18:11;
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                                                                              - protein search, using sw model
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AAC90721
AAC70721
AAC96758
AAW18869
AAW18869
AAW18251
AAY99905
AAM00074
AAU02803
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length: 2000000000
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1 AHRIDPGWSGCIVL
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Match Length
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Maximum DB seq
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Amino acid sequence Human regulatory m Lung cancer associ Seq ID 92 from USS Seq ID 91 from USS Seq ID 91 from USS Seq ID 91 from USS Streptococcus pneu C glutamicum prote Corynebacterium gl Seq ID 93 from USS Seq ID 93 from USS Seq ID 93 from USS Seq ID 93 from USS Seq ID 93 from USS

AAW59197 AAW40086 AAW55085 AAG90786

AAB76739 AAW59199

AAB93461 AAY29189 AAW93948 AAB58403 AAW59198 AAW40087

Arabidopsis thalia Arabidopsis thalia Chimeric endogluca Chimeric endogluca

ALIGNMENTS

M. vaccae antigen Partial amino acid Humicola insolens

AAW40088 AAW60128 AAY14874 AAW57420

AAG07220 AAG61558 AAW04936

TD AAW72853 standard; Peptide; 14 AA.  XX  XX  XX  XX  XX  AAW72853;  XX  DT 01-MAR-1999 (first entry)  XX  DE Escherichia coli dCTP deaminase uridine-binding motif.  XX  Polymerase enhancing factor; PEF; dUTPase; PCR; amplification;  XX  WO9842860-A1.  XX  XX  XX  XX  XX  XX  XX  XX  XX	4 AA. se uridine-binding motif.
AAW72853; 01-MAR-1999 (first entry) Escherichia coli dCTP deaminas Polymerase enhancing factor; P sequencing; replication. Escherichia coli. W09842860-Al. 01-OCT-1998. 20-MAR-1998; 98WO-US05497. 24-OCT-1997; 97US-0957709. 21-MAR-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, HOGrefe H; WPI: 1998-542284/46.	se uridine-binding motif.
Ol-Mar-1999 (first entry) Escherichia coli dCTP deaminas Polymerase enhancing factor; P sequencing; replication. Escherichia coli. W09842860-Al. Ol-OCT-1998, 98WO-US05497. 24-OCT-1997; 97US-0957709. 21-Mar-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, HOGrefe H; WPI: 1998-542284/46.	se uridine-binding motif.
Escherichia coli dCTP deaminas Polymerase enhancing factor; P sequencing; replication.  Escherichia coli.  WO9842860-Al.  01-OCT-1998; 98WO-US05497.  24-OCT-1997; 97US-0957709.  21-MAR-1997; 97US-0822774.  (STRA-) STRATAGENE.  Hansen CJ, HOGrefe H;  WPI; 1998-542284/46.	se uridine-binding motif.
Polymerase enhancing factor; Psequencing; replication. Escherichia coli. WO9842860-Al. 01-OCT-1998. 20-MAR-1998; 98WO-US05497. 24-OCT-1997; 97US-0957709. 21-MAR-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, HOGrefe H; WPI: 1998-542284/46.	
Sequencing; replication.  Escherichia coli.  WO9842860-Al.  01-OCT-1998.  20-MAR-1998; 98WO-US05497.  24-OCT-1997; 97US-0957709.  21-MAR-1997; 97US-0822774.  (STRA-) STRATAGENE.  Hansen CJ, Hogrefe H;  WPI: 1998-542284/46.	PEF; dUTPase; PCR; amplification;
Escherichia coli. W09842860-Al. 01-OCT-1998. 20-MAR-1997; 97US-0957709. 24-OCT-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, HOGrefe H; WPI: 1998-542284/46.	•
WO9842860-Al. 01-OCT-1998. 20-MAR-1998; 98WO-US05497. 24-OCT-1997; 97US-0957709. 21-MAR-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, HOGrefe H; WPI: 1998-542284/46.	
01-OCT-1998.  20-MAR-1998; 98WO-US05497.  24-OCT-1997; 97US-0957709.  21-MAR-1997; 97US-0822774.  (STRA-) STRATAGENE.  Hansen CJ, HOGrefe H;  WPI; 1998-542284/46.	
20-MAR-1998; 98WO-US05497. 24-OCT-1997; 97US-0957709. 21-MAR-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, HOGTEFE H; WPI; 1998-542284/46.	
24-OCT-1997; 97US-0957709. 21-MAR-1997; 97US-0822774. (STRA-) STRATAGENE. Hansen CJ, Hogrefe H; WPI; 1998-542284/46.	
(STRA-) STRAIAGENE.  Hansen CJ, Hogrefe H;  WPI; 1998-542284/46.	
Hansen CJ, Hogrefe H; WPI; 1998-542284/46.	
WPI; 1998-542284/46.	
Polymeriase enhancing tactor proteins, extracts a improve the polymerisation activity of nucleic a use in amplification, sequencing and replication	Polymerase enhancing factor proteins, extracts and complexes - improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

us-08-957-709-77.rag

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This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX79002) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 35 novel genes and their fragments (nucleic acid sequences: AAX7901-X79064; amino acid sequences AAX14411-Y14464) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 53 polynucleotides, based on which tissues they are most highly expressed in (see AAX79011 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
  New isolated human genes and the secreted polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; SEQ ID NO: 6520; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                               42.9%; Score 6; DB 20; Length 53; 100.0%; Pred. No. 5.9; 0; Indels iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum protein fragment SEQ ID NO: 6520.
                                     Claim 11; Page 203; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG92766
ID AAG92766 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 6; Conservative
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N-PSDB; AAH67985.
                                                                                                                                                                                                                                                                                                                                                             53 AA;
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41 ridpgw 46
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schiothenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                          This is the uridine-binding motif of the dCTP deaminase of Eschericha coil. Sequences are provided (see AAW72849-57) of the uridine-binding motifs of dUTPases and dCTP deaminases of Pyrococcus furiosus (see AAW72847), Methanococcus jannaschii, Pyrococcus furiosus (see AAW72847), Methanococcus jannaschii, Bosulfurolobus ambivalens, Escherichia coil, yeast, human and herpesvirus; a consensus (see AAW72848) is also provided. A claimed method of enhancing a nucleic acid polymerase reaction comprises performing the reaction in the presence of one or more of the following: a polymerase enhancing factor (PEF), a dTPPase, a cfollowing: a polymerase enhancing factor (PEF), a dTPPase, a ctivity comprises one or more of sequences provided in AAW72848-57. A claimed protein having PEF activity comprises one or more of sequences given in AAW72848-57.

Kits are provided for replicating nucleic acids, for site-directed mutagenesis, for nucleic acid sequencing or for amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 14; DB 19; Length 14; 100.0%; Pred. No. 3.7e-09; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Duan R, Ebner R, Ferrie AM, Florence C;
KA, Greene JM, Olsen HS, Rosen CA, Ruben SM;
Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein encoded by gene 45 clone HCFBJ91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY14455 standard; Protein; 53 AA.
Claim 71; Page 47; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970S-0061463.
970S-0061527.
970S-0061529.
970S-0061532.
970S-0061536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
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N-PSDB; AAX79055.
                                                                                                                                                                                                                                                                                                                                         Sequence 14 AA;
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09-OCT-1997;
09-OCT-1997;
09-OCT-1997;
09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1998;
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Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY14455;
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Gaps

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Indels

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Length 733;

42.9%; Score 6; DB 22; 100.0%; Pred. No. 41; Pred. No. 41; 0; Mismatches

Conservative

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Matches

Best Local Similarity

Query Match

9 SGCIVL 14

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                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
            mutant of coryneform bactérium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases
                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast, fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration.
                                                                                                                                                                                                                              DB 22; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL; Nelissen BJW, Reekmans RJ;
                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S cerevisiae apoptosis associated protein YFL015C.
                                                                                                                                                                                                                           42.9%; Score 6; DB 22
100.0%; Pred. No. 19;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           AAG70721 standard; Protein; 733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2000; 2000WO-BE00077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                           Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                 256 AA;
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                                                                                                                                                                                                                                                                                                                   223 idpgws 228
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                                                                                                                                                                                                                                                                                       4 IDPGWS 9
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number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the S. cerevisiae

proteins of the invention.

733 AA;

Sequence

The present invention provides the protein and coding sequences of a

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Auto13501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides cor serine/threonine kinases and the polymeptides may be used in the provention, diagnosis and treatment of diseases associated with cancers (especially cancers of hematopoletic origin), cardiovascular cancers (especially cancers of hematopoletic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), inflammatory disorders (e.g. asthma), infectious parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. inflammatory disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used as for gene therapy and as DNA probes in diagnostic assays.

The protein kinase epolypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
                                                                                                                                                                                                                                            Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Pred. No. 47;
iive 0; Mismatches (
                                                                                                      AAU03556 standard; Protein; 884 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Figure 2; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-2000; 2000WO-US32085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0167482.
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                           Human protein kinase #56.
                                                                                                                                                                                                                                                                                                   reproductive disorder.
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Clary D;
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Best Local Similarity
Matches 6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-343950/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS06756
                                                                                                                                                                                                                                                                                                                                                                     WO200138503-A2.
24-NOV-1999;
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Flanagan P,
                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2001
                                                                                                                                         AAU03556;
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AAG96758

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The present sequence represents a Pasteurella multocida strain R1913 ManH neutraminidase immunogenic peptide. The present invention also describes: an immunogenic composition comprising a recombinant neuraminidase from P. multocida (shown in AAW48668) or the immunogenic peptides shown in AAW48869 to AAW48869. Or the immunogenic assay kit for the diagnosis and/or detection of P. multocida, comprising an antibody specific to P. multocida neuraminidase and antibody. The neuraminidase protein and immunogenic peptides can be used to immunise and protect animals, e.g. sheep, cattle, rabbits, dogs, cats, chickens, turkeys and humans against P. multocida diseases such as fowl cholera, shipping fever in cattle, respiratory tract infections, abscesses and systemic oligonucleotides derived from it, or the antibody can be used to diagnose P. multocida infections.
                                                                                                                                                                                                                                                                                                                  Pasteurella multocida neuraminidase - useful for protecting animals and humans from P. multocida infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellulose; CBD; hemicellulosic substrate;
Trichoderma reesei; cellulase; terminal A region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 35.7%; Score 5; DB 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0
                                                                                                                                                                                                       (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR15251 standard; Protein; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 26; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carbohydrate binding domain #8.
                                                                                                             97WO-US18668
                                                                                                                                                    96US-0028876,
96US-0028482,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO NORDISK A/S
      Pasteurella multocida.
                                                                                                                                                                                                                                                                                WPI; 1998-271747/24.
                                                                                                                                                                                                                                              Lee MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||
|7 ridpg 21
                                        WO9816649-A1
                                                                                                               15-OCT-1997;
                                                                                                                                               16-OCT-1996;
15-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RIDPG 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-1990;
                                                                           23-APR-1998.
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AAR15251
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella multocida strain R1913 NanH; neuraminidase; detection; diagnosis; fowl cholera; shipping fever; respiratory tract infection; abscess; systemic infection; immunoassay; immunogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
                                                                                                                                                                                                                                                                              Human; complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 10; 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella multocida neuraminidase immunogenic peptide.
                                                                                                                                                                                                                                         Human complementary peptide, SEQ ID NO: 2952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 5; DB 2
Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 466; 646pp; English.
                                                                                                                              AAG96758 standard; Peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW48869 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Sco
Similarity 100.0%; Pr
5; Conservative 0;
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                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts GW, Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEOM LTD.
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                     320 dpgwsg 325
5 DPGWSG 10
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                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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4 pgwsg 8
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                                                                                                                                                                                                     18-SEP-2001
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Best Local S
Matches 5
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AAW48869
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                                                                                                  This CBD is homologous to a terminal A region of Trichoderma reesei cellulases and effects binding of a protein to an insoluble cellulosic or hemicellulosic substrate. It is one of ten specific CBD's (see AAR15244-R15253) which correspond to the generic CBD formulae in AAR15242 and AAR15243. The CBD is incorporated into a fusion protein comprising a catalytic domain from a cellulase, e.g. a Bacillus endoglucanase, and optionally comprising a linking B domain from e.g. a fungal endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency virus (HIV) genetic vaccine involves obtaining a first nucleotide sequence from a HIV patient, redesigning and assembling it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing nucleotide sequence construct with optimized codons for human
                                           New fungal (hemi)cellulose degrading enzymes - for prodn. of lig. fuel gas and feed protein, have specified carbohydrate binding domain
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide encoded by Snut 1700Eagl DNA used in HIV DNA vaccine.
                                                                                                                                                                                                                                              DB 12; Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; human immunodeficiency virus; vaccine; AIDS; snut;
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 Hastrup S;
                                                                                                                                                                                                                                                   100.0%; Pred. ...
                                                                                                                                                                                                                                              Score 5;
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                                                                                                                                                                                                                                                                                                                                                                           AAY99905 standard; Peptide; 60 AA.
Hjort CM,
                                                                               Claim 20; Page 45; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 silent nucleotide substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; 104; 150pp; English.
                                                                                                                                                                                                                                              35.7%;
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                                                                                                                                                                                                                                                                    Conservative
Woldike HF, Hagen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-387778/33.
N-PSDB; AAA49074.
                       WPI; 1991-353766/48
                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                           32 AA;
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                                                                                                                                                                                                                                                                                          7 GWSGC 11
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09-APR-1999;
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                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                AAY99905;
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Matches
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The present invention relates to a nucleotide construct with optimised codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The construct uses codons from highly expressed mammalian proteins to code for each derivative of an early, primary HIV envelope gene. The first stage in the production of the construct was the cloning of an HIV

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envelope gene. A nucleotide sequence encoding this gene was then created using codous from highly expressed mammalian genes. The present sequence is the peptide encoded by one of the snuts (AAA49006-A49079) that were created by redesigning the nucleotide construct so that restriction enzyme sites surrounded functional regions of the sequence. The snuts were then assembled into pieces (AAA49080-A49092). Each derivative of the envelope gene (AAA49097-A49097) was then built using the pieces. The HV DNA vaccine may be used as a prophylactic vaccine and as a therapeutic vaccine in HIV infected patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel moss nucleic acid molecules encoding a carbohydrate metabolism related protein useful for modulating production of fine chemicals such as carbohydrates, cofactors and enzymes from microorganisms and plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to nucleic acid molecules AAH88708 - AAH88796 isolated from Physcomitrella patens (a moss), which encode carbohydrate metabolism related proteins (CMRP) represented in AAM00022 - AAM00110. Included in the invention is a vector containing the CMRP CDNA, and a host cell transformed with the vector. The host cell (a microorganism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium or Brevibacterium, moss or algae or a plant cell) is useful for producing a fine chemical such as carbohydrates, cofactors and/or enzymes. The nucleic acid molecules are suitable for modifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moss; carbohydrate metabolism related protein; CMRP; sugar; cofactor; fine chemical production; carbohydrate; polysaccharide.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-Deoxy-D-arbino-heptulosonate 7-phosphate synthase sequence #142.
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                                                                                                                                                                                                                                                                  Length 60;
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Reski |
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Schmidt R,
                                                                                                                                                                                                                                                         DB 2
81;
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100.0%; Pred. No. 81;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM00074 standard; Protein; 60 AA.
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Duwenig E,
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physcomitrella patens
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N-PSDB; AAH88760.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                           60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM00074;
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related Brevibacteium species and Acetobacter xylinum and Chlorella to make it a better or more efficient producer of one or more file chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs having altered activities which indirectly impact the production of one or more desired fine chemicals indirectly impact shalls705 - AAH80707 are used in the sequencing of the CMRP cDNA sequences of the invention.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid and amino acid sequences, isolated from the Taxus genus, useful for the synthetic production of Taxol and related taxolds, intermediates within the Taxol biosynthetic pathway, and other taxoid derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxygenase; Japanese yew; Taxol; taxoid; Taxol biosynthetic pathway; transgenic organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taxus cuspidata RT-PCR generated amplicon polypeptide #4.
                                                                                                                                                                          35.7%; Score 5; DB 22; Length 60;
100.0%; Pred. No. 81;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                              AAU02803 standard; Protein; 63 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 5; Conservative
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N-PSDB; AAS05148.
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Length 63;

DB 22; . 84;

Score 5; D Pred. No.

35.7%;

Query Match Best Local Similarity

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AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode. AAE01631-AAE01660 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene amount of the new protein in a sample or by determining the mount of the new genes. Specific uses are described for each of the
                                                                                                                                                                                                                                                                               Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; heamatopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy: neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; Alzheimer's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorfasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; majogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                   Human gene 22 encoded secreted protein HT4ES80, SEQ ID NO:167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Mature_human_secreted_protein
20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                      AAE01617 standard; Protein; 70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
/note= "Encoded
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30-JUN-2000; 2000US-0215137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2000; 2000WO-US30037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM, Komatsoulis GA,
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-316490/33.
N-PSDB; AAD05460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                       9 SGCIV 13
                                                            11||||
31 sqciv 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
. 5;
                                                                                                                                                                                                                    17-JUL-2001
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                                                                                                                                                                                      AAE01617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                         12
                                                                                                                                        AAE01617
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and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foctal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, alsergies, neurological disorders (e.g., Alzheimer's disease, canforders) alsergies, neurological disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin adjoin due to culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunossasy service requence represents a human secreted protein of the invention.
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70 AA; Sequence

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Gaps
                                   0;
           DB 22; Length 70;
                                   0; Indels
           35.7%; Score 5; DB 2
100.0%; Pred. No. 90;
Live 0; Mismatches
Query Match
Best Local Similarity 100.00
These 5; Conservative
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ð 용 RESULT 13 AAG03260

AAG03260 standard; Protein; 95 AA. 06-OCT-2000 (first entry) AAG03260; 

Human secreted protein, SEQ ID NO: 7341.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

Homo sapiens

EP1033401-A2

06-SEP-2000.

21-FEB-2000; 2000EP-0200610.

99US-0122487 26-FEB-1999;

GEST ) GENSET

Giordano J; Duclert A, Dumas Milne Edwards J,

WPI; 2000-500381/45 N-PSDB; AAC03266. New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

Claim 13; SEQ ID 7341; 71pp + CD-ROM; English.

The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30

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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' UTR is rarely included to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used to obtain full length cDNAs and genomic character an also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
               untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mappling procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic, forensic, gene therapy and chromosome mapping procedures
different tissues. EST sequences usually correspond mainly to the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                  35.7%; Score 5; DB 21; Length 95; llarity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; SEQ ID 7871; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein, SEQ ID NO: 7871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG03790 standard; Protein; 101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
N-PSDB; AAC03796.
                                                                                                                                                                                                                                                                                                    Local Similarity
nes 5; Conserv
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29 pgwsg 33
                                                                                                                                                                                                                                                                                                                                                                    PGWSG 10
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                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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The polynucleotide sequences given in AAG59738 to AAG59787 encode the human secreted proteins given in AAB4577 to AAB34686. AAB34627 to AAB34686 represent human secreted proteins plant polynucleotide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and calls the genes are expressed in Example of activities include: antiatriviti. Immunosuppressive; antirhenment.; antiproliferative; cardiant; vasotropic; cerebroprotective; noctropic; ophthalmological. The polynucleotides and proteins can be are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep: They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include cancers of the breast or liver, cardiovascular disorders.

Cerebrovascular disorders, andiogenesis, nervous system disorders.

Cerebrovascular disorders, andiogenesis, nervous system disorders.

The proteins can also be used to aid wound healing and epithelial cell
                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antishmatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; cancer; cardiovascular disorder; infection; cerebrovascular disorder; infection; cerebrovascular disorder; anglogenesis; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein sequence encoded by gene 35 SEQ ID NO:95.
                                                                                           ó,
                                                    Length 101;
                                                                                         Indels
                                                  35.7%; Score 5; DB 21; Lo
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM, Komatsoulis G;
                                                                                                                                                                                                                                                            AAB34611 standard; Protein; 102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 384; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0125360.
99US-0138626.
99US-0168662.
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                                                                                                                                                                                                                                                                                                                                    26-JAN-2001 (first entry)
                                Ouery Match
Best Local Similarity 100..
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N-PSDB; AAC59772.
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101
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                                                                                                                            6 PGWSG 10
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                                                                                                                                                  11111
82 pgwsg 86
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11-JUN-1999;
03-DEC-1999;
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                                                                                                                                                                                                                                                                                                 AAB34611;
Sequence
õ
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CC proliferation, to prevent skin aging due to sunburn, to maintain organs are before transplantetion, for supporting cell culture of primary tissues. CC to regenerate tissues and in chemotaxis. The proteins can also be used a food additive or preservative to increase or decrease storage or capabilities. AAC59729 to AAC59737 and AAB34576 represent sequences used cC in the exemplification of the present invention.

XX

SQ Sequence 102 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; [111]

DD 54 pgwsg 58
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Search completed: January 31, 2002, 13:18:12 Job time: 173 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:37:47 ; Search time 130.99 Seconds (without alignments) 15.633 Million cell updates/sec

Run on:

US-08-957-709-78 14 Title: Perfect score:

1 VGLIDSDYQGQLMI 14 Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

473505 segs, 146272329 residues Searched:

Word size :

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Listing first 45

SPTREMBL_17:* Database :

sp_archea:* sp_bacteria:*

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:* sp_virus:*
sp_vertebrate:* sp_organelle:* sp_phage:* sp_rodent:* sp_plant:* sb_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

# STIMMARTES

					SUMMAKIES	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	10	71.4	139	. 7	O9F7S4	O9f7s4 uncultured
~	10	71.4	150	7	Q9JZU7	09izu7 neisseria m
m	10	71.4	150	7	Q9JUW1	
4	10	71.4	151	7	Q9HTN3	
S	6	64.3	155	7	09PGZ6	Ogpqz6 xylella fas
9	9	42.9	139	10	Q9LSA1	Oglsal arabidopsis
7	9	42.9	232	σ	003945	003945 bacteriopha
œ	9	42.9	279	Ŋ	Q9U8P7	
6	9	42.9	280	7	P95727	
10	9	42.9	355	7	Q9RP73	09rp73 pasteurella
11	9	42.9	388	7	Q99x85	099x85 staphylococ
12	9	42.9	404	Н	029700	029700 archaeoglob
13	9	42.9	433	Ŋ	Q9NKA0	O9nkaO drosophila
14	9	42.9	438	Ŋ	69VJQ3	O9viq3 drosophila
15	9	42.9	455	٣	Q9Y7W5	09y7w5 saccharomyc
16	9	42.9	464	10	Q9SGA8	Ogsqa8 arabidopšis
17	9	42.9	517	m	Q9C1Z8	09c1z8 pichia past
18	9	42.9	586	٣	Q9URE1	Q9urel saccharomyc
19	9	42.9	286	3	Q9P986	Q9p986 saccharomyc

Q9p985 saccharomyc Q9p984 saccharomyc O31382 bradyrhizob Q9zt83 arabidopsis	09x9p5 streptococc 09p797 schizosacch 017517 caenorhabdi 050463 mycobacteri		/5 mus xylel therm mycob bacte droso	V4V8H0
3 Q9P985 3 Q9P984 2 O31382 10 Q9ZT83	2 Q9X9P5 3 Q9P797 5 Q17517 2 O5O463	2 09FBR4 4 09P111 6 P79114 6 09NYA7	1 (2507) 2 (29PB90 1 (29PR0) 2 (0777) 2 (200775) 5 (29VX03)	
	847 1142 1148 1214	1272 1540 2052 2058	-	
		44444 2002 2002 2000 2000	355.7 355.7 355.7 355.7	35.7 35.7 35.7 35.7 35.7
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### ALIGNMENTS

RESULT

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SEQUENCE FROM N.A.
MEDLINE=20446260; PubMed=10988064;
Beja O., Aravind L., Koonin B.V., Suzuki M.T., Hadd A., Nguyen L.P.,
Jovanovich S.B., Gates C.M., Feldman R.A., Spudich J.L., Spudich E.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                            DeLong E.F.; "Bacterial rhodopsin: evidence for a new type of phototrophy in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PREDICTED DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE.
uncultured proteobacterium EBAC31A08.
Bacteria; Proteobacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%; Score 10; DB 2; Length 139; 100.0%; Pred. No. 0.001; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        139 AA; 14883 MW; ODCA7E61F9E16C62 CRC64;
   139 AA.
   PRT;
                                                                                                                                                                                                                                                                                         EMBL, AF279106; AAG10445.1; -.
InterPro; IRRO01428; durpase.
Pfam; PF00692; durpase; l.
ProDom; PD000946; durpase; l.
                                                                                                                                                                                                                                                           Sea.";
Science 289:1902-1906(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VGLIDSDYQG 10
                                                                                                                             NCBI_TaxID=133804;
                                                                                                                                                                                                                                                                                                                                                          Hydrolase.
SEQUENCE
Q9F7S4
Q9F7S4;
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150 AA. 09JZU7; 01-OCT-2000 (TrEMBLrel. 15, Created) PRT; PRELIMINARY; Q9JZU7 093207 ID 0 AC 0 DT 0

RESULT

us-08-957-709-78.rspt

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Query Match 71.4
Best Local Similarity 100
Matches 10; Conservative
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Q9PGZ6
                                                                                                                                  g
                                                                                                                                                                                                                                    δλ
                                                                                                                                           The Sequence From N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

X MEDLINE-20175755; PubMed-10710307;

XA TELLELIN H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eitelin H., Saunders N.J., Heidelberg J.F., Dodson R.J.,

Reison J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Ra Eisen J.A., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.R.,

Ra Mason T., Clecko A., Parksey D.S., Blair E., Citcone H., Clark E.B.,

RA Mason T., Clecko A., Parksey D.S., Blair E., Citcone H., Clark E.B.,

RA Mason T., Clecko A., Masignani V., Pizza M., Grandi G., Sun L.,

RA Salth H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

RT Schene genome sequence of Neisseria meningitidis serogroup B strain

REMBL; AE002441; AAF41302.1; -.

BR TIGR: NB00893: -.

BR TIGR: NB00893: -.

BR TIGR: PF006945; duTPase.

SCHEDON: PD000946; duTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERORTOPE 4A;

MEDILINE-2022556; Pubmed-10761919;

MEDILINE-2022556; Pubmed-10761919;

A Parkhill J., Achtman M. James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Chillingworth T.,

Bayles R.M., Davis P., Morelli G., Brown D., Chillingworth T.,

A Jagels K.M., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria

menigitidis 22491.;

"Complete DNA sequence of a serogroup A strain of Neisseria

menigitidis 22491.;

REMBL; All62755; CAB84374.1;

REMBL; All62755; CAB84374.1;

REMBL; PRO0692; dUTPasse. 1.

R. Probom; PD000946; dUTPasse. 1.
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEDXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE.
NUBBOR3:
Nelsseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID-491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 10; DB 2; Length 150; 100.0%; Pred. No. 0.0011; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
FUTATIVE DECXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE
FUT 31-01-23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9EFB0077F7CBD12C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Complete proteome.
SEOUENCE 150 AA; 16285 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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STRAIMPAOUL:

MEDLINE-20437337; PubMed=10984043;

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hidnagle W.O., Kowalik D.J., Lagrou M.,

A Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Raich K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

Complete genome sequence of Pseudomonas aeruginosa PAOI, an

opportunistic pathogen.";

Nature 406:959-964(2000).

R InterPro: IPRO01428; dUTPase.

R InterPro: IPRO01428; dUTPase.

R Pfam; PF00692; dUTPase; 1.

R ProDom: PD000946; dUTPase; 1.

R Hydrolase; Complete proteome.

SEQUENCE 151 AA; 15920 MW; 7F87AD5DEF031A48 CRC64;
                                                   Gaps
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MEDLINE=20365717; PubMed=10910347;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L., M.C., Araya J.E., Bala G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylella fastidiosa.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                 OBJUTUS PRELIMINARY; PRT; 151 AA.
OBJUTUS;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYNTDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE.
DUT OR PAS31.
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Length 150;
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09PGZ6;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
71.4%; Score 10; DB 2; Le 100.0%; Pred. No. 0.0011; tive 0; Mismatches 0;
                                                                                           SEQUENCE FROM N.A. STRAIN=PAO1;
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STRAIN=AX4;
Mitra B.N., Yoshino R., Kato M., Morio T., Urushihara H., Tanaka Y.;
"Sequence analysis of a water channel protein gene agpA in
Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome structure of the Lactobacillus temperate phage phi gle: the whole genome sequence and the putative promoter/repressor system."; Gene 187:45-53(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97225795; PubMed-9073065;
Kodaira K.I., Oki M., Kakikawa M., Watanabe N., Hirakawa M.,
Yamada K., Taketo A.;
           Length 139;
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PHIGIE COMPLETE GENOMIC DNA.
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EMBL; AB032841; BAA85158.1; -.
HSSP; P11244; 1FX8.
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PROSITE; PS00221; MIP; UNKNOWN_1.
SEQUENCE 279 AA; 29905 MW; 1B4928E57ACC7EA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X98106; CAA66755.1; -.
SEQUENCE 232 AA; 25836 MW; 6A77FBA26AFC1742 CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
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Last annotation update)
           DB 10;
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100.0%; Pred. No. 41;
iive 0; Mismatches
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           42.98; Score 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17)
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Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutino L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Farga J.S., Franca S.C., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Radioan M. Gannier M., Goldman M.H.S., Gomes S.L., Gibber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Langer E.L., Kitajima J.P., Krieger J.E., Mardins E.M.F., Lopes C.R., Machado J.A., Machado M.A., Madeira H.M.F., Marino C.L., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Mardins E.A.L., Martins E.A.L., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mn. 0.014;
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EMBL; AB026654; BAB01802.1; -.
SEQUENCE 139 AA; 15966 MW; 696B1DEA844218C7 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MVE11.
Arabidopsis thaliana (Mouse-ear cress).
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MEDLINE=20277480; PubMed=10819329;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 178:6873-6881(1996).
-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
EMBL: U72144; AAC44655.1; --
HSSP; P50163; 2AE1.
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycesacsacious Streptomyces
NCBI_TaxID=42684;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PASTEURIAL AI. IKDA PROTEIN.
Pasteurella haemolytica.
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

LO R.Y.C., Hills T.L., Kostrzynska M., McKerral L.J.;

"Analysis of the capsule biosynthetic cluster of Pasteurella haemolytica Al.";

Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF170495; AAF08246.1; --
Hypothetical protein.

SEQUENCE 355 AA. 41088 MW, 35DADE832699123A CRC64;
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InterPro; IPR002193, Abh_short_C2.
InterPro; IPR002147; Abh_short_C2.
Pfam; PF00165; adh_short, 1.
Oxidoreductase.
SEQUENCE 280 AA; 29849 MW; 20F8B51A21E76135 CRC64;
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                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created).
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1-CYCLOHEXENYLCARBONYL COA REDUCTASE.
CHCA.
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                                                                                                                                                                                                                  280 AA.
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NCBI_TaxID=75985;
                                                                 109 VGLIDS 114
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                                   1 VGLIDS 6
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P95727;
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SETRAIN-WC-16, DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-976, Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodgson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Merlavage A.R., Medenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., Meckenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., MoNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yauzaki J., Kanehisa M.,
Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Archaea; Buryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 388;
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EMBL, AP003129; BAB41345.1; -.

CCMD1ete protecome.

SEQUENCE 388 AA; 43232 MW; CC1085A7DE8A5B89 CRC64;
                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SA0125 PROTEIN.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
THREONINE SYNTHASE (THRC-1).
                                                                                                                                                                                                                                                               Staphylococcus aureus subsp. aureus N315.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 55; Matches 6; Conservative 0; Mismatches
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388 AA.
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Matches 6; Conserv
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STRAINEY, CN BW SP.

ARDLINE-99403001; PubMed-10471707;

Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,

Boyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,

Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,

Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,

Celniker S., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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STRAIN-Y, CHE WAS PR.
STRAIN-Y, CHE WAS PR. ST.
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
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                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
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  Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                  InterPro; IPR001926; PALP.
Pfan: PF00291; PALP; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 404 AA; 43941 MW; 05C2E77770C26050 CRC64;
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48733 MW; 93A43238B0FB7C77 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2001 (TrEMBLrel. 17, Last annotation update)
BG:DS00929.8 PROTEIN.
YELLOW-C OR BG:DS00929.8 OR CG4182.
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100.0%; Pred. No. 58;
tive 0; Mismatches
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Genetics 153:179-219(1999).
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EMBL; AE001066; AAB90683.1;
TIGR; AF0551; -.
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253 VGLIDS 258
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                                              Venter J.C.;
Sadow P.W.,
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REPLOINTER JOJG6006; PubMed-10731132;

RADDIANE-20196006; PubMed-10731132;

RADDIANE-20196006; PubMed-10731132;

RADIANE-20196006; PubMed-10731132;

RADIANE-20196006; Mortman J. E., Idhards S., Ashburner M. Henderson S.N.,

Sutton G.G., Wortman J. E., Richards S., Ashburner M. Henderson S.N.,

RADIANE R. C., Rogers Y. H. C., Blazej R. G., Champe M., Pfelifer B.D.,

RAD Bandon R. C., Rogers Y. H. G., Blazej R. G., Champe M., Pfelifer B.D.,

RAD Ballew R. M., Basu A. Baxendal J. Bayraktacoll L., Beasley E. M.,

RAD Ballew R. W., Basu A. Baxendal J. Bayraktacoll L., Beasley E. M.,

RAD Ballew R. D., Botchan M. R., Bouck J. Brokstein P., Botchier P.,

RAD Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RAD Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

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RAD Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RAD Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RAD Cherry J. M., L. Harvey D., Heinan T. J., Weil M. Harris M.,

RAD Harris N. L., Harvey D., Heinan T. J., Weil M. Harris M.,

RAD Harris N. L., Harvey D., Heinan T. J., Weil M. Harris M.,

RAD Harris N. L., Harvey D., Heinan T. J., Weil M. Harris M.,

RAD Harris N., Moy M., Murphy B., Murphy L., Murphy D., Mohrefi A.,

RAD Lasko P., Lei Y. Levitzky A.A., Li J., Li Z., Liang Y., Lin X.,

RAD Lasko P., Lei Y. Levitzky A.A., Li J., Li Z., Liang Y., Lin X.,

RAD Mattel B., Mointcsh T. C., McLeod M.P., Merkelbe J. M.,

RAD Mattel B., Mointcsh T. C., McLeod M.P., Merkelbe J. M.,

RAD M. Nelson R.A., Nuvon K., Nuskern D. R., Ressen M.G.,

RAD RAD M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,

RAD RAD M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,

RAD RAD M., RAD M., Murphy B., Weinschool W., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., San R.,

RAD M., Rad M., Rad M., Rad M., Rad M., Rad M., Rad M., Rad M., Rad M., Rad M., Rad M., Ra
                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG4182 PROTEIN.
YELLOW-C OR BG:DS00929.8 OR CG4182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.9%; Score 6; DB 5;
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EMBL; AE003646; AAF53432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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PRELIMINARY;
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RESULT

370 GLIDSD 375

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Search completed: January 31, 2002, 13:37:49 Job time: 174 sec

321 GLIDSD 326

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 31, 2002, 13:20:16 ; Search time 78.64 Seconds (without alignments) 13.561 Million cell updates/sec

US-08-957-709-78 Perfect score:

1 VGLIDSDYQGQLMI 14 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

219241 seqs, 76174552 residues Searched:

0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

PIR\_68:\* Database :

pirl:\*
pir2:\*
pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description      | dUTP pyrophosphata | deoxyuridinetripho | dUTP pyrophosphata | probable durp pyro | deoxyuridine 5'-tr | dUTP pyrophosphata | deoxyuridine 5'-tr | dUTP pyrophosphata | dUTPase XF0150 [im | hypothetical prote | hypothetical prote | C      | homothallic switch | homothallic switch | nitrous-oxide redu | probable calcium c | phenylalaninetRN | lysyl aminopeptida | H+-transporting AT | probable calcium c | e su   | myosin X - bovine | myosin X - human | myosin X - mouse |        | Ö      |        | hypothetical prote | hypothetical prote |
|-----------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------|-------------------|------------------|------------------|--------|--------|--------|--------------------|--------------------|
| SUMMARIES | QI               | WPECDU             | D86040             | B84995             | D81877             | C81146             | H64104             | C82982             | S44300             | A82843             | T13226             | S51571             | G69318 | S59301             | JC2407             | T44660             | B85045             | S73374           | JU0191             | PXBYVA             | T18770             | G70953 | T18519            | A59267           | A59297           | D82579 | JS0250 | D37949 | B70909             | D65046             |
|           | Length DB        |                    |                    |                    | 150 2              |                    |                    | 151 2              |                    |                    |                    |                    |        |                    |                    |                    |                    |                  | 849 2              |                    |                    | 1214 2 |                   | 2058 2           |                  | 4      | 53 2   | 6      |                    | 99 2               |
| œ         | Query<br>Match I | 100.0              | 100.0              | 100.0              | 71.4               | 71.4               | 71.4               | 71.4               |                    | 64.3               | 42.9               | -                  | ٠      | •                  | •                  | •                  | •                  |                  | 42.9               |                    | ς.                 | ς.     | ä                 |                  | ς.               | 'n.    | 35.7   |        |                    | 35.7               |
|           | Score            | 14                 | 14                 | 14                 | 10                 | 10                 | 10                 | 10                 | 10                 | σ                  | 9                  | 9                  | 9      | 9                  | 9                  | 9                  | 9                  | 9                | 9                  | 9                  | 9                  | 9      | 9                 | 9                | 9                | 5      | 5      | 2      | S                  | Ŋ                  |
|           | Result<br>No.    | -                  | 7                  | ٣                  | 4                  | 2                  | 9                  | 7                  | ω                  | 6                  | 10                 | 11                 | 12     | 13                 |                    | 15                 | 16                 | 17               | 18                 | 19                 | 20                 | 21     | 22                | 23               | 24               | 25     | 56     | 27     | 28                 | 29                 |

|        | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | probable durp pyro | hypothetical prote | probable duTP pyro | DutP nucleotidohyd | acetyltransferase, | hypothetical prote | protein tyrosine p | spoliga homolog - | hypothetical 18.7K | heat shock protein | hypothetical prote |
|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| B82270 | S55211             | G86681             | D86753             | н86800             | T18053             | C69515             | D72124             | D86498             | C82464             | F75125             | T10278             | D39441            | S21858             | C84997             | T48362             |
| ~      | ~                  | ~                  | 7                  | 7                  | 7                  | ~                  | 7                  | 7                  | 7                  | 7                  | 7                  | ~                 | 7                  | ~                  | 7                  |
| 100    | 178                | 139                | 139                | 139                | 141                | 143                | 145                | 145                | 151                | 156                | 160                | 161               | 163                | 170                | 170                |
| 35.7   | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7              | 35.7               | 35.7               | 35.7               |
| ıΩ     | ď                  | 'n                 | 'n                 | ഗ                  | Ŋ                  | വ                  | 2                  | S                  | Ŋ                  | Ŋ                  | വ                  | Ŋ                 | Ŋ                  | Ŋ                  | Ŋ                  |
| 30     | 3.1                | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                | 43                 | 44                 | 45                 |

### ALIGNMENTS

219241

durp pyrophosphatase (EC 3.6.1.23) - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Species: 1-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 24-Sep-1999
C;Accession: A30388: B65165; Q00497
R;Lundberg, L.G.; Thoresson, H.O.; Karlstroem, O.H.; Nyman, P.O.
EMBO J. 2, 967-971, 1983
A;Title: Nucleotide sequence of the structural gene for dUTPase of Escherichia coli K
A;Reference number: A30388; MUID:84057777
A;Recession: A30388
A;Molecule type: DNA
A;Residues: 1-151 < CLUN>
A;Ross-references: GB:X0174; NID:941296; PIDN:CAA25859.1; PID:941297
A;Rolidues: T. 1453-1462, 1997
A;Ritle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64200, MUID:97426617
A;Reference number: B65166

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-151 <BLAT>
A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000441; GB:U00096; NID:q1790063; PIDN:AAC76664.1; PID:q17900 A;Experimental source: strain K-12, substrain MG1655 C;Comment: This enzyme catalyzes the hydrolysis of dUTP (deoxyuridine 5'-triphosphate ar concentration of dUTP.

A; Map position: 82 min

C;Superfamily: dUTP pyrophosphatase C;Keywords: hydrolase; nucleotide metabolism

Gaps ., Length 151; Indels Query Match 100.0%; Score 14; DB 1; L Best Local Similarity 100.0%; Pred. No. 7.4e-09; Matches 14; Conservative 0; Mismatches 0;

0

1 VGLIDSDYQGQLMI 14 δŏ

85 VGLIDSDYQGQLMI 98 qq

## RESULT

D86040

deoxyuridinetriphosphatase [imported] - Escherichia coli (strain 0157:H7)
C;Specias: Escherichia coli
C;Specias: Escherichia coli
C;Accession: 1086040
C;Accession: D86040
E;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001

85 VGLIDSDYQGQLMI 98

Q

1 VGLIDSDYQGQLMI 14

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H0410TP pyrophosphatase (EC 3.6.1.23) - Haemophilus influenzae (strain Rd KW20)
C.Species: Haemophilus influenzae
C.Species: Haemophilus influenzae
C.Date: Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
C.Date: Bandon, R.C.; Fine, L.D.; Fitchmann, J.L.; Glodek, A.; Kelley, J.M.; Macidman
C.D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Puhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 465-512, 1995
A.Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A.Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A.Recession: H64104
A.Status: nucleic acid sequence not shown; translation not shown
A.Residues: 1.151 CTIGRA
A.Residues: 1.151 CTIGRA
A.Residues: 1.151 CTIGRA
A.Rocessuerreferences: GBB1032776; GB:L42023; NID:g1573969; PIDN:AAC22615.1; PID:g1573979
C.Superfamily: dUTP pyrophosphatase
C.Superfamily: dUTP pyrophosphatase
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                                                     Length 150;
                                                                                                                                          0; Indels
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                                               DB 2; Le
0.00023;
                                               Ouery Match 71.4%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.0 Best Local Similarity 100.0%; pred. No. 0.1 Mismatches 10; Conservative 0; Mismatches
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C; Superfamily: retroviral proteinase
                                                                                                                                                                                                                               1 VGLIDSDYQG 10
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published duTP pyrophosphatase (EC 3.6.1.23) NMA1112 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: O5-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
C;Accession: D81877
A;Reference number: A81775; MUID:20222556
A;Accession: D81877
A;Reference number: A81775; MUID:20222556
A;Accession: D81877
A;Residues: 1-150 CPAR>
A;Accession: D81877
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A;Acces
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUD:21074935; PMID:11206551

A; Reference number: A85480; MUD:21074935; PMID:11206551

A; Status: preliminary

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-151 <STO>

A; Cross-references: GB:AE005174; NID:g12518396; PIDN:AAG58784.1; GSPDB:GN00145; UWGP:Z5C

A; Experimental source: strain O157:H7, substrain EDL933

A; Genetics:

A; Genetics:

A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3

B48495

GUTP pyrophosphatase (EC 3.6.1.23) [imported] - Buchnera sp. (strain-APS)

C.Species: Buchnera sp.

C.Species: Buchnera sp.

C.Accession: B84995

A.Shidenobu, S.; Watenabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A.Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.

A.Reference number: A84930; MUID:20445173

A.Accession: B84995

A.Accession: B84995

A.Accession: B84995

A.Accession: B84995

A.Accession: B84995

A.Residues: 1-154 <STO>

A.Residues: 1-154 <STO>

A.Reperimental source: GR:AP000398; GSPDB:GN00144

A.Experimental source: strain APS

C.Gonettcs:
A.Genetcs:
A.Gene
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100.0%; Score 14; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 14; Conservative 0; Mismatches 0; Indels
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85 VGLIDSDYQGQLMI 98

Db

1 VGLIDSDYQGQLMI 14

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A'Experimental Source: Strain 965C

R'Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurames, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, B.E.; La

r. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A;Authors: da Silva, A.C.R.; de Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.D.

A;Reference number: A59328

A;Rochents: annotation

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Lactobacillus phage phi-gle (") C; Species: Lactobacillus phage phi-gle (") C; Date: 13-Aug-1999 #text_change 21-Jul-2000 (") C; Accession: T1328 (") C; Accession: T1328 (") C; Accession: T1328 (") C; Accession: T137 (") C; M; M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taket Gene H7, 45-73, 1997 (") A; Title: Genome structure of the Lactobacillus temperate phage phi gle: the whole gen A; Reference number: 217631; MUID:97225795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pypothetical protein 293 - Rhizobium meliloti
C;Species: Rhizobium melloti
C;Species: Rhizobium melloti
C;Accession: S51571, 843166
R;Rossbach, S.; Kulpa, D.A.; Rossbach, U.; de Bruijn, F.J.
Mol. Gen. Genet. 245, 11-24, 1994
A;Title: Molecular and genetic characterization of the rhizopine catabolism (mocABRC)
A;Reference number: S51569; MUID:95147842
A;Status: nucleic acid sequence not shown; translation not shown
A;Wolecule type: DNA
A; Cross-references: GB: AE003868; GB: AE003849; NID: 99104930; PIDN: AAF82963.1; GSPDB: GN
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C; Genetics:
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C;Superfamily: Lactobacillus phage phi-gle hypothetical protein R232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 9; DB 2; L 100.0%; Pred. No. 0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-232 <KOD>
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100.0%; Pred. No. 11;
Live 0; Mismatches
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C; Superfamily: dUTP pyrophosphatase
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les 9; Conservative C
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les 6; Conserv
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Matches 6
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S51571
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                                        d02843

d0TPase XF0150 [Imported] - Xylella fastidiosa (strain 9a5c)

d0TPase XF0150 [Imported] - Xylella fastidiosa

d15-pecies: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C;Accession: A82843

Ranonyous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below
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dUTP pyrophosphatase (EC 3.6.1.23) - Coxiella burnetii
C;Species: Coxiella burnetii
C;Species: Coxiella burnetii
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C;Accession: S44300
R;Thiele, D.; Willems, H.; Oswald, W.; Krauss, H.
submitted to the EMBL Data Library, May 1994
A;Reference number: S44297
A;Accession: S44300
A;Status: preliminary
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Best Local Similarity 100.
Matches 10; Conservative
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A;Molecule type: DNA
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      A; Accession: $67790

A; Roceaule type: DNA
A; Residues: 1-586 - RAAS-
A; Cross-references: EMBL: 274275; NID: 91431382; PIDN: CAA98806.1; PID: e253273; PID: 9143
A; Experimental Source: strain $288C
C; Genetics:
A; Genetics:
A; Genetics:
A; Cross-references: SGD: $50002386; MIPS: YDL227C
A; Map position: 4L
C; Puroficion:
C; Function:
C; Function:
C; Keywords: DNA binding; nucleus; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o;
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. 26;
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches
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(66918)

thereonine synthase (EC 4.2.99.2) thrC-1 AF0551 [similarity] - Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Accession: G69318

R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

C; Accession: G6318

R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Welson, K.E.; Ketchum, K.A.; Dodson

R; Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocaphe, J.D.; Weidman, J.F.; McDonald, L.

A; Atthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

A; Atthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

A; Atthors: Utterback, T.; Cotton, W.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

A; Reference number: A69250; MUID: 98049343

A; Reference number: A69250; MUID: 98049343

A; Accession: G69318

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Residues: 1-404 «KLE>

A; Cross-references: GB: AE001066; GB: AE000782; NID: 92689389; PIDN: AAB90683:1; PID: 9265006

C; Superfamily: threonine dehydratase

C; Superfamily: producted prosphate (Lys) (covalent) #status predicted
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S59301
homothallic switching endonuclease - yeast (Saccharomyces cerevisiae)
NiAlternate names: HO endonuclease; homothallism protein; protein D0827; protein VDL227c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Dec-1995 #text_change 29-Oct-1999
R;Raveh, D.
Submitted to the EMBL Data Library, August 1995
A;Reference number: S59301
A;Reference number: S59301
A;Reference number: S59301
A;Reference number: S29301
A;Reference number: S29301
A;Reference number: S29301
A;Residues: 1-586 cRAv
A;Cross references: EMBL:X90957; NID:9984693; PIDN:CAA62447.1; PID:9984694
A;Cross reference number: A2340, 1966
A;Title: Structure of the Saccharomyces cerevisiae HO gene and analysis of its upstream A;Reference number: A25309; MUID:87089786
A;Accession: A2530
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A;Accession: A2530
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A;Accession: A2530
A;Accession: A2530
A;Accession: A2
A;Residues: 1-293 <ROS>
A;Cross-references: EMBL:X78503; NID:g468758; PIDN:CAA55268.1; PID:g468761
A;Experimental source: strain L5-30
A;Experimental source: strain L6-30
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches
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A:Cross-references: EMBL:AJ002531; PIDN:CAA05518.1
A:Experimental source: strain USDA110
C;Genetics:
C;Genetics: nos2
C;Superfamily: nitrous-oxide reductase
C;Keywords: oxidoreductase

0; Gaps Query Match
42.9%; Score 6; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels

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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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| 35.7 622 4 US-09-305-381-2 Se 53.7 623 1 US-08-734-925-2 Se 53.5.7 630 3 US-08-771-986A-2 Se 53.5.7 636 4 US-08-771-986A-1 Se 53.7 666 4 US-08-982-785A-11 Se 53.7 76 1 US-08-021-601-2 Se 53.7 776 1 US-08-021-601-2 Se 53.7 776 1 US-08-0461-551-2 Se 53.7 776 1 US-08-461-551-2 Se 53.7 776 1 US-08-461-551-2 Se 53.7 849 1 US-08-461-551-2 Se 53.7 866 3 US-08-461-551-2 Se 53.7 866 3 US-08-487-691-18 Se 53.7 866 3 US-08-487-691-17 Se 53.7 866 3 US-08-487-691-12 Se 53.7 864 1 US-08-487-691-12 Se 53.7 864 1 US-08-487-691-12 Se 53.7 865 3 US-08-486-269A-12 Se 55.7 865 3 US-08-486-269A-12 Se 55.7 865 3 US-08-487-691-2 Se 55.7 86                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | SULT 1 5048824 405-7 50408067, Application US/08824405 50508067, Application US/08824405 50508067, Application US/08824405 50508067, Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Conservation Co | COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: Diskette COMPU | Similarity 100.0%; Score 14; DB 2; Length 151 Similarity 100.0%; Pred. No. 4.2e-08; 4; Conservative 0; Mismatches 0; Indels |
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CORRESPONDENCE ADDRE. STREET: 4000 Bell STREET: Philadelphi STATE: PA COUNTRY: USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | COMPUTER READABLE FRANCHIER READABLE FRANCHIER READABLE FOR MEDIUM TYPE: District of the computer: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER: IBM COMPUTER SYSTEM: SOFTWARE: EastSE CURRENT APPLICATION WHOBE FILING DATE: ATTORNEY/AGENT INFO; NAME: BLOOM, All REGISTRATION NUMBER REFERENCE/DOCKET ITELECOMMUNICATION ITELEX: INFORMATION FOR SEQ II SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCE CHARACTERIS SEQUENCES: SITRANDEDNESS: SITRANDEDNES | atch<br>cal                                                                                                                 |
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US-09-106-582-54

US-09-106-582-54

Sequence 54, Application US/09106582

Sequence 54, Application US/09106582

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
CORRESPONDENCES: 73

CORRESPONDENCES: SEED and BERRY LLP
STREET: STED and BERRY LLP
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CORRESPONDENCES: 73

CORRESPONDENCES: SEED and BERRY LLP
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
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100.0%; Pred. No. 21;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/FORCET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 54 ; LENGTH: 340 ; TYPE: PRT ; ORGANISM: Ehrlichia sp. ; ORGANISM: Ehrlichia sp. (25-09-295-028-54
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US-08-563-892A-16
'Sequence 16, Application US/08563892A
'Patent No. 5976819
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-582-54
                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv.
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INFORMATION FOR ESQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 340 amino acid
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                                                                                                                                                                                                                                                      Sequence 54, Application US/08975762

Patent No. 6207169

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP.
STREEF: 6500 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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US-09-295-028-54
Sequence 54, Application US/09295028
Sequence 54, Application US/09295028
Sequence 54, Application US/09295028
Sequence 54, Application US/09295028
Sequence 54, Application US/09295028
SERENCAMT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF EHRLICHIA INFECTION
FILE REFERENCE: 210121.439C4
CURRENT APPLICATION NUMBER: US/09/295,028
CURRENT FILING DATE: 1999-04-20
NUMBER OF _SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: SOUR COLUMNIA CENTER; FILCH AVENUE STATE: Washington COUNTR: Washington COUNTR: Washington ZIP: 98104
COMPUTER READABLE FORM: WEDTUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OF PERATION FOR SOFTWARE: PATORIT RE-Base #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/975,762 FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
42.9%; Score 6; DB A Best Local Similarity 100.0%; Pred. No. 21 Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
NAME: Mark, David J.
NEGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439
TELECOMMUNICATION INFORMATION:
TELEPAN: 206-622-4900
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-762-54
                                                                     85 VGLIDSDYQGQLMI 98
                                      1 VGLIDSDYQGQLMI 14
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2 SDYQGQ 7
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US-08-975-762-54
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Sequence 27, Application US/09025151

Sequence 27, Application US/09025151

Patent No. 618735

GENERAL INFORMATION:
APPLICANT: Legrain, Pierre
APPLICANT: Fromont, Michaline
APPLICANT: Fromont, Michaline
TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS
TITLE OF INVENTION: INTEREST: US/09/025,151

CURRENT APPLICATION NUMBER: US/09/025,151

CURRENT APPLICATION NUMBER: US/09/025,151

SOFTWARE: PATENTIN VOIL 2.0

SEQ ID NOS: 29

LENGTH: 67

LENGTH: 67
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APPLICANT: V1 uela, Eladio
APPLICANT: V1 uela, Eladio
APPLICANT: V1 uela, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 67;
                                                                                                                                                                                                                                                                                                                                                                                        Length 50;
                                                                                                                                                                                                                                                                                                                                                                                        35.7%; Score 5; DB 1; 100.0%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08307499; Patent No. 5651972; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae US-09-025-151-27
                                                                                                     REFERENCE/DOCKET NUMBER: 1677
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)683-4109
TELEY: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
FILING DATE: 19920624
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                           ; LENGTH: 50 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-903-456-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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Best Local Similarity
The 5; Conserve
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27 GLIDS 31
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Patent No. 5574144
GENERAL INFORMATION:
APPLICANT: KAMBOJ, Rajender
APPLICANT: ELLIOTT, Candace
APPLICANT: BLIOTT, Candace
TITLE OF INVENTION: THE EAA4 FAMILY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                        APPLICANT: Finkel, Terri H.

PAPLICANT: Rozdzial, Moshe M.

TITLE OF INVENTION: PRODUCT AND PROCESS TO REGULATE ACTIN
TITLE OF INVENTION: DOLYMERIZATION IN T LYMPHOCYTES
TOWNSHORDENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 27;
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/563,892A
FILING DATE: 21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 5; DB 2; Pred. No. 24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRARATION NUMBER: 33,005
REGISTRAFOCKET NUMBER: 2879-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.7%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-563-892A-16
                                                                                                                                                                                               STATE: COLOLUC COUNTRY: U.S.A. 70: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 DSDYQ 14
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US-07-903-456-5
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APPLICANT: ERTESVAG, HELGA
APPLICANT: SKJAR-RABEK, GUDMUND
APPLICANT: SKJAR-RABEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES;
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES;
TITLE OF INVENTION: DNA COMPOUND C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O.BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: Z2042
COMPUTED FOR STATES CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ore 5; DB 4; Length 142;
red. No. 1.1e+02;
Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OMPOTER: IBM PC COMPATIBLE
OMPOTER: DEM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURRHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UF35.1.FWCC1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
FILING DATE:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
FILING DATE: 1-JUL-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION NUMBER: US 07/342,212
FILING DATE: 31,794
RECISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: 31,794
RELEPHONE: 904-375-8100
TELECHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-187-942C-43
Sequence 43, Application US/08387942C
; Sequence No. 5939289
; GENERAL INFORMATION:
APPLICANT: FRYENAC, HELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pr
Matches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-268-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 IDSDY 8
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US-09-258-22
Sequence 22, Application US/09299268
Sequence 22, Application US/09299268
Sequence 22, Application US/09299268
Sequence 22, Application US/09299268
Sequence 22, Application US/09299268
SPECIANT: Wilela, Eladio
APPLICANT: Wilela, Eladio
APPLICANT: Glbs, E.P.J.
TITLE OF INVENTION: Use OF Recombinant Swine Poxvirus as a TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS: 60
CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 50
COUNTRY: Qainesville
STATE: Plotida
COUNTRY: U.S.A.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: READABLE: PC-DOS/MS-DOS
COPERATING SYSTER: PC-DOS/MS-DOS
COPERATING SYSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 142;
                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US /08/307, 499
FILING DATE:
CLASIPICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION 435
RIOR APPLICATION 435
RIOR APPLICATION 1435
RIOR APPLICATION WHER: US 07/342,212
FLING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: UF 31,794
REFERENCE/DOCKET NUMBER: UF 31,794
REFERENCE/DOCKET NUMBER: UF 31,794
REFERENCE/DOCKET NUMBER: UF 31,794
REFERENCE/DOCKET NUMBER: UF 31,794
REFERENCE/DOCKET NUMBER: UF 31,794
RELEPAN: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.7%; Score 5; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0;
   STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-307-499-22
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DB 1; Length 212;
                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,965A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REFERENCE/DOCKET NUMBER: 32,073
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRA: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08462169B
Patent No. 5773252
GENERAL INFORMATION:
APPLICANT: John Greene and Craig A. Rosen
TITLE OF INVENTION: Fibroblast Growth Factor-15
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-441 (PF203)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%; Score 5;
100.0%; Pred. Nc
tive 0; Misma1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,169B
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                           Query Match 35.7%; Score 5; DB 2; Length 153; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09357251

Sequence 2, Application US/09357251

Sequence 2, Application US/09357251

GENERAL INFORMATION:

APPLICANT: Fanco, S. Carl

APPLICANT: Forozco, Layo O.

APPLICANT: Schwaber, James S.

TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase

FILE REFERENCE: BB-1193

CURRENT FILING DATE: 1999-07-20

CURRENT FILING DATE: 1999-07-20

EARLIER APPLICATION NUMBER: 60/093,530

EARLIER PILING DATE: July 21, 1998

NUMBER OF SEQ ID NOS: 37

SOFTWARE: MICROSOFT Office 97

LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Greene Ph.D., John M.
APPLICANT: Greene Ph.D., Joachim R.
APPLICANT: Greene Ph.D., Joachim R.
APPLICANT: Rosen, Craig R.
APPLICANT: Rosen, Craig R.
AUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greener Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 5; DB 4
100.0%; Pred. No. 1.3
tive 0; Mismatches
REFERENCE/DOCKET NUMBER: 1809-106P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08462965A
; Patent No. 5728546
              TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8050
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-942C-43:
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Zea mays
US-09-357-251-2
                                                                                                                                                                                                                                                                                                                                                                                                                                            138 YQGQL 142
                                                                                                                                                                                                                                                                                                                                                                                                    8 YOGOL 12
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21 GLIDS 25
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US-08-462-965A-2
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red. No. 1.5e+02;
Mismatches 0; Indels
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                                                                                                                             RESULT 14
US-09-103-079-21
Sequence 21, Application US/09103079A
Fatent No. 6013477
GENERAL INFORMATION
APPLICANT: Greene, John M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION Fibroblast Growth Factor 15
FILE REFERENCE: PF203D1
CURRENT APPLICATION NUMBER: US/09/103,079A
CURRENT FILING DATE: 1998-06-05
MUMBER FILING DATE: 1998-06-05
NUMBER OF SQD ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SSO ID NO 21
LENGTH: 212
TYPE: PRF
GROWN HOME Sapiens
US-09-103-079-21
                                                                                                                                                                                                                                                                                                                                                            Query Match 35.7%; Score 5; DB 3 Best Local Similarity 100.0%; Pred. No. 1.5 Matches 5; Conservative 0; Mismatches
                                         Score 5;
Pred. No
                                     Query Match
Best Local Similarity 100.
Matches '5; Conservative
; MOLECULE TYPE: PROTEIN US-08-462-169B-21
                                                                                             175 YQGQL 179
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Peptide #2254 enco

Staphylococcus aur Saccharomyces uvar

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Saccharomyces carl

Sulfated fucose-co

Human ORFX ORF1784

Prostate tumour as ARH1 peptide mimet Valphal2.1 / Jalph T cell receptor al Multisubunit immun

Excitatory amino a YJR022W a yeast pe Peptide #4496 enco Peptide #4611 enco

Minimum DB seq Maximum DB seq

Word size

Searched:

Database :

score:

Perfect

Run on:

Sequence:

Scoring table:

Human colon cancer Chlamydia pneumoni H. pylori GHPO 107 Eucalyptus grandis

Peptide #6669 enco S. epidermidis ope Swinepox virus Hin

Peptide #5399 enco Fragment of human

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Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases, for
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase enhancing factor; PEF; dCTP deaminase; PCR; amplification; sequencing; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli dUTPase uridine-binding motif.
                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                               AAB23251
AAW82639
AAY78561
AAY70155
AAR72471
                                                                                                                                                  AAB42020
AAY11681
AAB24303
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AAB38061
AAR45368
AAY33818
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AAY34660
AAW98755
AAB25167
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                     AAG56812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US05497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0957709
97US-0822774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
Hansen CJ, Hogrefe H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-542284/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRA-) STRATAGENE.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09842860-A1
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21-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW72854;
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 RESULT
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Peptide #2619 enco
Peptide #2501 enco
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Human normal bladd
                                                                       Search time 140.03 Seconds (without alignments) 7.406 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                             /SIDSZ/gcgdata/geneseq/geneseqp/AAl980.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqpAAl981.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqpAAl981.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqpAAl981.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqpAAl981.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp/AAl984.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqpAAl986.DAT:*
/SIDSZ/gcgdata/geneseq/geneseqp/AAl986.DAT:*
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/SIDSZ/gcgdata/geneseq/geneseqp/AAl980.DAT:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                       Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                             522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                        January 31, 2002, 13:18:12
                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                     OM protein – protein search, using sw model
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AAM16091
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AAM28248
AAW38508
AAM20396
AAM34854
AAM34854
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Gapop 60.0 , Gapext 60.0
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1 VGLIDSDYQGQLMI 14
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                 This is the uridine-binding motif of the dUTPase of Escherichia coli. Sequences are provided (see AAM72849-57) of the uridine-binding motifs of dUTPases and dCTP deaminases of Pyrococcus furiosus (see AAM72847), Methanococcus jannaschii, Desulfurolobus ambivalens, AAM72847), Methanococcus jannaschii, Desulfurolobus ambivalens, AAM72848 is also provided. A claimed method of enhancing a nucleic acid polymerzae reaction comprises performing the reaction in the presence of one or more of the following: a polymerase enhancing factor (PEF), a dUTPase, a protein that turns-over dUTP and protein having one or more of the sequences provided in AAM72848-57. A claimed protein having PEF activity comprises one or more of sequences given in AAM72848-57. Kits are provided in AAM72848-57. A claimed protein acids, for site-directed mutagenesis, for nucleic acid sequencing or for amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment; EST; expressed sequence tag; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides and their nucleic acids, useful for treatment bladder tumour and identification of therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human normal bladder tissue EST encoded protein 27.
                                                                                                                                                                                                                                         100.0%; Score 14; DB 19;
100.0%; Pred. No. 1.4e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A, Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                  71; Page 47; 161pp; English.
                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 14; Conserv
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of fallures because of ESTS from different libraries representing different parts of the same unknown gene distorting the estimated frequency of occurrence in a particular tissue. AAY6029-Y60591 represent protein fragments encoded by the human normal bladder tissue cDNA library derived EST fragments represented in AAZ42122-Z42248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #2525 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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Pred. No. 7;
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ID AAM16091 standard; Protein; 66 AA.
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|larity 100.0%; Pl
| Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UN4-2000; 2000US-0608408.
03-AUG-2000; 2000US-063366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GS-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2001 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                          32 AA;
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24 lidsdy 29
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The present invention relates to novel single exon nucleic acid probes clear Asia (Month) and Asia (Month) and a periode concoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumnours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at tp.wipo.int/pub/published_pct_sequences.
                                                                                                                                    Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                   Peptide #2501 encoded by probe for measuring breast gene expression.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 12559; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%; Score 6; 100.0%; Pred. No
AAM03819 standard; Protein; 66 AA.
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2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                           2000US-0207456.
2000US-0608408.
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                                                                   (first entry)
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Best Local Similarity 100.
Matches 6; Conservative
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21-SEP-2000;
27-SEP-2000;
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                                 AAM03819;
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                                                                                                                                                                                                                                                                                                                                         Peptide #2619 encoded by probe for measuring placental gene expression.
                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
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                                               Length 66;
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                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                           microarray; human; placenta; antenatal diagnosis;
                                              Score 6; DB 22;
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11arity 100.0%; Score 6; DB 2 11arity 100.0%; Pred. No. 13; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR;
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                                 42.9%; Scc.
100.0%; Pred
0; M
                                                                                                                                                                                                                                      AAM28582 standard; Protein; 66 AA.
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26-MAY-2000; 2000US-0207456.
30-UNY-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-02359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human genetic disorders.
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Best Local Similarity
'-hac 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder
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51 1dsdyg 56
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99
                                                                                                                 4 IDSDYQ 9
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Sequence
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Probe;

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Gaps

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Staphylococcus aureus protein of unknown function.

RESULT AAM03819

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Length 66; Indels Nicholas RO;

Hodgson JE, Knowles DJC,

96US-0017670.

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This sequence represents a Streptococcus pneumoniae protein that, based on homology with a Lactobacillus helveticus protein, is an ISLZ protein, and is encoded by a DNA sequence of the invention. The DNA sequences strain of the DNA sequences of the invention can be used to compendate proteins of the invention can be used to calcivity of the proteins of the invention can be used to calcivity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic immunisation. They can look be used to induce an immunological response in a mammal by cancilation with the S. pneumoniae proteins or delivery of the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The proteins can be used to identify antimicrobial compounds which are capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian extracellular matrix proteins on in-dwelling devices or in wounds, to block protein.

C. and be used to infedential initiated other than by the implantation of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.
                                                                                                                                                                                                                                                                                                Novel Streptococcus pneumoniae proteins and related DNA - useful for diagnosing anti-microbial agents for treatment of bacterial infections
                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Pages 292-293; 483pp; English.
                                                                                                                                        (SMIK.) SMITHKLINE BEECHAM CORP (SMIK.) SMITHKLINE BEECHAM PLC.
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N-PSDB; AAT98575.
                                                                    14-MAY-1997;
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                                 20-NOV-1997.
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Stodola RK;
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            Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Staphylococcus aureus protein of unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCCH 9 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce antibacterial action. These vaccines and antibodies with a host to produce specific antibodies with a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S. aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae protein; genetic immunisation; antagonist; Immunological response; incculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound; pathogenesis.
                                                                                                                                                                                                                                                                                                                  Hodgson JE, Knowles DJC, Nicholas RO;
Rosenberg M, Ward JM;
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llarity 100.0%; Pred. No. 15;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 556; 989pp; English.
                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                             97WO-US02318.
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                                                                                                                                                                                                                                                                                                                    Burnham MK,
Reichard RW,
                                                                                                     Staphylococcus aureus
                                                                    toxic shock syndrome
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N-PSDB; AAT84155.
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Best Local Similarity
Matches 6; Conserv
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Pratt JM,
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Peptide #6830 encoded by probe for measuring cervical gene expression.
                          Gaps
                                                                                                                                                                                                                          Probe; human; microarray; gene expression; cervical epithelial cell;
                       ó
Ouery Match

42.9%; Score 6; DB 19; Length 104;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                              AAM20396 standard; Protein; 106 AA.
                                                                                                                                                                                                                                      cervical cancer
                                             5 DSDYQG 10
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                                                                                                                                                                          12-OCT-2001
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Streptococcus pneumoniae

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104 AA;

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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
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                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
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analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 106;
                                                                                                                                                 analyzing gene expression in human placenta
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Mismatches
                                                                                                                                                                             Claim 27; SEQ ID No 35123; 654pp; English.
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                                                                Rank DR;
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                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                Chen W,
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2000US-0207456.
2000US-0608408.
2500US-0632366.
2000US-0234687.
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04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                            from human placenta. The
human genetic disorders
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Best Local Similarity
6, Conserv?
                                                                Hanzel DK,
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92 idsdyg 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human single exon nucleic acid probes (SENP: see AA11068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical useful in grading and/or staging of diseases of the cervix, notably everycal cervical cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #8891 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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genetic disorder.
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                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 25222; 487pp; English
                                                                                                                                                                                                             Rank
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100.0%; Pre
0; 7
                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                             Chen W,
                                                            2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0608408.
2000US-0632366.
                                                                                                            2000US-0234687.
2000US-0236359.
               30-JAN-2001; 2001WO-US00670
                                                                                                                                             2000GB-0024263
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2000US-0236359
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Best Local Similarity 100.v.
6; Conservative
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                                                                                                                                                                                                             Penn SG, Hanzel DK,
                                                                                                                                                                                                                                          WPI; 2001-488901/53
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                              26-MAY-2000;
30-JUN-2000;
                                                                                                                                             04-OCT-2000;
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                                                                                            03-AUG-2000;
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Indels

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Length 107;

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(SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are defived from human HeLea cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                             cervical cancer.

Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see ANII)15-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #2381 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                       42.9%; Score 6; DB 22; Length 107; Ilarity 100.0%; Pred. No. 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe: microarray; human; placenta; antenatal diagnosis; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                    AAM28344 standard; Protein; 107 AA.
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26-MAY-2000; 2000US-0207456.
30-UNY-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                           Sequence 107 AA
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92 idsdyg 97
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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                                 Gaps
                                                                                                                                                                                                                                                                      Peptide #2254 encoded by probe for measuring breast gene expression.
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                                 0; Indels
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42.9%; Score 6; DB 22;
100.0%; Pred. No. 19;
iive 0; Mismatches C
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ilarity 100.0%; Pred. No. 19;
Conservative 0; Mismatches
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                                                                                                                                                                         AAM03572 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
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26-MAY-2000, 2000US-0207456.
30-UJN-2000; 2000US-0603408.
03-AUG-2000, 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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 Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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|92 idsdyg 97
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                                                                 4 IDSDYQ
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AAG91790;

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AAG91790 RESULT

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990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
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990S-0131449.
990S-0132407.
990S-0132484.
990S-0132485.
990S-0132487.
990S-0132487.
990S-0134286.
990S-0134286.
990S-0134286.
990S-0134219.
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990S-0134219.
990S-0134370.
990S-0134370.
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99US-0127462.
99US-0128234.
99US-0128714.
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99US-0130077.
99US-0130449.
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99US-0136782.
99US-0137222.
99US-0137528.
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99US-0138540.
99US-0138847.
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99US-0139452.
99US-0139453.
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99US-0139455
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18-OCT-2000 (first entry)
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                                                                                                                          termination sequence
                                                                                                                                                                  Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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                                                          AAG91790 standard; Protein; 132 AA
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100.0%; Pre-
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                                           (first entry)
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Best Local Similarity
Matches 6; Conserval
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36 glidsd 41
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Tateishi N,
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AAG56812 standard; Protein; 133 AA.

RESULT 14

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AAG56812

AAG56812 ID AAG5 XX AC AAG5

Sequence

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 73116.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;

Arabidopsis thaliana protein fragment SEQ ID NO: 77060.

| 28-JUN-1999; 99US-0.<br>29-JUN-1999; 99US-0.<br>30-JUN-1999; 99US-0.<br>01-JUL-1999; 99US-0.<br>02-JUL-1999; 99US-0.<br>06-JUL-1999; 99US-0.<br>08-JUL-1999; 99US-0.<br>08-JUL-1999; 99US-0. | PR 13-0101-1999; 9908-0143842.  PR 15-701-1999; 9908-0144085.  PR 16-701-1999; 9908-0144085.  PR 19-701-1999; 9908-0144331.  PR 19-701-1999; 9908-0144331.  PR 19-701-1999; 9908-0144331.  PR 19-701-1999; 9908-0144331.  PR 20-701-1999; 9908-0144331.  PR 20-701-1999; 9908-0144331.  PR 20-701-1999; 9908-0144331.  PR 21-701-1999; 9908-0144331.  PR 21-701-1999; 9908-0144318.  PR 22-701-1999; 9908-0145088.  PR 23-701-1999; 9908-0145088.  PR 23-701-1999; 9908-014508.  PR 24-A0G-1999; 9908-014508.  PR 24-A0G-1999; 9908-014508.  PR 03-A0G-1999; 9908-014508.  PR 04-A0G-1999; 9908-014508.  PR 04-A0G-1999; 9908-014508.  PR 13-A0G-1999; 9908-014703.  PR 13-A0G-1999; 9908-014938.  PR 13-A0G-1999; 9908-014938.  PR 13-A0G-1999; 9908-014938.  PR 23-A0G-1999; 9908-014938.  PR 13-A0G-1999; 9908-014938.  PR 23-A0G-1999; 9908-014939.  PR 23-A0G-1999; 9 |
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42.9%; Score 6; DB 21; Length 133;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels
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Search completed: January 31, 2002, 13:18:13 Job time: 174 sec

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8 YQGQLM 13 ||||||| 54 Yqgqlm 59

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 13:37:49; Search time 130.99 Seconds

Title: US-08-957-709-79

Perfect score: 14
Sequence: 1AGVVDRDYTGEVKV 14
Scoring table: OLIGO Gapext 60.0
Searched: 473505 seqs, 146272329 residues

Word size: 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|                                                                                                                          | Q99212 homo sapten<br>Q2863 oryctolagus<br>Q9cj55 lactococcus<br>Q97791 oryctolagus<br>Q91791 oryctolagus<br>Q9810 gallus gall<br>Q98018 gallus gall<br>Q10466 homo saplen |
|--------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 386 2<br>387 3<br>387 3<br>397 3<br>406 10<br>406 10<br>619 1<br>619 1<br>625 1<br>1028 2<br>1039 2<br>1031 13<br>1132 4 | <b>4444444</b>                                                                                                                                                             |
| 0.11.02.02.02.02.02.02.02.02.02.02.02.02.02.                                                                             | 3 2 8 4 4 4 4 4 4 4 3 8 8 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                              |

## ALIGNMENTS

|                  |                 |                                   |                     |                   |              |                                                         |                                                                    |                  |    |                    |                |                                                                 |                                                    |                                                                      |              |                                                         |     |                    |                |                                      |                                                          |                             |                             |                          |                             |                         |   |                | 0;           |           |            |
|------------------|-----------------|-----------------------------------|---------------------|-------------------|--------------|---------------------------------------------------------|--------------------------------------------------------------------|------------------|----|--------------------|----------------|-----------------------------------------------------------------|----------------------------------------------------|----------------------------------------------------------------------|--------------|---------------------------------------------------------|-----|--------------------|----------------|--------------------------------------|----------------------------------------------------------|-----------------------------|-----------------------------|--------------------------|-----------------------------|-------------------------|---|----------------|--------------|-----------|------------|
|                  |                 |                                   |                     |                   |              |                                                         | ces.                                                               |                  |    |                    |                | r L.,                                                           |                                                    | thesis                                                               |              |                                                         |     |                    |                |                                      |                                                          |                             |                             |                          |                             |                         |   |                | Gaps         |           |            |
|                  |                 |                                   |                     |                   |              |                                                         | tomy                                                               |                  |    |                    |                | naue                                                            |                                                    | uksc                                                                 |              |                                                         |     |                    |                |                                      |                                                          |                             |                             |                          |                             |                         |   |                | 0;           |           |            |
|                  |                 | ate)                              | pdate)              |                   |              | acteridae;                                              | Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. |                  |    |                    |                | Trefzer A., Hoffmeister D., Westrich L., Stockert S., Weitnauer | d A.;                                              | "Function of glycosyl transferase genes involved in the biosynthesis |              | databases.                                              |     |                    |                |                                      | databases.                                               |                             |                             |                          |                             | 21A3B2A2E55168B2 CRC64: |   | Length 148;    | 0; Indels    |           |            |
|                  | 148 AA.         | ce upd                            | annotation update)  |                   |              | ctinob                                                  | tomyce                                                             |                  |    |                    |                | , Stoc                                                          | chthol                                             | invol                                                                |              | к/ровл                                                  |     |                    |                |                                      | к/ровл                                                   |                             |                             |                          |                             | E55168                  |   | DB 2;          | hes          |           |            |
|                  | 14              | )<br>guen                         | nota                |                   |              | a; A                                                    | trep                                                               |                  |    |                    |                | h<br>L.                                                         | , Be                                               | enes                                                                 |              | nBan                                                    |     |                    |                |                                      | nBan                                                     |                             |                             |                          |                             | R2A2                    |   | 2              | Mismatches   |           |            |
|                  | PRT;            | Created)<br>Last sequence update) | Last an             | N.                |              | bacteri                                                 | neae; S                                                            |                  |    |                    |                | Westric                                                         | nzel J.                                            | erase g                                                              |              | EMBL/Ge                                                 |     |                    |                | hold A.                              | EMBL/Ge                                                  |                             |                             |                          |                             |                         |   | Score 7; DB 2; | 0            |           | ٠          |
|                  | ARY;            | el. 13,                           | TrEMBLrel. 17, Last | 16.3 KDA PROTEIN. |              | ; Actino                                                | eptomyci                                                           |                  |    |                    |                | ter D.,                                                         | K., Kue                                            | l transf                                                             |              | to the                                                  |     |                    |                | ., Becht                             | to the                                                   | 0212.1;                     | DUF24.                      |                          | F24; 1.                     | 148 AA: 16268 MW:       |   | 50.08;         |              |           |            |
|                  | PRELIMINARY;    | (TrEMBLrel.                       | (Tremblr            | 16.3 KD           | fradiae.     | rmicutes                                                | les; Str                                                           | 906;             |    | M N.A.             | 7;             | Hoffmeis                                                        | Bindseil                                           | glycosy                                                              | A.";         | CT-1999)                                                |     | M N.A.             | 7;             | strich L                             | UL-1999)                                                 | 61; AAF0                    | R002577;                    | 8; DUF.24                | 4032; DU                    | 48 AA                   |   | ]arit          | Conservative | 7         | 98         |
| T 1              | 9RPA4<br>9RPA4; | 01-MAY-2000                       | 01-JUN-2001         | HYPOTHETICAL      | Streptomyces | Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; | Actinomyceta                                                       | NCBI_TaxID=1906; | [] | SEQUENCE FROM N.A. | STRAIN=T#2717; | Trefzer A.,                                                     | Fuchser J., Bindseil K., Kuenzel J., Bechthold A.; | "Function of                                                         | of urdamycin | Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases | [2] | SEQUENCE FROM N.A. | STRAIN=T#2717; | Faust B., Westrich L., Bechthold A.; | Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. | EMBL; AF164961; AAF00212.1; | InterPro; IPR002577; DUF24. | Fram; FruibsB; DUFZ4; I. | ProDom; PD004032; DUF24; 1. | SECTENCE 1              |   | Query Match    | Matches 7; ( | 1 AGVVDRD | 80 AGVVDRD |
| RESULT<br>O9RPA4 | AC D            | TO<br>TO                          |                     |                   |              |                                                         |                                                                    |                  |    |                    |                |                                                                 |                                                    |                                                                      |              |                                                         |     |                    |                |                                      |                                                          |                             |                             |                          | DR<br>F                     |                         | ľ | Que            | Mat          | QY        | qq         |

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RESULT Q19635

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STREATIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-980404313; Dubmed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Ouackenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loffus B.D.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., 20 cotton M.D., Spriggs T., Artiach P., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Wason T.M., Olsen G.J., Fraser C.M., Smith H.O., Weese C.R.,
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STRAIN-TM300;

Manchine-1, Lindgren P.E., Neubauer H., Goetz F.;

Pantel I., Lindgren P.E., Neubauer H., Goetz F.;

Pantel I., Lindgren P.E., Neubauer H., Goetz F.;

Identification and characterization of the Staphylococcus carnosus mitrate reductase operon.

Mol. Gen. Genet. 259:105-114(1998).

EMBL, AF02224, AAC82242.).

Pfam; PF00384; molybdopterin. I.

Pfam; PF00384; molybdopterin. I.

PROSTE: PS00551; MOLYBDOPTERIN PROK. I; UNKNOWN. I.

SEQUENCE 1224 AA; 138358 WW; 978D33279862C820 CRC64;
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Archaeo; Buryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
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Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1901 (TrEMBLrel. 17, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus carnosus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBL_TaxID+1281;
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Conservative
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MEDLINE-94150718; PubMed-7906398;
MEDLINE-94150718; PubMed-7906398;
MIJSON R., AINSCOURD R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Kershaw J., Kirsten J., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Lastster N., Latreille P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Staden R., Saunders D., Shownkeen R.
Smaldon N., Smith A., Somhhammer E., Staden R., Sulston J.,
Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"2.2 Mo of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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004387, 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MR 105,000 OUTER DYNEIN ARM DOCKING COMPLEX PROTEIN.
CDA3.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonadaceae: Chlamydomonas.
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MEDLING=97311076; PubMed=9166407;

Koutoulis A., Pazour G.J., Wilkerson C.G., Inaba K., Sheng H.,

Takada S., Witman G.B.;

"The Chlamydomonas reinhardtii ODA3 gene encodes a protein of touter dynein arm docking complex.";

C.Call Biol. 137:1069-11080(1997).

EMBL: AF001309; AAC49732.1;

EMBL: AF001309; AAC49732.1;

SEQUENCE 749 AA; 83376 MW; 8ED440836EB6DF6B CRC64;
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Pred. No. 39;
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361 AA; 41249 MW; F83965FC6C1B42C6 CRC64;
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Last sequence update)
Last annotation update)
                                                  361 AA.
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                                                  PRELIMINARY;
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EMBL; Z68161; CAA92297
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SEQUENCE
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DT 01-JUL.
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GN ODA3.
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Length 1224; 0; Indels

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Score 6;

42.98;

Query Match 42.9 Best Local Similarity 100. Matches 6; Conservative

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TRANSPOSON-WAS-TYPE, TN1546-LIKE;
MEDLINE=98195721; PubMed=9534232;
MEDLINE=98195721; PubMed=9534232;
MEDLINE=98195721; PubMed=9534232;
Minhakhin L.S., Petrova M.A., Mindlin S.Z., Volodin A.A., Kalyaeva E.S., Tiedge G.M., Hobman J.L., Brown N.L., Nikifirov V.G.;
"Horizontal spread of mer operons among gram-positive bacteria in
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-1- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                     DB 13; Length 113;
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PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
SEQUENCE 132 AA; 15988 MW; E6628416136E2A94 CRC64;
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Last sequence update)
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5. 75;
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100.0%; Pred. No. 75;
tive 0; Mismatches
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100.0%; Pred. No. 65;
tive 0; Mismatches
                    MEDLINE=97439845; PubMed=9294191;
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TRANSPOSON-TN3-TYPE, TN1546-LIKE;
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EMBL; Y09024; CAA70225.1; -.
InterPro; IPR000551; HTH_MerR.
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PRINTS; PR00040; HTHMERR.
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Matches 6; Conservative
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     TISSUE=SPIRAL INTESTINE;
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Matches 6; Conserv
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70 GWVDRD 75
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MEDLINE-9743845; PubMed=9294191;
MEDLINE-9743845; PubMed=9294191;
JOHNSEN A.H., JOENSON L., Rourke I.J., Rehfeld J.F.;
"Elasmobranchs express separate cholecystokinin and gastrin genes.";
Proc. Natl. Acad. Sci. U.S.A. 94:10221-10226(1997).
EMBL; 297360; CAB10586.1; -.
EMBL; 297360; CAB10586.1; -.
PROSITE; PRO01651; Gastrin.
PROSITE; PRO01651; Gastrin. 1.
PROSITE; PRO01651; Gastrin: 1.
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Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
"The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE001112; ABB91292.1; -.
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                                                                            InterPro; IROJ331; DUF153.
InterPro; IROJ331; DUF153.
Pfam; PF03579; DUF153; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 107 AA; 11614 MW; F6CB538BDF6D9B4B CRC64;
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GASTRIN-8.
3AECD41ACC551565 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. 65;
tive 0; Mismatches
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Squalus acanthias (Spiny dogfish).

PREPROGASTRIN

RESULT
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[1] SEQUENCE FROM N.A. NCBI\_TaxID=7797;

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SEGUENCE FROM N.A.
STAIN-WIGHT-5;
Bogdanova E.S., Minakhin L.S., Bass I.A., Hobman J.L., Brown N.L.,
Nikiforov V.G.;
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"MATCOMMENTS."
"SUBMITTED (DEC.1996) to the EMBL/GenBank/DDBJ databases.
-: SIMILARIY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL: Y09906; CAA711.
INTERPO: JERO00551, HTH_MERR.
SMART; SM00422; HTH_MERR.
SMART; SM00422; HTH_MERR.
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SMART; SM00422; HTH_ME
Nikiforov V.G.;
"Mercoury transposons in Gram-positive bacteria in natural environments.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL REGULATORS.
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Interpro; IPRO0551; HTH MerR.
Pfan; PF00376; merR; 1.
PRINTS; PR0040; HTHMERR.
SMART; SM0422; HTH_MERR.
PROSITE; PS00552; HTH_MERR.
DNA-DINGING; Transcription regulation.
EQUADENCE 132 AA, 15929 WW; F7A88B1544DCAB28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9F4C0;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-UMAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
REGULATORY PROFEIN.
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Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=33935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 75; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 75; Matches 6; Conservative 0; Mismatches
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70 GVVDRD 75
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70 GVVDRD 75
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054602
ID 054602
AC 054602;
DT 01-JUN-
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MEDLINE-88195721; PubMed-9534232;
Bogdanova E.S., Bass I.A., Minhakhin E.S., Petrova M.A., Mindlin S.Z., Volodin A. Kalyaeva E.S., Tledge G.M., Hobman J.L., Brown N.L., Nikifirov V.G.;
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STRAIN=FA6-12;
Bogdanova E.S., Minakhin L.S., Bass I.A., Hobman J.L., Brown N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Horizontal spread of mer operons among gram-positive bacteria in atural environments.";
Microbiology 144:609-620(1998).
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-!-SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL: x99457; CAA67018.1; -.
PITALEPRO; IPRO00551; HTH_MerR.
PRINTS; PRO0040; HTHWERR.
PRINTS; ROMO042; HTH_MERR.
PROSTE; PSO0525; HTH_MERR.
PROSTE; PSO0525; HTH_MERR.
PROSTE; PSO0525; HTH_MERR.
PROSTE; PSO0542; HTH_MERR.
PROSTE; PSO0544; HTH_MERR.
PROSTE; PSO0544; HTM, MERR.
PROSTE; PSO0545; HTM, MERR.
PSO0545; HTM, MERR.
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PSO0545; HTM, MERR.
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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Last annotation update)
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Bacillus/Staphylococcus group; Exiguobacterium.
NCBL_TaxID=44751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus licheniformis.

Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.

NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 42.9%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
MERR.
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086214;
01-NOY-1998 (TrEMBLEEL: 08, C.
01-NOY-1998 (TrEMBLEEL: 08, L.
01-JUN-2001 (TrEMBLEEL: 17, L.
REGULATORY PROTEIN.
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70 GVVDRD 75
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Bacteria; Firm
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AC 09F4C7
AC 09F4C7
DT 01-MAR-
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Ng W.L., DasSarma S.;
"Minimal replication origin of the 200-kilobase Halobacterium plasmid
pNRC100.";
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Ng W.L., DasSarma S.;
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MEDLINE-93012964; PubMed-1398080;
Malladay J.T., NG W.L., DasSarma S.;
"Genetic transformation of a halophilic archaebacterium with a gas vesicle gene cluster restores its ability to float.";
Gene 119:131-136(1992).
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                                                                                                                                                                                 MEDLINE-88201675; PubMed=3448465;
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                                                                                    Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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MEDLINE-93139036; Pubmed-8423144;
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MEDLINE=91323716; PubMed=1864501;
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                                                  Halobacterium sp. (strain NRC-1).
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                                                                    Plasmid pNRC100
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(In) Robb F.T., Place A.R., Sowers K.R., Schreier H.J., Dassarma
                                                                                                                                  DasSarma S., Arora P., Lin F., Molinari E., Yin L.R.; "Wild-type gas vesicle formation requires at least ten genes in gyp gene cluster of Halobacterium halobium plasmid pNRC100."; J. Bacteriol. 176:7646-7652(1994).
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Ng W.L., Cluffo S.A., Smith T.M., Bumgarner R.E., Loretz C.,
Faust J., Seto J., Slagel J., Hood L., DasSarma S.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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Cold Spring Harbor Laboratory Press, New York (1995).
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Syst. Appl. Microbiol. 16:560-568(1994).
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Bacteriol. 175:4584-4596(1993).
                                                                                                        MEDLINE=95095934; PubMed=8002589;
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Ng W.L., Ciufo S.A.,
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DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE HYPOTHETICAL 32.2 KDA PROTEIN.
OS Acotobacter vinelandil.
OC Acotobacter vinelandil.
OC Acotobacter.
OX NCBI_TAXID-154;
RN 11
RP SEQUENCE FROM N.A.
C STRAIN-TRANS;
RA Dean D R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ Gatabases.
RM Hypothetical protein.
SQ SEQUENCE 287 AA; 32170 MM; 6541031DD01B7D3D CRC64;
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT TAL.

GN 17AL.

CN Pasteurella multocida.

CC Pasteurella.

CN NCBI_TAXID=747;
RN [1]
RP SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN MAY B.J. Zhang Q. Li L.L., Paustian M.L., Whittam T.S., Kapur V.

RN MAY B.J. Zhang Q. Li L.L., Paustian multocida Pm70.";
RN Proc. Natl. Acad Scil. G. S. Ack05686;
DR Pfam; PP006198; Aransaldolase.

DR Pfam; PP006198; Aransaldolase.

DR Pfam; PP006198; Transaldolase.

DR PGOSTEE; PS00058; Transaldolase.

SQ SEQUENCE 317 AA; 35007 MM; 4DCAOCFED73458DA CRC64;
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Matches 6; Conservative 0; Mismatches 0; Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AZ297529; CAC03733.1; -. Hypothetical protein: SEQUENCE 279 AA; 31298 MW; 91473D0FE3B31491 CRC64;
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24 GVVDRD 29
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265 YTGEVK 270
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Search completed: January 31, 2002, 13:37:50 Job time: 175 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein – protein search, using sw model

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January 31, 2002, 13:20:17 ; Search time 78.64 Seconds (without alignments) 13:561 Million cell updates/sec

1 AGVVDRDYTGEVKV 14 US-08-957-709-79 Perfect score: Sequence:

OFICO Scoring table: 219241 seqs, 76174552 residues Searched:

Gapop 60.0 , Gapext 60.0

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219241 Total number of hits satisfying chosen parameters: Word size

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | Description | dUTP pyrophosphata | hypothetical prote |        | conserved hypothet | ATP synthase F1, c |        | mercuric resistanc | regulatory protein | merR1 protein [imp | hypothetical prote |        | ω.     | transaldolase B [i | hypothetical prote |        | probable acyl-CoA | related to INORGAN | probable acyl-CoA | hypothetical prote | hypothetical prote | anthranilate synth | anthranilate synth | aldehydeferredox | aldehydeferredox | probable hydroxama | connectin 1 - chic | isoleucyl-tRNA syn | DNA-directed RNA p | prot   |
|-----------------------------------------|-------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------|
| SUMMARIES                               | 1D          | S38189             | T21136             | T08101 | A69547             | C71855             | C64661 | A32239             | T45509             | T44501             | E64126             | T08285 | S40535 | H85480             | T40385             | н82308 | F83496            | T51225             | E83213            | T45863             | B83295             | G81892             | E81132             | A75101           | G71072           | C83588             | PN0689             | D82293             | C82923             | G86643 |
| 2                                       | 9 :         | 7                  | ď                  | ~      | ~                  | N                  | 7      | ~                  | ~                  | ~                  | 7                  | 7      | 7      | ~                  | 7                  | 7      | 7                 | 7                  | 7                 | ~                  | 7                  | 7                  | ~                  | ~                | 7                | 7                  | ~                  | <b>⊘</b> 1         | ~                  | ~      |
| 1                                       | Leng Li     | 147                | 361                | 749    | 107                | 123                | 124    | 132                | 132                | 132                | 185                | 206    | 317    | 317                | 355                | 376    | 379               | 387                | 394               | 406                | 438                | 491                | 491                | 621              | 625              | 802                | 811                | 949                | 1434               | 1983   |
| &<br>Query                              | Maccil      | 100.0              | 50.0               | 50.0   | 42.9               | 42.9               | 42.9   | 42.9               | 42.9               | 42.9               | 42.9               | 42.9   | 42.9   |                    | 42.9               | 42.9   |                   | 42.9               | -:                | ٠.                 | ς.                 | ٠                  |                    |                  | ٠.               | •                  | •                  | 42.9               | 42.9               | •      |
| 9                                       | 300re       | 14                 | 7                  | 7      | 9                  | 9                  | 9      | 9                  | 9                  | 9                  | <b>.</b>           | 9      | 9      | ø                  | 9                  | 9      | 9                 | 9                  | 9                 | 9                  | 9                  | 9                  | 9                  | 9                | 9                | 9                  | 9                  | 9                  | 9                  | 9      |
| Result                                  | 2           | -                  | 7                  | м      | 4                  | S                  | 9      | 7                  | 8                  | 6                  | 10                 | 11     | 12     | 13                 | 14                 | 15     | 16                | 17                 | 18                | 19                 | 20                 | 21                 | 22                 | 23               | 24               | 25                 | 56                 | 27                 | 28                 | 29     |

| hypothetical prote | connectin/titin - | titin, cardiac mus | ferredoxin (fdx-2) | hypothetical prote | hypothetical prote | hypothetical prote | exogenous DNA-bind | hypothetical prote | probable dioxygena | leghemoglobin - fa | lamellar cuticular | lamellar cuticular | Ig kappa chain V r | histidine decarbox | hypothetical prote |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T45584             | T42633            | I38344             | F69270             | E64575             | A69342             | T07551             | D30338             | T48765             | F75334             | T12133             | A37370             | B37370             | KVMSC1             | DCLBHB             | C75451             |
| 7                  | N                 | ٦                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | ٦                  | 7                  | 7                  |
| 3071               | 4162              | 26926              | 9                  | 61                 | 67                 | 77                 | 86                 | 100                | 103                | 107                | 110                | 110                | 111                | 114                | 116                |
| 42.9               | 42.9              | 42.9               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               |
| 9                  | 9                 | ဖ                  | ഗ                  | ស                  | S                  | Ŋ                  | S                  | ഗ                  | S                  | S                  | ഹ                  | ഹ                  | ស                  | Ŋ                  | Ŋ                  |
| 30                 | 31                | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

durp pyrophosphatase (EC 3.6.1.23) precursor, mitochondrial - yeast (Saccharomyces ce N;Alternate names: protein YBR1705; protein YBR252w (Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 22-Jun-1999 C;Accession: S38189; S46133; S39578; S36425 R;Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M. Yeast 9, 1131-1137, 1993 A;Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A;Reference number: S38185; MUID:94078675

A; Molecule type: DNA A; Residues: 1-147 <DOI>

<u>ст</u> A;Cross-references: GB:L20296; NID:g311101; PIDN:AAA65611.1; PID:g311106 R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, submitted to the Protein Sequence Database, August 1994

A; Reference number: \$45940
A; Accession: \$46133
A; Molecule type: DNA
A; Residues: 1-147 < AIG>
A; Cross-references: EMBL: 236121; NID: 9536670; PIDN: CAA85215.1; PID: 9536671; MIPS: YBR2
B; Gadsden, M.H.; McIntosh, E.M.; Game, J.C.; Wilson, P.J.; Haynes, R.H.
EMBO J. 12, 4455-4431, 1993
A; Title: dUTP pyrophosphatase is an essential enzyme in Saccharomyces cerevisiae.
A; Reference number: \$39578; MUID: 94038925

A; Molecule type: DNA
A; Residues: 1-9, N', 11-147 <GAD>
A; Residues: 1-9, N', 11-147 <GAD>
A; Residues: 1-9, N', 11-147 <GAD>
A; Cross-references: EMBL: X74263; NID: 9398183; PIDN: CAA52322.1; PID: 9398184
A; Cross-references: EMBL: X74263; NID: 9398183; PIDN: CAA52322.1; PID: 9398184
B; Gadsden, M.; McIntosh, E.; Game, J.; Wilson, P.; Haynes, R.
submitted to the EMBL. Data Library, July 1993
submitted to the EMBL. Data Library, July 1993
A; Reference number: S36425
A; Reference number: S36426

A; Accession: S36425

A;Molecule type: DNA A;Residues: 1-9,'N',11-95,'V',97-138,'R',140-146,'K' <GA2>

A; Cross-references: EMBL: X74263

A,Gene: SGD:DUT1 A,Cross-references: SGD:S0000456; MIPS:YBR252w A,Map position: 2R

A; Genome: nuclear

C; Superfamily: retroviral proteinase C; Keywords: hydrolase; mitochondrion; nucleotide metabolism; proteinase F:1-15/Domain: transit peptide (mitochondrion) #status predicted <TNP> F:16-147/Product: dUTP pyrophosphatase #status predicted <MAT>

Gaps ; 0 Query Match

100.0%; Score 14; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 14; Conservative 0; Mismatches 0; Indels

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Cypecies: Helicobacter pylori
Cypecies: Helicobacter pylori
Cypecies: Helicobacter pylori
Cypecies: Helicobacter pylori
A, Variety: Strain J99
Cybate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
Cybate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
CyAccession: C71855
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. ; Ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A; Reference number: A71800; MUID:99120557
A; Reference number: A71800; MUID:99120557
A; Residues: preliminary
A; Molecule type: DNA
A; Cross-references: GB.A.E001533; GB:AE001439; NID:94155636; PIDN:AAD06638.1; PID:9415
A; Experimental source: strain J99
C; Superfamily: H+-transporting ATP synthase epsilon chain
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod J. Flastchmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A. Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.

A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A; Areference number: A69250; MUID:98049343

A; Reference number: A69547

A; Reference number: A69550; MUID:98049343

A; Reduction preliminary; nucleic acid sequence not shown; translation not shown

A; Readides: L-107 < KLE>

A; Cross-references: GB:AE001112; GB:AE000782; NID:g2689435; PIDN:AAB91292.1; PID:g265

C; Superfamily: conserved hypothetical protein MJ0580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6

Godolinase F1, subunit epsilon - Helicobacter pylori (strain 26695)

C.5Actes: Helicobacter pylori
C.5Deciles: Helicobacter pylori
R.7Deciles: Helicobacter pylori
R.7Deciles: R. S. Sequence_revision 09-Aug-1997 #text_change 22-Jun-1999
C.5Accession: C.64661
R.7Deciles: R. A. S. Sequence C. S. S. September, R. A. September, R. S. September, R. S. Bordovsky, M.; Rarpk, P.D.; Shith, H.O.; Fraser, A. Aluthors: Wallin, E.; Hayes, W. S.; Bordovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A. Recence number: A64520; MUID:97394467
A. Recence number: A64520; MUID:97394467
A. Section: C64661
A. Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 12; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11arity 100.0%; Pred. No. 13; Conservative 0; Mismatches
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Best Local Similarity
Matches 6; Conserva
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22 TGEVKV 27
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16 YTGEVK 21
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PUBLIC 1999

Outer dynein arm docking complex protein ODA3 · Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change O8-Oct-1999
C;Accession: T08101
C;Clate: 21-May-1999 #sequence_revision 21-May-1999 #text_change O8-Oct-1999
C;Accession: T08101
A; Total Biol. 137, 1069-1080, 1997
A;Title: The Chlamydomonas reinhardtii ODA3 gene encodes a protein of the outer dynein a A;Reference number: 216354; MUID:97311076
A;Reference number: 216354; MUID:97311076
A;Stetus: pre-liminary: translated from GB/EMBL/DDBJ
A;Getule type: mRNA
A;Residues: 1-749 <a href="https://documber.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/result-number.com/r
                                                                                                                                                                                                                                                                           RESULT 2
T136
hypothetical protein F20C5 4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caecasion: T2136
R;Matthews, P.
Submitted to the EMBL Data Library, December 1995
A;Reference number: 219381
A;Reference number: 219381
A;Reference number: 219381
A;Reference number: 219381
A;Reference number: 219381
A;Reference number: 219381
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-361 -WIL)
A;Residues: 1-361 -WIL)
A;Residues: 1-361 -WIL)
A;Residues: 21-361 -WIL)
A;Residues:
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                                                         14
                                                                                                            81 AGVVDRDYTGEVKV 94
                                                         1 AGVVDRDYTGEVKV
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hypothetical protein HI1488 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: B64126
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
C;Accession: E64126
R;Fleischmann, R.D.; Schirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoglagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gehem, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Reference number: A64000; MUID:95350630
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A;Cross-references: GB:U32826; GB:L42023; NID:g1574322; PIDN:AAC23133.1; PID:g1574324
C;Superfamily: Haemophilus influenzae hypothetical protein H11488
                                                                                                                                                                                                                                                                                                                                   744501
merRl protein [imported] - Clostridium butyricum
C;Species: Clostridium butyricum butyricum
C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T44501
E;Narita, M.; Koizumi, T.; Huang, C.; Endo, G.
submitted to the EMBL Data Library, March 1999
A;Description: Broad-spectrum mercury resistance and its genetic characterization of
                                                                                                                              Gaps
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A;Status: nucleic acid sequence not shown; translation not shown
                                                                        Length 132;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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A;Experimental source: isolate Mersaru
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                                                                      Score 6; DB 2;
Pred. No. 14;
0; Mismatches
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C; Superfamily: transcription repressor glnR
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C;Superfamily: transcription repressor glnR
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100.0%;
                                                                                                                              Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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70 GVVDRD 75
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70 GVVDRD 75
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77 TGEVKV 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             mercuric resistance operon regulatory protein - Bacillus sp.
(Species: Bacillus sp.
C.Species: Bacillus sp.
C.Date: 12-Oct-1989 #sequence_revision 12-Oct-1989. #text_change 15-Oct-1999
C.Accession: A32239; A3227
R.Helmann, J.D.; Wang, Y.; Mahler, I.; Walsh, C.T.
J. Bacteriol. 171, 222-299, 1989
A.Title: Homologous metalloregulatory proteins from both gram-positive and gram-negative
A.Reference number: A32239; MUID:89123021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Status: preliminary; not compared with conceptual translation
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Moste S. 1-132 < HELD.
J. Bacteriol. 171, 83-92, 1989
A.Title: Nucleotide sequence of a chromosomal mercury resistance determinant from a Baci A.Reference number: A32227; MUID:89123092
                  A,Cross-references: GB:AE000619; GB:AE000511; NID:g2314276; PIDN:AAD08173.1; PID:g2314286.5. C;Genetics:
A;Start codon: GTG
C;Superfamily: H+-transporting ATP synthase epsilon chain
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C;Species: Exiguobacterium sp.
C;Date: 3. Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45509
R;Bogdanova, E.S.; Bass, I.A.; Minhakhin, L.S.; Petrova, M.A.; Mindlin, S.Z.; Volodin, A Microbiology 144, 609-620, 1998
A;Title: Horizontal spread of mer operons among Gram-positive bacteria in natural envirch A;Reference number: 222993; MUID:98195721
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A;Cross-references: EMBL:X99457; NID:g3413183; PIDN:CAA67818.1; PID:g3413184
A;Experimental source: strain TC38-2b
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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o. 14;
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100.0%; Pred. No. 14;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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A; Residues: 1-124 <TOM>
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70 GWVDRD 75
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C;Genetics:

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Apporthetical protein SPBC3E7.11c - fission yeast (Schizosaccharomyces pombe)
C)Species: Schizosaccharomyces pombe
C)Species: Schizosaccharomyces pombe
C)Accession: T40385
R)Lyne, M: Wood V. Rajandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
R)Lyne, M: Wood V. W: Rajandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
A)Reference number: 221924
A)Rocession: T40385
A; Status: preliminary; translated from GB/EMBL/DDBJ
A)Rolecule Fype: DMS
A)Rolecule Fype: DMS
A)Rolecule Fype: DMS
A)Rolecule Rype: DM
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A: Introns: 30/2; 54/3
C: Superfamily: dnaJ amino-terminal homology
F:9-75/Domain: dnaJ amino-terminal homology < DNJ>
                                                                                                                                                                                                                                           Query Match 42.9%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches
C;Superfamily: human transaldolase
C;Keywords: transferase
F;132/Active site: Lys #status predicted
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265 YTGEVK 270
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265 YTGEVK 270
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transaldolase (EC 2.2.1.2) B - Escherichia coli
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Species: Secherichia coli
C;Species: 13-3an-1995 sesquence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: $40535; #64720
C;Accession: $40535; #64720
C;Accession: $40535; #64720
R;Yura, T:; Mori, H:; Nagal, 
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C;Superfamily: Halobacterium plasmid pNRC100 hypothetical protein H0748
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RESULT 15
H82308
oxaloactate decarboxylase, beta chain VC0551 [imported] - Vibrio cholerae (strain N1696 c; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: H82308
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
A; Reference number: A82035; MUID:20406833
A; Residuee: 1.376 <a href="https://documents/record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-record-reco
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A;Map position: 1
C;Superfamily: Propionigenium modestum methylmalonyl-CoA decarboxylase beta chain
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5 VVDRDY 10
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Scoring table:

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Database :

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Polymerase enhancing factor proteins, extracts and complexes -
improve the polymerisation activity of nucleic acid polymerases,
use in amplification, sequencing and replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymerase enhancing factor; PEF; dUTPase; PCR; amplification; sequencing; replication.
                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
AAY01519
AAU05396
AAW25728
AAB37654
AAB37655
AAW82454
AAM19992
AAM33697
                                                                                  AAR56632
AAR56631
AAG18871
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AAG61462
AAG04411
AAB16405
AAW77684
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AAW28215
AAM17893.
AAM30402
AAM05546
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AAG41380
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AAG32119
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AAB79203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast dUTPase uridine-binding motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW72855 standard; Peptide; 14 AA.
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97US-0822774
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 1462
26926
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                               Hansen CJ, Hogrefe H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRA-) STRATAGENE.
 W09842860-A1.
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  AAW72855;
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  RESULT
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Human ORFX ORF110
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UDP-N-acetylglucos
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Staphyloccus aureu
                                                                       Search time 140.03 Seconds (without alignments)
7.406 Million cell updates/sec
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/ SIDSZ/gcgdata/geneseq/geneseqp/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gcgdata/geneseg/geneseqp/AA2000.DAT:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         522463 seqs, 74073290 residues
                                                                       January 31, 2002, 13:18:13;
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                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries
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AAW26735
AAW27783
AAW20256
AAW96156
AAW96156
AAY70130
AAY70137
AAY34508
AAY34508
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Maximum DB seq length: 200000000
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Match Length
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                         This is the uridine-binding motif of yeast dUTPase. Sequences are provided (see ANW72849-57) of the uridine-binding motifs of the dUTPases and dCTP deaminases of Pyrococcus furiosus (see also Escherichia coli, yeast, human and herpesvirus; a consensus (see ANW72843) is also provided. A claimed method of enhancing a nucleic acid polymerase reaction comprises performing the reaction in the presence of one or more of the following: a polymerase enhancing protein having one or more of the following: a polymerase enhancing protein having one or more of the sequences provided in ANW72848-57. Sequences pivon in ANW72848-57. Kits are provided for replicating sequences given in ANW72848-57. Kits are provided for replicating sequencing or for site-directed mutagenesis, for nucleic acid sequencing or for amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                            Query Match

100.0%; Score 14; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ORFX ORF110 polypeptide sequence SEQ ID NO:220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB40346 standard; Protein; 102 AA.
Claim 71; Page 47; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127728.
05-APR-2000; 2000US-0540763.
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N-PSDB: AAC74555.
                                                                                                                                                                                                                                                                 14 AA;
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which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX acquences have activities such as: cytostatic; hepatotropic; vulnerary; antipportiatic; antiportiant; antiartitic; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; antidiabetic; hypotensive; dermatological; immunosuppressant; antidiabetic; hypotensive; dermatological; antidiabetic; hypotensive; dermatological; antidiabetic; hypotensive; dermatological; antidiabetic; predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy; or politicative disorders, neurodegenerative disorders, neurodegenerative disorders, neurodegenerative disorders, osteoarthitis, graft vs host disease, cardiovascular disease, osteoarthitis, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus cryterial or fungal infection, malaria, autoimmune disorders, asthma, allories, benefit and cartilage damage, nocturnal haemoglobinuria, antilifanmatory disease; to enhance compliant in thrombosis; and as contraceptive.
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Novel nucleic acids and peptides derived from open reading frame X, sasful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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50.0%; Score 7; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                             Claim 11; Page 547-548; 5507pp; English.
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N-PSDB; AAT99449.
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Pantel I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               based on homology with an Acinetobacter calcoaceticus protein, is believed to be a UDP-N-acetylglucosamine l-carboxyvinyltransferase (enoy)pyruvate transferase, UDP-N-acetylglucosamine enoy)pyruvyl transferase). The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents a Staphylococcus aureus protein, that,
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - nsed
Recombinant S. carnosus nitrate and nitrite reductase proteins - useful for reducing nitrate and nitrite in nitrate-polluted material
                                                                        This protein comprises the G subunit of nitrate reductase NarGHJ encoded by nuclectides 4140-7814 of an isolated nitrite reductase and nitrate reductase gene region (see AAT99449) of Staphylococus carnosus. The invention relates to recombinant proteins (see AAW26733-49) involved in the reduction of nitrate and nitrite in Scarnosus, and the use of these proteins, or cells enroding them, in free or immumobilised form to reduce nitrate and nitrite in water, vegetables and other nitrate and/or nitrite polluted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide(s) from Staphylococcus aureus strain WCUH29 slate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                          DB 18; Length 1224;
                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                    100.0%; Preu. ...
                                                                                                                                                                                                                                                                                        Score 7; 1
Pred. No.
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                                             Claim 1; Page 29-32; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW27783 standard; Protein; 44 AA
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Matches 7; Conservative
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Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-424969/39.
                                                                                                                                                                                                                                           1224 AA;
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|875 vvdrdyt 881
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                                                                                                                                                                                                            materials
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                        Query Match
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expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is a H. pylori outer membrane protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial and the predicted coding regions defined by computer evaluation. To identify likely H. pylori artigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant beneated to to the known or exported membrane proteins. Having identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic, vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and defermined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
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                                                                                                                                                                                                            Length 44;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                            DB 18;
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                                                                                                                                                                                                        Score 6; DB 18; Pred. No. 9.7; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  AAW20256 standard; Protein; 124 AA.
                                                                                                                                                                                             42.9%; Scc.
100.0%; Pred
0; A
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95US-0487032.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                          44 AA;
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                     Staphyloccus aureus MurA protein fragment from open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus aureus UDP-N-acetylglucosamine enolpyruvitransferase (murA) polypeptides and polynucleotides -useful as diagnostic reagents and for prevention and treatment of Streptococcus aureus infections
                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus; murA; anitbodies; antibiotics; therapy; Infection; UDP-N-acetylglucosamine enolpyruvitransferase; diagnosis; bacteriocidal; bacteriostatic; osteomyelitis; septic arthritis; septic thrombophlebitis; acute bacterialendocarditis; toxic shock syndrome; scalded skin syndrome; food poisoning; treatment;
                                                              DB 18; Length 124; . 24;
                                                                                              0; Indels
                                                            42.9%; Score 6; DB 1
100.0%; Pred. No. 24;
Live 0; Mismatches
                                                                                                                                                                                                                                       AAW96156 standard; Protein; 252 AA.
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                                                                                                                                                                                                                                                                                                       (first entry)
                                                              Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
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             124 AA;
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                                                                                                                          8 YTGEVK 13
                                                                                                                                                      17 ytgevk 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogen.
                                                                                                                                                                                                                                                                       AAW96156;
               Sequence
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus aureus UDP-N-acetylglucosamine enolpyruvitransferase (murA) polypeptides and polynucleotides -useful as diagnostic reagents and for prevention and treatment of Streptococcus aureus infections
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                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus; murA; anitbody; antiblotic; therapy; infection; UDP-N-acetylglucosamine enolpyruvltransferase; diagnosis; bacteriocidal; bacteriostatic; osteomyelitis; septic arthritis; septic thrombophlebitis; food polsoning; acute bacterialendocarditis; toxic shock syndrome; scalded skin syndrome; treatment; immunogen.
                Length 252;
                                                  0; Indels
                DB 20;
5. 45;
              42.9%; Score 6; DB 2
100.0%; Pred. No. 45;
iive 0; Mismatches
                                                                                                                                                                                                    AAW96155 standard; Protein; 421 AA.
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                                                                                                                                                                                                                                                                                                        Staphyloccus aureus MurA protein.
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Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
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                                                                                9 TGEVKV 14
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Length 421;

DB 20;

Score 6;

42.98;

Query Match

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The present sequence is a MurA protein from Staphylococous aureus genomic DNA library. The protein has UDP-N-acetylglucosamine 1-carboxyvinyltransferase activity.

The present sequence is useful in preparation of vaccines for prevention or attenuation of Staphylococcal infections (especially Saureus infections) which may cause conditions such as neonatal conjunctivitis, osteomyelitis, skin infections and toxic shock syndrome. The present sequence is also useful for detecting Staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus polypeptide useful for preventing or attenuating a Staphylococcal infection comprises one of 32 sequences of 100-1277 amino acids or their fragments
                                                                                      Vaccine; antibacterial; prevention; attenuation; detection; staphylococcal infection; neonatal conjunctivitis; skin infection; toxic shock syndrome; osteomyalitis; MurA; UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
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                                                     Staphylococcus aureus MurA protein (HGS016).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 14; 144pp; English.
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                     06-JUN-2000 (first entry)
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                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                     Bailey CC, Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-237864/20.
N-PSDB; AAZ51222.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus polypeptide useful for preventing or attenuating a Staphylococcal infection comprises one of 32 sequences of 100-1277 amino acids or their fragments
                     Gaps
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                   Indels
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                                                                                                                                                                                                                                                                               Staphylococcus aureus MurA protein (HGS004).
   Pred. No. 71;
                     Mismatches
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100.0%; Pred. No. 71;
Live 0; Mismatches
                                                                                                                                                                        AAY70130 standard; Protein; 421 AA.
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                   ;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US19726
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                                                                                                                                                                                                                                           06-JUN-2000 (first entry)
                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-237864/20.
 Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                    13 tgevkv 18
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|3 tgevkv 18
                                                    9 TGEVKV 14
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                                                                                                                                                                                                           AAY70130;
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RESULT
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(CSLC-) CSL LTD.
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                       23-APR-1998;
05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
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                                                                                                                                  gingivitis
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                                                                                                                                                                                                           AAX91536 to AAX91801 encode two hundred and sixty six antigenic borphorymonas gingivalis (PG) polypeptide sequences given in AAX94318 to AAX91802 to AAX91809 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial extivity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; antigenic.
                                                                                                                           MA;
                                                                                                                                                                        preventing
                                                                                                                                                                                                                                                                                                                 Length 867;
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                                                                                                                           Margetts MB,
                                                                                                                                                                       Antigenic Porphorymonas gingivalis peptides gingivitis
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Pred. No.
                                                                                                                                                                                              Claim 1; Page 491-492; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphorymonas gingivalis protein PG47.
                                                                                                                                                                                                                                                                                                                                                                                                   AAY34381 standard; Protein; 875 AA.
                                                                                                                          DM,
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100.08; Pre
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                    98AU-0005028.
97AU-0001182.
98AU-0001546.
98AU-0002564.
98AU-0002211.
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97AU-0000839.
97AU-0001182.
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98AU-0003654.
98AU-0004917.
       98WO-AU01023
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphorymonas gingivalis
                                                                                                                        Agius CT, Barr IG,
Ross BC, Rothel LJ,
                                                                                                                                                WPI; 1999-385613/32.
N-PSDB; AAX91726.
                                                                                                                                                                                                                                                                                          867 AA
                                                                                                          (CSLC-) CSL LTD.
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522 rdytge 527
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                     04 - AUG - 1998;
10 - DEC - 1997;
31 - DEC - 1997;
30 - JAN - 1998;
10 - MAR - 1998;
05 - APR - 1998;
05 - MAY - 1998;
22 - MAY - 1998;
29 - JUL - 1998;
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10-DEC-1997;
31-DEC_1997;
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       10-DEC-1998;
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AAX91536 to AAX91801 encode two hundred and sixty six antigenic borphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to AAX34583. AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebral tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A carcinogenesis-inhibiting gene - useful for genetic treatment of cerebral tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .°
                                                                                                                                                                                                  Patterson MA;
                                                                                                                                                                                                                                                                                                                                                   for preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; DB 20; Le
Pred. No. 1.3e+02;
0; Mismatches 0;
                                                                                                                                                                                                  Margetts MB,
                                                                                                                                                                                                                                                                                                                                                Antigenic Porphorymonas gingivalis peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 346-348; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY01519 standard; Protein; 1462 AA
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                                                                                                                                                                                                  DW,
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Best Local Similarity 100.0%; Pr
Matches 6; Conservative 0;
                                                                                                                                                                                               Hocking Dr
Webb EA;
                    98AU-0003128.
98AU-0003338.
98AU-0003654.
98AU-0004917.
98AU-0002911
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Ross BC, Rothel LJ,
                                                                                                                                                                                                                                                                      WPI; 1999-385613/32.
N-PSDB; AAX91599.
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N-PSDB; X026546.
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26926 AA;

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Synthetic
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                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reubi J;
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                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence representing human titin (also known as connectin)

1. State described in an invention relating to a novel method for determining

2. Whether a subject has or is at risk of developing a titin-related

3. Sample from the subject and detecting the presence of a mutation

4. The mutation in the cardiac specific exon NSB) in the

5. The pickwick mutation in the cardiac specific exon NSB) in the

6. Similar to mammalian the subject has or is at risk of

6. Similar to mammalian heart failure is used as a model. The method is

8. Similar to mammalian heart failure is used as a model. The method is

8. Useful for detecting an increased likelihood of heart disease, such as

8. Useful for detecting an increased likelihood of heart disease, such as

8. Useful for detecting on increased likelihood of heart disease, such as

8. Useful for detecting on increased likelihood of heart disease, such as

8. Useful for detecting on increased likelihood of heart disease, such as

8. Useful for detecting on increased likelihood of heart disease, such as

8. Useful for detecting on increased likelihood of heart disease, to creat

8. Conspounds that can be used to treat

8. Compounds identified using the methods may be used to treat patients

8. Compounds identified using the methods may be used to treat patients

8. Compounds identified using the methods may be used to treat patients

8. Compounds identified using the methods may be used to treat patients

8. Compounds identified using the methods may be used to treat patients
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                            The present sequence represents a protein with carcinogenesis-inhibiting activity. The gene is useful for the genetic treatment of cerebral
                                                                                                                                                                                                                                                                                                                                                                                                          Human; titin; connectin; pickwick mutation; cardiac specific exon; N2B; titin-related disease; zebrafish; heart fallure; heart disease.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining if a subject has or is at risk of developing a titin-related disease or condition, particularly heart failures, comprises detecting the presence of a mutation in the titin gene
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                                                                                                                                  Length 1462;
                                                                                                                                                             Indels
                                                                                                                                DB 20; Le
                                                                                                                               42.9%; Score 6; DB 2
100.0%; Pred. No. 2.1
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Human titin (connectin) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 57-111; 114pp; English.
                                                                                                                                                                                                                                                                                         AAU05396 standard; Protein; 26926 AA
Claim 1; Page 15-19; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-2001; 2001WO-US01212.
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                              Conservative
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                                                                                     1462 AA;
                                                                                                                               Query Match
Best Local Similarity
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                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Labelled cholecystokinin analogue 2 (CCK 25-33) for detecting tumours.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholecystokinin analogue; CCK receptor; detection; malignant; localisation; tumour; magnetic resonance imaging; MRI; label.
Length 26926;
                                                            Indels
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42.9%; Score 6; DB 22; Ls 100.0%; Pred. No. 2.8e+03; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                        AAW25728 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MLCW ) MALLINCKRODT MEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1998 (first entry)
                                                            Conservative
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   Query Match
Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                  9 TGEVKV 14
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The present invention relates to peptides showing cholecystokinin (CCK)-8 extivity, which can be used to treat neuropathies in the peripheral nervous system (PNS). The present sequence is one such peptide. The peptides of the present invention may be used to treat neuropathies in the PNS associated with diabetes mellitus, cancer treatment such as cytostatica, hearing impairment and/or visual handicap, alcohol-induced neuropathy, damage induced by surgery and dystrophy.
                                                                                                                                                                                           Antidiabetic; cytostatic; auditory; cholecystokinin-8; CCK-8; neuropathy; peripheral nervous system; diabetees mellitus; cancer treatment; cytostatica; hearing impairment; visual handicap; alcohol-induced neuropathy; dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manufacturing a medicament for treating neuropathies in the peripheral nervous system comprises use of a substance showing cholecystokinin-8 activity -
                                                                                                                                                                    Cholecystokinin peptide fragment analogue #33.
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                        'note- "Tyr-(S03Ba1/2)"
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                               /note= "Asp(OBut)"
                                                                                                                                                                                                                                                                                                                                                                                          'note= "Asp(OBut)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KARO-) KAROLINSKA INNOVATIONS AB.
                                                                                                                                                                                                                                                                                                                                                                'note= "Thr(But)"
                                                                                         AAB37654 standard; peptide; 9 AA.
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                                                                                                                                            23-MAR-2001 (first entry)
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Modified-site
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Query Match 35:7%; Score 5; DB 22; Length 9; Best Local Similarity 100.0%; Pred. No. 4.3e+05; Matches 5; Conservative 0; Mismatches 0; Indels Matches 5; Conservative 0; Mismatches 0.

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Q996d4 Q996d3 2996d5

564 AA

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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Bightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
EMBL; Z49969; CAA90270.1; -.
SEQUENCE 564 AA; 63998 MW; 1637EDDCDCC4631D CRC64;
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Last sequence update)
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Mismatches
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Pred. No.
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O76623
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100.0%; Pre
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Best Local Similarity 100.
Matches 7; Conservative
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                                        Caenorhabditis elegans.
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Q9jr33 neisseria m
O02206 caenorhabdi
Q99zkl streptococc
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                                                                      ; Search time 130.99 Seconds (without alignments) 15.633 Million cell updates/sec
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streptococc
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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sp_mammal:*
sp_mhc:*
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Lin W.C., Whitman W.B.;
Lin W.C., Whitman W.B.;
Lin W.C., Whitman W.B.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
SEQUENCE 101 AA; 11426 MW; BD7A24CFDF64152F CRC64;
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Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
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1-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 11.4 KDA PROTEIN.
HYPOTHETICAL II.4 KDA PROTEIN.
Archaea: Enryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                     Length 88;
   EMBL; AL162754; CAB84093.1; -.
InterPro; IPR003849; DUF219.
Pfam; PF02699; DUF219; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 88 AA; 9725 MW; C751556C99C8EE44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TAPOTHETICAL PROTEIN TA0304.
                                                                                                                                                                                  Ouery Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred No. 28; Matches 6; Conservative 0; Mismatches
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73 GWIDAG 78
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Q9P9E8;
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SEQUENCE FROM N.A.

STRAIN-MCS8 / SERGOROUP B;

MEDLINE-2017575; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Heod D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.E., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Viderback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., Complete genome sequence of Neisseria meningitidis serogroup B strain
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STRAIN-22491, SERCOTOPE 4A;
MEDLINE-2022556; PubMed-10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morell G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Sprath B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
menigitidis 22491.";
Nature 404:502-506(2000).
                                                                                                                                         O9K0J1 PRELIMINARY; PRT; 88 AA.

O9K0J1

O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)

O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)

O1-OTT-2000 (TrEMBLrel. 17, Last annotation update)

NHOGOG:

NHOGOG
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Oj-Car-2000 (Tremblrel. 15, Created)
Ol-Jun. 2001 (Tremblrel. 17, Last sequence update)
Ol-Jun. 2001 (Tremblrel. 17, Last annotation update)
NYPOTHETICAL PROTEIN NMAO811.
NMAO811.
NMAO811.
Bacteria meningitidis (serogroup A).
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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EMBL; AE002416; AAF41033.1; -.
InterPro; IPR003849; DUF219.
Pfam; PF02699; DUF219; 1.
Complete proteome.
SEQUENCE 88 AA; 9709 MW; C751556C81A8EE44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 6; DB 2;
Pred. No. 28;
0; Mismatches
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Best Local Similarity 100.0%; Pr
Matches 6; Conservative 0;
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50 AGFKGK 55
FKGKITL 8
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Gaps

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Q9NEY7 9

Q9NEY7

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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 217-96(1996).
EMBL: ALG50289; CAC1671.1.; - SEQUENCE 228 AA; 23839 MW; C4249A9CBDDIC75B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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25077 MW; 2362E8F7434D56CE CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE ESTERASE.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 62; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                      228 AA.
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MEDLINE=97000351; PubMed=8843436;
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SEQUENCE FROM N.A.
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40 IDAGFK 45
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genome sequence of the nematode C.elegans: A platform for
                                         Length 101;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1,2-DIHYDROXYNAPHTHALENE DIOXYGENASE 2 (FRAGMENT).
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100.0%; Pred. No. 33;
Live 0; Mismatches
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100.0%; Pred. No. 31;
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Science 282:2012-2018(1998).
                                    Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
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77 GWIDAG 82
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71 AGFKGK 76
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STRAIN-A3(2);
Strain A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2000) to the EMBL/GenBank/PDBJ databases.
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SETAILNEDSM 1617 / P2;
MEDLINE-SM 1617 / P2;
MEDLINE-97055432; PubMed-8899719;
Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
Liu O.Y., Penny S.L., Young F., Schenk M.E., Gaasterland T.,
Doolittle W.F., Ragan M.A., Charlebois R.L.;
"Organizational characteristics and information content of an archaeal genome: 156 kb of sequence from Sulfolobus solfataricus P2.";
MOI. Microbiol. 22:175-191(1996).
ENBL: Y08256; CAA69435.1;
ENBL: Y08256; CAA69435.1;
SEQUENCE 233 AA; 26215 MW; 5E3AE64515CAAD90 CRC64;
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09L2D4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-TW-2001 (TrEMBLrel. 17, Last annotation update)
01-TW-2001 (TrEMBLrel. 17, Last annotation update)
10-TW-2001 (TrEMBLrel. 15, Last
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Archaea: Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
NCBL_TaxID=2287;
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STRAIN-XC;

MEDLINE-97175539; PubMed-9023194;

Tsukioka Y., Yamashita Y., Oho T., Nakano Y., Koga T.;

Tsukioka Innction of the dTDP-rhamnose synthesis pathway in Streptococcus mutans.;

J. Bacteriol. 179:1126-113-1136-1134.1997).

EMBL: D78182; BAA11245.1;

SEQUENCE 232 AA; 26030 MW; D078E11994604525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 232;
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Oliver K., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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42.9%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches
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STRAIN-MAS(2);
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STRAIN-MAS(2);
STRAIN-MAS(2);
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL131187; CAB69773.1;
InterPro; IPR002781; DUF81.
FPGINS: PF01925; DUF81; 2.
Hypothetical protein.
SEQUENCE 260 AA: 25996 MW; DA0F43E1197BACE1 CRC64;
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STRAIN-BRISTOL NO.

WILSON R., Ainscough R., Anderson K., Baynes C., Berks M.,

Wilson R., Ainscough R., Anderson R., Eavel D., Coulson A.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Culson A.,

Bonfield J., Burton J., Durbin R., Favello A., Fullton L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Jones M., Kershaw J., Kirsten L., Stopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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SERAIN-BRIGTOL N2;
Waterston R:
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 021324; AAA662562.1; -.
HSSP; PR0276; 1AH4.
InterPro: IPR001395; Aldo, ket_red.
Pfam; PF00248; aldo_ket_red.
PFINTS; PR00069; ALDKETRDJASE.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
C35D10 6
Casonrhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.9%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches
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Q18483
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Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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53 GFKGKI 58
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S. Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                       Length 287;
                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL16206; CAB8239.1; -.
Interro; IRR00082; 2nf-C2H2.
Pfam; PF00096; zf-C2H2; 1.
SWART; SM00355; ZnF_C2H2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS01057; ZINC_FINGER_C2H2_2; 1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 296 AA; 32129 WW; 4B2DAABEAAIFIE9D CRC64;
PROSITE; PS00062; ALDOKETO_REDUCTASE_2; UNKNOWN_1. SEQUENCE 287 AA; 32840 MW; 9E9B4979E5F20D54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HISTONE DBACETYLASE-LIKE PROTEIN.
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                                                                                       DB 5;
3. 78;
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                                                                                  42.9%; Score 6; DB 5
100.0%; Pred. No. 78;
ive 0; Mismatches
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01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-JUN-2001 (TrEMBLrel. 17,
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                                                                Query Match
Best Local Similarity 100.0
Lace 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Aquifex aeolicus.
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31 IDAGFK 36
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Q9LZR5;
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SEQUENCE 352 AA; 37808 MW; 3BF480E6E097ACD2 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
THREONINE SYNTHASE.
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100.0%; Pred. No. 93;
tive 0; Mismatches
                                                                                                                                                                                                                                                         42.9%; Score 6; DB 2;
100.0%; Pred. No. 83;
iive 0; Mismatches
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PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: January 31, 2002, 13:37:42 Job time: 167 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392:353-358(1998).
EMBL; AE000689; AAC06690.1; -.
InterPro; IPR000634; dehydrtse_ser_thr.
InterPro; IPR001926; PALP.
Mature 392:353-358(1998).

EMBL; AE000754; AAC07589.1; -.
InterPro; IPR000205; NAD_binding.
InterPro; IPR0003099; PBH.
InterPro; IPR000594; Thir_family.
Pfam; PF02153; PBH; 1.
Complete proteome.
SEQUENCE 311 AA; 34849 MW; CCA6
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                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Lines 6; Conserve
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us-08-957-709-74.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:39:18 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec Run on:

US-08-957-709-74 14 1 AGWIDAGFKGKITL 14 Title: Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 segs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Word size :

100059

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|                               |                                    |        |        |             |                 |                  |        |        |         |                    |     |                    |       |                 |                 |                 |       |        |         |                 |        |        |                 |        |        |        |       | •              |                |                 |                 |
|-------------------------------|------------------------------------|--------|--------|-------------|-----------------|------------------|--------|--------|---------|--------------------|-----|--------------------|-------|-----------------|-----------------|-----------------|-------|--------|---------|-----------------|--------|--------|-----------------|--------|--------|--------|-------|----------------|----------------|-----------------|-----------------|
| Description                   | 872 methanococc<br>971 eubacterium |        | -      |             | x96 clostridium |                  |        |        | mus mus | P21195 oryctolagus |     | Q10499 schizosacch | _     | 749 bacteriopha | 111 saccharomyc | 6d5 homo sapien | -     |        | sorghum | 925 sorghum bic | •••    |        | 159 triticum ae |        |        |        |       | 138 pyrococcus | 280 pyrococcus | 396 rattus norv | 031 mus musculu |
| Des                           | 057872<br>P50971                   | P10356 | 057721 | P43991      | 09wx96          | P14220<br>085692 | P44513 | P12244 | P09103  | P21                | P04 | 010                | 032   | P03             | P34             | <b>09y</b>      | 046   | 09y6d6 | 009198  | P21925          | P81008 | P20158 | P20159          | P20230 | P21924 | P22798 | P3975 | 09v138         | 059280         | 968390          | P11(            |
| SUMMARIES<br>ID               | DCD_METJA<br>TRXB_EUBAC            | (EAST  | METJA  | IAEIN       | MOAA_CLOPE      | MEGEL            |        |        |         | II                 |     |                    | MYCLE |                 | YEAST           |                 | SOVIN |        | SORBI   | _SORBI          | MAIZE  |        | ī               |        |        |        | ACSU  |                | PYRHO          |                 | P15_MOUSE       |
| DB                            |                                    |        | ~4     | <del></del> |                 |                  | -      | -      | Н       | -                  | Н   | -                  | Н     | Н               | Н               | -               | Н     | Н      | Н       | -               | -      | -      | -               | -      | Н      | -      | ٦     | -              | Н              | _               | Н               |
| %<br>Query<br>Match Length DB | 204                                | 443    | 103    | 183         | 323             | 338              | 356    | 508    | 209     | 509                | 509 | 575                | 731   | 1132            | 1160            | 1785            | 1849  | 1849   | 47      | 47              | 47     | 47     | 47              | 47     | . 48   | 91     | 92    | 115            | 116            | 119             | 126             |
| &<br>Query<br>Match           | 100.0                              | 50.0   | 42.9   | · i         | 42.9            | . ~              |        | •      | ς.      |                    | ς.  | 42.9               |       |                 | ς.              | ς.              | N     | 42.9   | 35.7    | 35.7            | 35.7   | S      | 2               | 2      | S      | S      | 35.7  | S              | 35.7           | 35.7            | 35.7            |
| Score                         | 14                                 | 7      | 9      | 9           | <b>9</b> 9      | ο ο              | 9      | 9      | 9       | 9                  | 9   | 9                  | 9     | ø               | 9               | 9               | 9     | 9      | S       | 2               | S      | 2      | 2               | S      | S      | Ŋ      | Ŋ     | S              | Ŋ              | 2               | ري              |
| Result<br>No.                 | 1 2                                | m      | 4      | S V         | 9 6             | - σο             | 6      | 10     | 11      | 12                 | 13  | 14                 | 15    | 16              | 17              | 18              | 19    | 20     | 21      | 22              | 23     | 24     | 25              | 26     | 27     | 28     | 29    | 30             | 31             | 32              | 33              |

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Gaps

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Query Match 100.0%; Score 14; DB 1; Length 204; Best Local Similarity 100.0%; Pred. No. 6.9e-08; Matches 14; Conservative 0; Mismatches 0; Indels

1 AGWIDAGFKGKITL 14

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| 047274 escherichia P47656 mycoplasma P75179 mycoplasma P53937 saccharomyc 092ww bacteriopha 048429 bacteriopha P52299 xenopus lae 09tlu3 bacteriopha 05873 methanococc 045234 bradyrhizob P5298 homo sapien 005642 sulfolobus | ALIGNMENTS  T. 1  DCD_MSTATA STANDARD: PRT; 204 AA. DCD_MSTATA DCD_MSTATA STANDARD: PRT; 204 AA. DCD_MSTATA D1.NOV-1997 (Rel. 35, Care ted) D1.NOV-1997 (Rel. 35, Last sequence update) DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD_MSTATA DCD |
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| REQ1_ECOLI<br>RS9_MYCGE<br>RS9_MYCGE<br>RS9_MYCGE<br>YN11_YEAST<br>REGQ_BPH13<br>CB2_XENLA<br>CB2_XENLA<br>CB2_XENLA<br>CB3_ERAJA<br>CS55_BRAJA<br>CS55_BRAJA<br>CS55_BRAJA                                                   | PRT;  uence otatio PHATE  43067  87; Zho erald instoc Weidma weidma weterso st M.A h H.O. h H.O. b DCTP inster inse. inse.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| REQ1<br>RS9<br>1 XN11<br>YN11<br>YN11<br>YN11<br>CB20<br>CB20<br>CB20<br>CB20<br>CB20                                                                                                                                         | Created) Last seque Last annot TILIST Seque Last annot TILIST Seque Last annot TILIST Seque Last annot TILIST Seque Linist |
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| 1122<br>1132<br>1132<br>1144<br>1144<br>1146<br>1146<br>1156                                                                                                                                                                  | STANDARD;  1. 35, Created)  1. 35, Last sec.  1. 40, Last and YTIDINE TRIPHOS  annaschii.  chaeota; Methar  chaeota; Methar  sec J.A., Fitz  ake J.A., Fitz  ake J.A., Fitz  ake J.A., Smit  sest C.M., Smit  sest |
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| 334<br>337<br>34<br>44<br>54<br>54<br>54<br>54<br>54                                                                                                                                                                          | RESULT DOCUMENTA DOTA DOTA DOTA DOTA DOTA DOTA DOTA DO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institutes are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   STRAIN-DSM 3953;
MEDLINE-9409119; PubMed-8223622;
Luebbers M., Andreesen J.R., The Components of glycine reductase from Eubacterium acidaminophilum. Cloning, sequencing and identification of the genes for thioredoxin reductase, thioredoxin and selenoprotein PA.";
Eur. J. Blochem. 217:791-798(1993).
                                                                                                                                          Eubacterium acidaminophilum.
Bubacterium: Firmicutes: Bacillus/Clostridium group; Clostridiaceae;
Eubacterium.
NCBL_TaxID-1731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 315;
                                                                                                                                                                                                                                                                                                       REVISION TO 275.
Andreesen J.R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                               01-6CT-1996 (Rel. 34, Created)
01-6CT-1996 (Rel. 34, Last sequence update)
01-6CT-1996 (Rel. 39, Last annotation update)
THIOREDOXIN REDUCTASE (EC 1.6.4.5) (TRXR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; DB 1;
Pred. No. 1.5;
0; Mismatches
                                                           315 AA.
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Interpro; IPR000103; Pyridine_redox_2.
Fam; PF00070; pyr_redox; 1.
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Best Local Similarity 100.0%; Powatches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L04500; AAB93303.1; -. HSSP; P09625; 1TDF.
131 AGWIDAGFKGKITL 144
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                         TRXB_EUBAC
P50971;
                                    RESULT 2
FRXB_EUBAC
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MEDLINE-90258894; PubMed=2166592;

MEDLINE-90258894; PubMed=2166592;

MEDLINE-90258894 PubMed=2166592;

Divergent overlapping transcripts at the PET122 locus in Saccharomycos cerevisiae...

Saccharomycos cerevisiae...

Mol. Cell. Biol. 10:3077-3035(1990).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AB330;
MEDLINE=89083497; PubMed=2849752;
Ohmen J.D., Kloeckener-Gruissem B., McEwen J.E.;
Ohmen J.D., Kloeckener-Gruissem B., McEwen J.E.;
"Molecular cloning and nucleotide sequence of the nuclear PET122 gene required for expression of the mitochondrial COX3 gene in S.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=S286/ AB972;
STRAIN=S286 / AB972;
Avain=S286 / AB972;
Avain=S286 / Ab972;
Avaines E., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
Chung E., Duncan M., Guzman E., Haricke-Smith S.,
Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                           01-MAR-1989 (Rel. 10, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HYPOTHETICAL 49.5 KBA PROTEIN IN UBP3-PET122 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 443;
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443 AA; 49490 MW; BCA67A4D3B9D7A14 CRC64;
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100.0%; Pred. No. 1.9;
iive 0; Mismatches
   443 AA.
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Nucleic Acids Res. 16:10783-10802(1988).
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   PRT;
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Best Local Similarity 100.
Matches 7; Conservative
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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SGD; S0000954; YER152C.
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SEQUENCE 44
YEY2_YEAST
P10356;
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Y273_METJA
ID Y273_METJA
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Gaps

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MOAA_CLOPE
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                                                                                                                                                                                                                                                                                Query Match
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MOAA_CLOPE
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                                                                                                                                                    ARAIN-JAL. / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8668087;
MEDLINE-96337999; PubMed-8668087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hill H.O., Woese C.R., Venter J.C.;
Klonk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MBDLINE-95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                             Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 103 AA; 11972 MW; BDE81755780AF7EB CRC64;
           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APOTHETICAL PROFEIN MU0273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
40, Last annotation update)
HYPOTHETICAL PROTEIN H10389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 6; DB 1
100.0%; Pred. No. 6.5
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                    Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67482; AAB98261.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=2190;
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                                                                                                        Methanococcus
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF MOLYBDOPTERIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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--- PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE MOAA / NIFB / PQQE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities 10.5
or send an email continue.

Rembl, AB07192; BAA76928.1; -.
Rembl, AB07192; BAA76928.1; -.
DR InterPro; IPR000385; MoaA_NifB_PqqE.
DR Pfam: PF01444; MoaA_NifB_PqqE.
DR PROSITE; PS01305; MoaA_NifB_PqqE.
DR PROSITE; PS01305; MoaA_NifB_PqqE.
DR Prosite; PS01305; MoaA_NifB_PqqE.
DR Pfam: PF01444.
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                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. 602C303C10A9B61B CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 6; DB 1; 100.0%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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183 AA; 21170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32722; AAC22047.1; -.
                                                                                                                                                                                                               Science 269:496-512(1995).
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Matches 6; Conserv
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NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 KGKITL 14
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KGKITL 7
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                                                             /enter J.C.;
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                                                                                                                                                                                                                         Megasphaera elsdenii.
Bacteria; Firmicutes; Bacillus/Clostridium group; Sporomusa subbranch;
                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT (ALPHA-ETF) (ELECTRON TRANSFER FLAVOPROTEIN LARGE SUBUNIT) (ETFLS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mino de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania del compania de la compania del compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania de la compania del compania del compania de la compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del compania del com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF072475; AAC31170.1; -.
InterPro; IFR001308; ETF_alpha.
Pfam; PF00766; ETF_alpha. 1.
PROSITE; PS00696; ETF_ALPHA; FALSE_NEG.
Electron transport; Flavoprotein; FAD.
NP_BIND
NP_BIND
SEQUENCE 338 AA; 36124 MW; 63FBD4CCFILLAE77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
o. 16;
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                          338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.9%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No.16;
Best Ches 6; Conservative 0; Mismatches
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STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; Pubmed=7542800;
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111111
255 AGWIDA 260
                                                                                                                                                                                                                                                                              Megasphaera.
NCBI_TaxID=907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGWIDA 6
                       ETFA_MEGEL
085692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
Wales R., Newman B.J., Pappin D., Gray J.C.;
"The extinist 33 kDa polypeptide of the oxygen-evolving complex of photosystem II is a putative calcium-binding protein and is encoded by a multi-gene family in pea."
a multi-gene family in pea."
plant Mol. Biol. 12:439-45[[1989].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pisum sativum (Garden pea)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Embales; Fabaceae; Papilionoideae; Vicleae; Pisum.
NCBI_TaxID=1888;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                     01-JÄN-1990 (Rel. 13, Created)
01-JÄN-1990 (Rel. 13, Last Sequence update)
01-JÄN-1990 (Rel. 13, Last Sequence update)
01-JGS-2001 (Rel. 140, Last annotation update)
0XYGEN-EVOLVING ENHANCER PROTEIN 1, CHLÖROPLAST PRECURSOR (OEE1) (33
KDA SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (OEC 33 KDA
SUBUNIT) (33 KDA THYLANCID MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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OXYGEN-EVOLVING ENHANCER PROTEIN
8F5F787616C5D8E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
Thylakoid; Membrane; Manganese.
TRANSIT 1 81 CHLOROPLAST (BY SIMILARITY).
Length 323;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 329;
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches
42.9%; Score 6; DB 1;
100.0%; Pred. No. 16;
ive 0; Mismatches
                                                                                                                                                                                                                                                                        329 AA
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S04132; S04132.
Mendel; 16708; PISsa;PsbO;mn16708.
InterPro; IPR002628; MSP.
Pfam; PF01716; MSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X15350; CAA33408.1; -. EMBL; D13297; BAA02554.1; -.
Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 AA;
                                                                                                                               234 GFKGKI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111111
278 KGKITL 283
                                                                                               7 GFKGKI 12
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Gaps

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SEQUENCE

RESULT . 8

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                                                                                                                                                                                                                                        of the ER.";
Cell 54:1053-1060(1988).
-!- FUNCTION: TRANSFER THE POLYSACCHARIDE SIDE-CHAINS OF GLYCOPROTEINS
-!- TO AN ASPARAGINE RESIDUE OF ASN-X-SER/THR SITES IN NASCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fiterPro; irno.

Pram; Pro0085; thiored; 4.

PRINTS; PR00421; THIOREDOXIN.

PROSITE; PS00014; ER_TARGET; 1.

PROSITE; PS00194; THIOREDOXIN; 1.

PROSITE; PS00194; THIOREDOXIN; 1.

PROSITE; PS00194; THIOREDOXIN; 1.

PROFITE; PS00194; THIOREDOXIN; 1.

PROFITE; PS00194; THIOREDOXIN; 1.
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88327849; Pubmed=2458190;
Geetha-Habib M., Noiva R., Kaplan H.A., Lennarz W.J.;
Glycosylation site binding protein, a component of oligosaccharyl transferase, is highly similar to three other 57 kd luminal proteins
                                                                                                                                                                                                                                                                                                                             PROTEINS.

CATALYTIC ACTIVITY: DOLICHYL DIPHOSPHOOLIGOSACCHARIDE + PROTEIN
L-ASPARAGINE = DOLICHYL DIPHOSPHATE + A GLYCOPROTEIN WITH THE
OLIGOSACCHARIDE CHAIN ATTACHED BY GLYCOSAMINE LINKAGE TO PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
20-AUG-2001 (Rel. 40, Last amnotation update)
PROYELN DISOULFIDE ISOMEARE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-
HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
PREVENT SECRETION FROM ER.
D2BAOE5872BE58BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: TO PROTEIN DISULFIDE ISOMERASE.
-!- SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.9%; Score 6; DB 1; 100.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000886; ER_target.
InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 2.
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
508
55
401
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                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 GFKGKI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GFKGKI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (P55) (ERP59).
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P09103;
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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ID_MOUSE_
AC P0910
DT 01-MA
DT 20-AU
DE HYDRC
DE (P55)
GN PDIA1
CO EURAIT
OC BURAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                             Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fubraman J.L., Geoghagen N.S.M., Grebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12244;
01-0CT-1989 (Rel. 12, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last anoquation update)
DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE PRECURSOR (EC 2.4.1.119) (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
                                                                                                                                                                                                                                                                                                    STRAIN-NTHI TN106;
MEDLINE-95012644; PubMed-7927717;
Sanders J.D., Cope L.D., Hansen E.J.;
"Identification of a locus involved in the utilization of iron by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                              Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S -> A (IN STRAIN TN106).
V -> I (IN STRAIN TN106).
S -> A (IN STRAIN TN106).
R -> K (IN STRAIN TN106).
S -> A (IN STRAIN TN106).
S -> A (IN STRAIN TN106).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00211; ABC_TRANSPORTER; 1.
Iron transport; Inner membrane; Transport; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 17. ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interpro: IPR003593; AAA.
Interpro: IPR003439; ABC_transportr.
Interpro: IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40360 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32695; AAC21775.1; -. EMBL; S72674; AAB32112.1; -. HSSP; P13569; INBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.98;
                                                                                                                                                                                                                                        Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00005; ABC_tran; 1
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABC TRANSPORTERS).
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                                                                                                                                                                            Venter J.C.;
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Gaps

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RESULT 10 GSBP\_CHICK ID GSBP\_CI AC P12244 DT 01-0CT DT 01-FEB DT 01-FEB DT 001-FEB DE DOLICHI DE CC 2.4

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Length 508; 0; Indels

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REMBL, J05602; AAA...

REMBL, J05602; AAA...

DR PIR, A38362.

DR HSSP, P07237; IMEK.

BR HSSP, P07237; IMEK.

DR RICEPPO; IPR000086; ER_target.

DR PRO0081; THIOREDOXIN.

DR PROSITE; PS00014; ER_TARGET; 1.

DR PROSITE; PS00014; FHIOREDOXIN.

DR PROSITE; PS00014; PHIOREDOXIN.

REGOX.active center; Isomerase; Endoplasmic reticulum; Repeat; Signal.

FT SIGNAL 1 50 POTENTIAL.

FT SIGNAL 1 50 POTENTIAL.

THIOREDOXIN: 2.

REDOX.ACTIVE (BY SIMILARITY).

1 50 PREVENT SECRETION FROM ER.

THAIN REDOX.ACTIVE (BY SIMILARITY).

50 PREVENT SECRETION FROM ER.

1 ONW; 093C8C18E209BAB5 CRC64;
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Filegel L. Newton E., Burns K., Michalak M.;

Indian Delay C. Chan and Company C. Burns K., Michalak M.;

Indian 265:15502(1990).

Indian 265:15496-15502(1990).

Indian 265:15496-15502(1990).

Indian 265:15496-15502(1990).

Indian E. CATALYLIC ACTIVITY: PROCEINAGE WITH THE NATIVE STRUCTURES.

Indian TRANS-4-HYDROXY L.PROLINE + 2-OXGLUTARATE + O(2).

Indian TRANS-4-HYDROXY L.PROLINE + SUCCINARE + CO(2).

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P04785; P13700;
13-AGG-1987 (Rel. 05, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
PROTEIN DISULEIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN)
(THYROXINE DEIODINASE) (EC 3.8.1.4) (IODOTHYRONINE 5'-MONODEIODINASE)
      20-ANG-2001 (Rel. 40, Last annotation update)
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-
HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINNING PROTEIN)
                                                                                                                        Oryctolagus cuniculus (Rabbit).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   norvegicus (Rat).
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282 GFKGKI 287
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                                                                                                           OR P4HB.
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                                                                                                                                                                                                                                                                                                          MEDINE-SOUTON: PubMed-2295602;
MEDINE-SOUTONOUT: PubMed-2295602;
MEDINE-SOUTONOUT: PubMed-2295602;
MEDINE-SOUTONOUT: MAINT STINIVASAN M., Haugejorden S.M., Green M.;
TERP72, an abundant luminal endoplasmic reticulum protein, contains three copies of the active site sequences of protein disulfide
1 isomerase...
1 January Chem. 265:1004-1101(1990).
2 January Chem. 265:1004-1101(1990).
3 MAIOL Chem. 265:1004-1101(1990).
4 ENGTION: PDI, THE BETA SUBBNIT OF PROLYL 4-HYDROXYLASE, AND THE CATALYTIC ACTIVITY: PRARRANGEMENT OF BOTH INTRACHAIN & INTERCHAIN DISULFIDE BONDS IN PROCELAGEN L-PROLINE + 2-OXOGLUTARATE + O(2)

- PROCOLLAGEN TRANS-4-HYDROXY-L-PROLINE + SUCCINATE + CO(2).
- SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
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                                                                                                     MEDLINE-88143996; PubMed-2830592; Ghong S.-Y.; Sukuda T., Parkison C., Cheng S.-Y.; Song Q.-H., Fukuda T. Parkison C., Cheng S.-Y.; Mucleotide sequence of a full-length cDNa clone encoding a mouse cellular thyroid hormone binding protein (p55) that is homologous protein disulfide isomerase and the beta-subunit of prolyl-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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DB6B3F5851088731 CRC64;
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01 MAY-1991 (Rel. 18, Last sequence update)
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100.0%; Pred. No. 22;
:ive 0; Mismatches
                                                                                                                                                                                                                                         hydroxylase.";
Nucleic Acids Res. 16:1203-1203(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCD; MCI:97464, P4hb.
InterPro; IPR000886; ER_target.
InterPro; IPR000886; ER_target.
InterPro; IPR000885; Thiored.
Pfam; PF00085; thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00014; ER_TRRGET; 1.
PROSITE; PS00194; THIOREDOXIN.
Redox-active center; Isomerase; End
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57143 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 6; Conservative
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P21195;
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CONFLICT
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PDI_RABIT
ID PDI_RAE
AC P21195;
DT 01-MAY-
DT 01:MAY-
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                                                                                                                                                                                                                                                                                                                                                                                     Boado R.J., Chopra I.J., Flink I.L., Campbell D.A.;
"Enzyme binding-inhibiting assay for iodothyronine 5'-monodeiodinase (5'-MD) and its application to isolation of complementary deoxyribonucleic acid clones for the 5'-MD in rat liver.";
Endocrinology 123:1264-1273(1988).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                  Boado R.J., Campbell D.A., Chopra I.J.;
"Nuclocities sequence of rat liver idochyronine 5'-monodeiodinase (5'
"MD): its identity with the protein disulfide isomerase.";
Biochem. Biophys. Res. Commun. 155:1297-1304(1988).
                                                                                                                                                                                                                                                                                                                                                                    Kamataki T.; "Identification of protein disulfide isomerase and calreticulin as
                                                                         Edman J.C., Ellis L., Blacher R.W., Roth R.A., Rutter W.J.; Sequence of protein disulphide isomerase and implications of its relationship to thioredayin."; Nature 317:267-270(1985).
                                                                                                                                                                                                                                                                                                                                                          ., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
                                                                                                                                                                                                                                           MEDLINE-88296303; PubMed-2841089;
                                                                                                                                                                                                                                                                                                                                    STRAIN=LEC; TISSUE=Liver;
MEDLINE=94072621; PubMed=8251535;
                                                                MEDLINE-86014354; PubMed=3840230;
                                                                                                                                                        MEDLINE-89025800; Pubmed=3178809;
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InterPro; IRR000063; Thiored.
Pfam; PF00085; thiored; 2.
PRINTS; PR00421; THIOREDOXIN.
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PROSITE; PS00194; THIOREDOXIN;
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EMBL; X02948; CAA26675.1; -.
EMBL; M21476; AAA40619.1; -.
PIR; A24595; ISRTSS.
PIR; A31118; A31118.
PIR; S06419; S06419.
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                                                                                                                                  SEQUENCE OF 28-509 FROM N.A.
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509
                                          SEQUENCE FROM N.A.
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                       NCBI_TaxID=10116;
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                                                       TISSUE-Liver;
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PROTEIN DISULFIDE ISOMERASE

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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                 REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
PREVENT SECRETION FROM ER.
AL -> P (IN REF. 1).
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Hypothetical protein; Flavoprotein.
SEQUENCE 575 AA; 62102 MW; 82F88DDD1E12E638 CRC64;
                                                                                                                                                                   3056107F5E8B1B54 CRC64;
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01-0CT-1996 (Rel. 34, Created)
20-AUG-2001 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE FLAVOROMEN C26F1.14C.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                 42.9%; Score 6; DB 1; 100.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%; Score 6; DB 1;
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InterPro; IPR001281; Rieske.
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Pfam; PF00355; Rieske; 1.
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RESULT 15

MASZ_MYCLE STANDARD, PRT; 731 AA.

O323171

DT 30-MAY-2000 [Rel: 39, Created)

DT 30-MAY-2000 [Rel: 39, Leated)

DT 30-MAY-2000 [Rel: 39, Leated)

DT 30-MAY-2000 [Rel: 39, Leated)

DT 30-MAY-2000 [Rel: 30, Last sequence update)

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Score 6; DB 1; Pred. No. 30; 0; Mismatches 100.0%; Pr ive 0; Query Match
Best Local Similarity 100.
Matches 6; Conservative 6 AGFKGK 11

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Gaps

Length 731;

Search completed: January 31, 2002, 13:39:19 Job time: 79 sec

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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-557-122A-37
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US-08-557-122A-30
US-08-557-122A-30
US-08-557-122A-36
US-09-256-212A-36
US-09-256-00206-4
US-08-159-339A-833
PCT-US96-00206-4
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US-08-51-565-6
US-08-51-565-1
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Perfect score:
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Polymerase Enhancing Factor (PEF) Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
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Sequence 55, Application US/08822774
Patent No. 6183997
GENERAL INFORMATION:
APPLICANT: HOGREFE, Holly
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isola
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isola
TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isola
TITLE OF INVENTION: and Methods for Purifying and Identify
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lenahan, P.L.L.C.
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
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                                                                                                        US-09-187-049-8
US-09-187-049-8
US-08-523-373-22
US-08-523-373-24
US-08-523-373-24
US-09-107-434-6
US-09-010-999-2
US-09-296-284-6
US-09-296-284-6
US-09-296-284-6
                                                       US-08-946-026-21
US-09-370-473-10
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CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULK, David J.
RESISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEO ID NO: 55
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 14 amino acids
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; ANTI-SENSE: NO
; FRAGMENT TYPE:
US-08-822-774-55
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PatentIn Release #1.0, Version #1.30
          11-DEC-1995
                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J.
REGISTRATION NUMBER: 33/28
REFERENCE/DOCKET NUMBER: 3980.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
INFORMATION FOR SEC ID NO: 27: SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 510 Amir
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
                                       APPLICATION NUMBER:
FILING DATE: 11-DEC
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                  linear
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283 GFKGKI 288
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US-08-557-122A-27
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                                                                                                                                                                                      GENERAL INFORMATION:

WHORE OF INFURTION: Fungal Protein Disulfide Isomerase
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
TORRESPONDENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58796640 No. 5879664th America, Inc.
STREET: New York
COUNTRY: United States of America
III7: New York
COUNTRY: United States of America
III7: New York
COUNTRY: United States of America
III7: New York
COUNTRY: Enable Form:
MEDIUM TYPE: Robopy disk
COMPUTER ENABLE FORM:
MEDIUM TYPE: Robopy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,122A
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J.
REFERENCE/DOCKET NUMBER: 33,728
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
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TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
TITLE OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58796640 No. 5879664th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%; Score 6; DB 2
100.0%; Pred. No. 27;
tive 0; Mismatches
                                                                                                     5-08-557-122A-37
Sequence 37, Application US/08557122A
Patent No. 5879664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08557122A Patent No. 5879664 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
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1 AGWIDAGFKGKITL 14
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282 GFKGKI 287
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US-08-557-122A-27
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RELIANT
RECHAINSON
RETHER NO. 5773245
GENERAL INFORMATION:
RECHAUSON
RECHAUSON
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REPLICANT:
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RESPONDENCE ADDRESSES
RUMBER OF SEQUENCES 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: A00 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
COMPUTER READABLE FORM:
REDIGN TYPE: Floppy disk
COMPUTER: BAP C COMPATIBLE
COMPUTER: BAP C COMPATIBLE
COMPUTER: BAP C COMPATIBLE
REDIGN SYSTEM: BC-082/MS-DOS
SOFTWARE: PATENTIN NATA:
REDIGN TYPE: BC-082/MS-DOS
SOFTWARE: PATENTIN NATA:
REPERENCE/ROCKET NUMBER: US/08/441,139
FILING DATE: 16-MAY-1995
REFIRENCE/ROCKET NUMBER: 8646
FELENCHMONTATION:
REFERENCE/DOCKET NUMBER: 8646
FELENCHMONTES: 516-742-4333
FELEFATION NUMBER: 516-742-4334
FELEFATION NUMBER: 516-742-4336
FELEFATION NUMBER: 516-742-4336
FELEFATION NUMBER: 516-742-4336
FELEFATION NUMBER: 516-742-4336
FELEFATION NUMBER: 516-742-4336
Length 509;
                                                0; Indels
   Score 6; DB 2
Pred. No. 27;
0; Mismatches
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APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Rhee, Sang-Ki
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Bun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REPREMENT: 133.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
       405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.7%; Score 5; DB 4
100.0%; Pred. No. 1.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                          3980.204-US
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/557,122A
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                                                      RY: United States of America 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-296-284-13; Sequence 13, Application US/09296284A; Patent No. 6204040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Gluconobacter suboxydans
                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1: 3052 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-557-122A-26
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Best Local Similarity J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                       New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||
| Db | 1462 GFKGKI 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 58796640 No. 5879664disk of No. 5879664th America, Inc.
                                                                                                                 Gaps
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                                                                             Length 510;
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                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                               Sequence 30, Application US/08557122A
Patent No. 587964
GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58796640 No. 587966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/08557122A
Patent No. 5879664
GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,122A
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
                                                                             DB 1;
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APPLICATIO...
FILING DAME: 11-C.
CLASSIFICATION: 435
ATTONNEY/GENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
FREFERDEC/POCKET NUMBER: 3980.204-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
                                                                           42.9%; Score 6; DB 1
100.0%; Pred. No. 27;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 6; DB 2
100.0%; Pred. No. 27;
tive 0; Mismatches
       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                           Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
; MOLECULE TYPE:
US-08-441-139-20
                                                                                                                                                                       111111
282 GFKGKI 287
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282 GFKGKI 287
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US-08-557-122A-30
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Gaps
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PGT-US96-00206-3
Sequence 3, Application PC/TUS9600206
Sequence 3, Application PC/TUS9600206
GENERAL INFORMATION:
APPLICANT: Immultogle Pharmaceutical Corporation
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATING RHEUMATOID ARTHRITS
NUMBER OF SEQUENCES:
ADDRESSE: Lappin & Kusmer
STREET: ADDRESSE: Lappin & Kusmer
STREET: ADD State Street
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
HEDDBUE FORM:
HEDDBUE READBUE FORM:
HEDDBUE READBUE FORM:
                                               ZIF: 02109

ZIF: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER PAPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00206
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 33.523
REFERENCE/DOCKET NUMBER: IXZ-014PCT
TELEPHONE: 617-466-6040
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE/CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: inear
MOLECULE TYPE: ineari
MOLECULE TYPE: ineari
ORGANISM: BOS taurus type II collagen
PCT-US96-00206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
FAPLICATION NUMBER: PCT/US96/00206
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.7%; Score 5; DB 5;
100.0%; Pred. No. 14;
tive 0; Mismatches
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NAME: REFECT, Ann-Louise
REGISTRATION NUMBER: 33,523
REFRENCE/DOCKET NUMBER: INZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-400 C.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.79
Best Local Similarity 100.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AGFKG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGFKG 5
                 COUNTRY:
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Sequence 833, Application US/08159339A

Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: USA
INUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
COUNTRY: USA
COUNTRY: USA
COUNTRY: BADABLE FORM:
MEDIUM TYPE: Diskete
COMMUTER READABLE FORM:
MEDIUM TYPE: Diskete
COMMUTER: OF JULION
TELEPHONE: (415) 576-0300
TELEFEX:
TELEDHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9600206
GENERAL INFORMATION:
APPLICANT: IMMULOAN:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATING RHEUMATOID ARTHRITIS
CORRESPONDENCE 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Lappin & Kusmer
STREET: 200 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.7%; Score 5; DB 3 Best Local Similarity 100.0%; Pred. No. 12 Best Local Similarity 100.0% insinatches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-159-339A-833
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1 AGFKG 5
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PCT-US96-00206-2
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RESULT 11

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APPLICANT: Luthra, Harvinder S.
APPLICANT: David, Chella S.
APPLICANT: David, Chella S.
APPLICANT: Zanelli, Eric.
TITLE OF INVENTION: H.A. DRB1 PEPTIDES WITH SPECIFIC BINDING
TITLE OF INVENTION: AFFINITY FOR HLA-DQ MOLECULES: PREVENTION AND
TITLE OF INVENTION: TREATMENT OF RHEUMATOID ARTHRITIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PILING DATE: 08/31/95
                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C., P.A. STREET: 60 South Sixth Street, Suite 3300 CITY: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/003001
TELECHNUICATION INFORMATION:
TELEPHONE: 612/335-6070
TELEFAX: 612/288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 5; |
Pred. No.
                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Policial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/07951565; Patent No. 5399347; GENERAL INFORMATION:
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IBM PC compatible
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100.0%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Darby & Darby STREET: 805 Third Ave. CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 612/288-9696
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-521-871A-5
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                COUNTRY:
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US-07-951-565-1
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                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TREATING RHEUMATOID ARTHRITIS NUMBER OF SEQUENCES: 7
ADDRESSENE: Lappin & Kusmer STREET: 200 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00206
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ImmuLogic Pharmaceutical Corporation
                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bos taurus type II collagen PCT-US96-00206-4
                                                                                      Bos taurus type II collagen
                                                                                                                                                        Score 5; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 5;
                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9600206
GENERAL INFORMATION:
                                                                                                                                        35.7%; bc.
100.0%; Pre
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: IMZ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-466-6040 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 amino acids
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.7
Best Local Similarity 100
Matches 5; Conservative
                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                      Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
GY: linear
amino acid
                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
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                                                                                                                                                                                                                              6 AGFKG 10
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                                                                                    ORGANISM:
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                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: BOS
STATE: MA
COUNTRY:
                                                                                                     PCT-US96-00206-3
                                                                                                                                                                                                                                                                                                                                   PCT-US96-00206-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-521-871A-5
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                                                  Gaps
                                                                                                                                                                                                                                                                                                                        APPLICANT: Trentham, David E.
APPLICANT: Weiner, Howard L.
TITLE OF INVENTION: Method of Treating Rheumatoid Arthritis with
TITLE OF INVENTION: Type II Collagen
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                  ;
                                                  0; Indels
Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Gaps
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                                                                                                                                                                                                        Length 26;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRECRIT Release #1.0, Version #1.25
SOFTWARE: PRECRIT Release #1.0, Version #1.25
SOFTWARE: PRECRIT RELEASE #1.0, Version #1.25
SOFTWARE: PRECRITOR NOTA: US-AR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLDERELIN JORGE A.
RESISTENCE/DOCKET UNBER: 29,021
RESISTENCE/DOCKET UNBER: 1383.0080000
TELEPEHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Benoist, C.
APPLICANT: Mathis, D.
APPLICANT: Mathis, D.
TITLE OF INVENTION: Transgenic Arthritic Mice
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: January 31, 2002, 13:15:12
Job time: 93 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-246-242-9; Sequence 9, Application US/08246242; Sequence No. 5675060; Patent No. 5675060;
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Partches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2500
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
STRANDEDNESS: unknown
TOPOLOGY: unknown
HOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kes
STREET: 1100 New York
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.7
Best Local Similarity 100
Matches 5; Conservative
          ; TOPOLOGY: linear
MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
GS-07-951-565-6
                                                                                             internal
                                                                                                                                                                                                                                                                                                                         6 AGFKG 10
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17 AGFKG 21
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18-07-97-91-565-6

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18-07-97-91-565-6

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18-07-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-565-91-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.7%; Score 5; DB 1; Best Local similarity 100.0%; Pred. No. 26; Matches 5; Conservative 0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,565
FILLIG DATE: 19920925
CLASSIFICATION: 424
ATTONNEY,FAGENT INFORMATION:
NAME: GOGOTIS, Adda C.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 1010/07300
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: 236697
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 anino acids
TYPE: AMINO ACID
TENGTH: AMINO ACID
TENGTH: AMINO ACID
TENGTH: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Gallus domesticus; TISSUE TYPE: collagen
US-07-951-565-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AGFKG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 1111
17 AGFKG 21
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:18:07; Search time 140.03 Seconds (without alignments) 7.406 Million cell updates/sec Run on:

US-08-957-709-74 14 Perfect score:

1 AGWIDAGFKGKITL 14 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

522463 seqs, 74073290 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

522463

Post-processing: Listing first 45 summaries

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

A\_Geneseq\_1101:\* Database :

/SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:\*
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDSZ/gcgdata/geneseq/geneseqp/AA1999 DAT:
/SIDSZ/gcgdata/geneseq/geneseqp/AA1990 DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB ID | DB | ID       | Description        |
|---------------|-------|----------------|-----------------------------|----|----------|--------------------|
|               | 14    | 100.0          | 14                          | 19 | AAW72850 | Methanococcus jann |
| 7             | 9     | 42.9           | 82                          | 21 | AAB59072 | Breast and ovarian |
| m             | 9     | 42.9           | 255                         | 22 | AAM01029 | CFE 32 protein seq |
| 4             | 9     | 42.9           | 260                         | 22 | AAB79890 | Corynebacterium qi |
| ß             | 9     | 42.9           |                             | 22 | AAG89903 | C qlutamicum prote |
| 9             | 9     | 42.9           |                             | 21 | AAB02857 | Human G protein co |
| 7             | 9     | 42.9           | 509                         | 22 | AAB93339 | Human protein sequ |
| œ             | 9     | 42.9           |                             | 22 | AAB94067 | Human protein sequ |
| 6             | 9     | 42.9           | -                           | 22 | AAB94129 | Human protein sequ |
| 10            | S     | 35.7           | 7                           | 21 | AAB35994 | Sorbitol dehydrode |
| 11            | S     | 35.7           | 13                          | 17 | AAW03105 | Bovine type II col |

| 9.1      | ige.     | ပ္ပ       | Peptide associated | Amino acid sequenc | Collagen II (CII) | /pe      | Rheumatoid arthrit | Rheumatoid arthrit | HII 250-270 peptid | Entry vector pENTR | Human type II coll | Fragment of human | Type II collagen p | Arthritis toleroge | Bovine type II col | Immunomodulatory p | Gene 33 human secr | Immunomodulatory p | Immunomodulatory p | Immunomodulatory p | Wheat gammal purot | Sorghum alpha-amyl | Human secreted pro | н        | b        | Arabidopsis thalia | Peptide #11451 enc | E        | Arabidopsis thalia | Fragment of human | EST      | Arabidopsis thalia | Arabidopsis thalia |
|----------|----------|-----------|--------------------|--------------------|-------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|----------|--------------------|-------------------|----------|--------------------|--------------------|
| AAW03106 | AA182005 | AAY 58994 | AAB84074           | AAB84108           | AAY82066          | AAW03107 | AAB96875           | AAB96873           | AAW53854           | AAB23766           | AAY26976           | AAY41477          | AAR51310           | AAR98363           | AAW03108           | AAB84091           | AAB39279           | AAB84093           | AAB84094           | AAB84095           | AAR33767           | AAR33766           | AAG01170           | AAR79479 | AAB12273 | AAG18359           | AAM37414           | AAU14925 | AAG50217           | AAY36443          | AAY12895 | AAG24263           | AAG16519           |
| 17       | 77       | 21        | 22                 | 22                 | 21                | 17       | 22                 | 22                 | 19                 | 21                 | 20                 | 20                | 15                 | 16                 | 17                 | 22                 | 21                 | 22                 | 22                 | 22                 | 14                 | 14                 | 21                 | 16       | 21       | 21                 | 22                 | 22       | 21                 | 20                | 20       | 21                 | 21                 |
| . 13     | T 3      | 13        | 13                 | 13                 | 15                | 16       | 16                 | 20                 | 21                 | 21                 | 22                 | 25                | 56                 | 26                 | 26                 | 27                 | 28                 | 31                 | 33                 | 33                 | 47                 | 48                 | 51                 | 53       | 23       | 09                 | 99                 | 72       | 75                 | 79                | 83       | 82                 | 87                 |
| 35.7     | 35.7     | 35.7      | 35.7               | 35.7               | 35.7              | 35.7     | S                  | 35.7               | S                  | 35.7               | 35.7               | 35.7              | .35.7              | 35.7               | 35.7               | 35.7               | 35.7               | S                  | 35.7               | 35.7               | 35.7               | 35.7               | 35.7               | 35.7     | 35.7     | 35.7               | 35.7               | 35.7     | 35.7               | 35.7              | 35.7     | 35.7               | 35.7               |
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| 12       | L3       | 14        | 15                 | 16                 | 17                | 18       | 19                 | 20                 | 21                 | 22                 | 23                 | 24                | 25                 | 26                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36       | 37       | 38                 | . 68               | 40       | 41                 | 42                | 43       | 44                 | 45                 |

## ALIGNMENTS

Methanococcus jannaschii dCTP deaminase uridine-binding motif. AAW72850 standard; Peptide; 14 AA (first entry) AAW72850; AAW72850 RESULT 

Polymerase enhancing factor; PEF; dCTP deaminase; PCR; amplification; sequencing; replication Methanococcus jannaschii.

WO9842860-A1.

01-OCT-1998

98WO-US05497. 20-MAR-1998; 97US-0957709. 97US-0822774. 24-OCT-1997; 21-MAR-1997;

(STRA-) STRATAGENE.

Hansen CJ, Hogrefe H;

WPI; 1998-542284/46.

Polymerase enhancing factor proteins, extracts and complexes -improve the polymerisation activity of nucleic acid polymerases, for use in amplification, sequencing and replication

Human protein sequ Human protein sequ Human protein sequ Sorbitol dehydroge Bovine type II col

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AAM01029;
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAM01029
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                   This is the uridine-binding motif of the dCTP deaminase of methanococus jannaschii. Sequences are provided (see AMW72849-57) of the uridine-binding motifs of dUTPases and dCTP deaminases of pyrococcus furiosus (see AAW72847), Methanococcus jannaschii, Desulfutolobus amblvalhans, Escherichia colli, yeast, human and herpesvirus; a consensus (see AAW72848) is also provided. A claimed herpesvirus; a consensus (see AAW72848) is also provided. A claimed method of enhancing a nucleic acid polymerase reaction comprises performing the reaction in the presence of one or more of the collination that turns-over dUTP and a protein having one or more of the sequences provided in AAW72848-57. A claimed protein having per activity comprises one or more of sequences given in AAW72848-57. (Kits are provided for replicating nucleic acids, for site-directed mutagenesis, for nucleic acid sequencing or for amplification (preferably PCR or RT-PCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breast and ovarian cancer associated antigen protein sequence SEQ ID 780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibbecterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human breast and ovarian cancer associated gene sequences and the polypetides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                             100.0%; Score 14; DB 19; Length 14; 100.0%; Pred. No. 1.7e-08; Live '0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 1244; 1299pp; English
Claim 71; Page 47; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   AAB59072 standard; Protein; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05881
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                               1 AGWIDAGFKGKITL 14
                                                                                                                                                                                                                                                                                                                             WPI; 2000-611515/58.
N-PSDB; AAF21975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200055173-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          AAB59072;
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AAB59072
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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist constraint sequences exhibit cytostatic; immunosuppressive; constraint sequences exhibit cytostatic; immunosuppressive; constraint antifungal; antifuncer; unlearing; hepatotropic; antidabetic; antifungal; antifuncer; vulnerary; anticonvulsant; antidabetic; antifungal; antifuncer; when the diagnosis of cancer, convincedide and protein sequences are used in the diagnosis; and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, allergies, autoimmune haemolytic anaemia, autoimmune themolytic anaemia, autoimmune themolytic anaemia, autoimmune themolytic anaemia, autoimmune themolytic anaemia, autoimmune themolytics arthuitis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as crebral anoxia and epilepsy; and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding conserved essential genes involved in bacterial replication which are potential targets for the treatment of antibiotic resistant bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to nucleic acids (AAH90701-AAH90918) encoding polypeptides (AAM01002-AAM01114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CEG For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davison DB, Bruccoleri RE;
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Thanassi JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM01029 standard; Protein; 255 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-2000; 2000WO-US35604.
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N-PSDB; AAH90728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 82 AA;
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15 fkgkit 20
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Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nuclectide sequence of interest is essential for viability of a bacterial cell or whether it resides within an open peron, by integrating an exogeneous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest comprising 200-500 base pairs) into the genomic sequence of interest which confers a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisease therapy. The nucleic acids also enable identification of targets sultable for the treatment of antibiotic resistant bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                             42.9%; Score 6; DB 22; Length 255;
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                                                                                                                                                                                                                                                                                                                                              AAB79890 standard; Protein; 260 AA
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99DE-1031428.
99DE-1031434.
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99DE-1031418.
99DE-1031419.
99DE-1031420.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                      AGFKGK 11
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agfkgk 13
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08-JUL-1999;
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08-JUL-1999;
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08-JUL-1999;
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08-JUL-1999;
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                                                                                                                                                                                              Sequence
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids from Corynebacterium glutamicum encoding metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 40
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 896-897; 1737pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 6;
llarity 100.0%; Pred. No
Conservative 0; Mismat
                                                                                                                                                                                                                                      99DE-1032926.
99DE-1032928.
99DE-1033004.
                                                                                                                                                                                                                                                                                          99DE-1033005.
99DE-1033006.
99US-0148613.
99DE-1040764.
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99DE-1041380.
99DE-1041394.
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99DE-1042076.
99DE-1042077.
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99DE-1040766.
                                                                        99DE-1032126.
99DE-1032130.
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                                                                                                                             99DE-1032206.
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N-PSDB; AAF72009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BADI ) BASF AG.
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agwida
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08-JUL-1999
08-JUL-1999
                                      38-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J3-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                            39-JUL-1
                                                                                                                                                                  -JUL-1
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                                                                                                                                                                                                                                                                                                                                                                      27 - AUG - 1
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                                                                                                                                                                                                                                                                                                                                  12-AUG-
                                                                                                                                                                                                                                                                                                                                                   27 - AUG - .
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Human G protein coupled receptor hMC4 (A244K) protein SEQ ID NO:136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents
                                                    Human; G protein coupled receptor; GPCR; transmembrane receptor;
identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Behan DP, Lehmann-Bruinsma K, Chalmers DT, (
Gore M, Liaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                        98US-0170496.
98US-0108029.
98US-0110060.
99US-0110060.
99US-0120416.
                                                                                                                                                                                                                                                                                                     990S - 0123946
990S - 0123945
990S - 0123948
990S - 0123948
990S - 0123949
990S - 0123951
990S - 0136436
990S - 0136439
990S - 0136439
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990S-0141448.
990S-0151114.
990S-015524.
990S-0156633.
                                                                                                                                                                                                  99WO-US24065
22-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317986/27.
N-PSDB; AAA46119.
                                                                                                                                              WO200022131-A2.
                                                                                                       Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1999;
03-SEP-1999;
29-SEP-1999;
29-SEP-1999;
29-SEP-1999;
                                                                                                                                                                                                 13-OCT-1999;
                                                                                                                                                                        20-APR-2000
                                                                                                                                                                                                                                                                                -FEB-1999
-FEB-1999
                                                                                mutant.
 The present invention provides a number of nucleotide and protein are asequences from the Corynetorm bacterium Corynebacterium glutamicum. These sequences from the Corynetorm bacterium, measuring expression amount and manalysing the expression profile or expression amount and amalysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacterium, and identifying a homologue of a gene derived amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed because and organic acids where the sequence data for this patent did not form part of the printed because and the present expensive form and the printed because the control of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                     Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                            Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 6; DB 22; Length 266; 100.0%; Pred. No. 41; Live 0; Mismatches 0; Indels
                                                                                                                   C glutamicum protein fragment SEQ ID NO: 3657.
                                     AAG89903 standard; Protein; 266 AA
                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                       16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                               18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Patent Office.
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N-PSDB; AAH65122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 AA;
                                                                                                                                                                                                            EP1108790-A2.
                                                                                         26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S,
Fateishi N,
                                                                                                                                                                                                                                      20-JUN-2001
                                                             AAG89903;
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          RESULT
AAG89903
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The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous constitutively activated versions the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB028859 represent sequences used in the exemplification of the present invention.
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0
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Best Local Similarity 100.0%; Predch No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels
Example 2; Page 176-177; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KGKITL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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AAB02857 standard; Protein; 332 AA.

AAB02857;

RESULT
AAB02857
ID AAB0:
XX
AC AAB0:
XX.-

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Chen

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Claim 8; SEQ ID 12449; 2537pp + CD ROM; English.
                                           Human protein sequence SEQ ID NO:12449
      AAB93339 standard; Protein; 509 AA.
                                                                                                                                                                    Isogai T, Nishikawa T,
                                                                                                                         27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
32-MAY-2000; 2000JP-0183767.
                                                                                                      28-JUL-2000; 2000EP-0116126.
                                                                                                                   99JP-0248036
                                                                                                                                     02-MAY-2000; 2000JP-0183767 09-JUN-2000; 2000JP-0241899
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                            of the present invention
                                                                                                                                                        (HELI-) HELIX RES INST
                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                                                                                                     full-length cDNAs
                               26-JUN-2001
                                                                   Homo sapiens
                                                                              EP1074617-A2
                                                                                                                   29-JUL-1999;
                                                                                           07-FEB-2001
                                                                                                                                                                           Ishii S,
                  AAB93339;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                    Ota T,
AAB93339
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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 3'-end sequence.
Complementary strand of a polynucleotide which comprises a feat of
sequence and an oligonucleotide comprises a sidence of
sequence complementary to the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connas seasily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18724 represent human cDNA sequences; AAH3640 to
AAH13633 to AAH18742 represent human cDNA sequences; AAH3620 to AAH13620 to A
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and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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242 kgkitl 247
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The present invention describes primer sets for synthesising 5602

(ull-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises at 3'-end sequence, where the

oligonucleotide which comprises at 3'-end sequence, where the

oligonucleotide which comprises at selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

connection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

cDNAs easily without any specialised methods. AAH03629 to AAH13632

AAH13633 to AAH13642 to AAH13632

represent clingonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Ye
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 14250; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:14250
                                                                                                                                                                                                                                                            AAB94067 standard; Protein; 673 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
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                                      111111
369 agfkgk 374
6 AGFKGK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                                                                                                  AAB94067;
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42.9%; Score 6; DB 22; Length 673;

Query Match

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0; Gaps

0; Indels

DB 22; Length 509;

42.9%; Score 6; DB 2 100.0%; Pred. No. 70; Live 0; Mismatches

Query Match 42.9 Best Local Similarity 100. Matches 6; Conservative

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RESULT 11
AAW03105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes primer sets for synthesising 5602 (111-length compared to the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence of an end of a sequence of the compination of the specification. The primers are useful for synthesising polynucleotides, nationary full-length convas are useful for synthesising polynucleotides, particularly full-length convas. The primers are useful for synthesising polynucleotides, particularly full-length convas. The primers are also useful for the full-length convas. The primers are also useful for she full-length convas. The primers allow obtaining of the proteins encoded by the full-length convas. The primers allow obtaining of the full-length convas. The primers allow obtaining of the full-length convas. The primers allow obtaining of the proteins and AAH13629 to AAH13629 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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                        Indels
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Pred. No. 88;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:14385.
                                                                                                                                                                                                                                  AAB94129 standard; Protein; 750 AA.
Best Local Similarity 100.0%; P
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-XAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                             (first entry)
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533 agfkgk 538
                                                               6 AGFKGK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                             26-JUN-2001
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Ishii S,
                                                                                                                                                                                                                                                                              AAB94129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule isolated from Glucocobatter suboxydans useful for the fermentative production of 2-keto-t-gulonic acid and L-sorbose from D-sorbitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol; L-sorbose production; 2-keto-L-gulonic acid.
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Length 750;
                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorbitol dehydrogenase subunit 2 internal peptide.
   DB 22;
. 96;
   Query Match 42.9%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                AAB35994 standard; Protein; 7 AA.
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(RHEE/) RHEE S.
(LEEE/) LEE E.
                                                                                                                                 6 AGFKGK 11
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| 606 agfkgk
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3 dagfk
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The present invention provides peptides, therapeutic compositions, and methods for treatment of rheumatoid arthritis in mammals, specifically in humans. The peptides of the invention comprise fragments of type Is collagen which bind specifically with human major histocompatibility complex proteins known to be genetically linked to susceptibility to rheumatoid arthritis. The therapeutic compositions of the invention comprise the peptides, alone or in combination with other collagen peptides. AAW03105-107 are claimed peptides which can be used to treat rheumatoid arthritis by down-regulating the autoimmune response, esp. rendering T cells non-responsive to the rheumatoid arthritis-related autoantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.
                                                                                                                                                                                                                                            New peptide fragments from human type II collagen - bind to specific major histocompatibility complex proteins and are useful, opt. with known collagen fragments, to treat rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
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                                                                                                                                                                       Sonderstrup-Mcdevitt G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen II (CII) peptide 261-273 SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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Pred. No. 38;
0; Mismatches
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100.0%; Pred
0; F
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                                                                                                                                                                                                                                                                                                                        Claim 1; Page 30; 46pp; English.
                                                                                                                                  (IMMU-) IMMULOGIC PHARM CORP
                                                        96WO-US00206.
                                                                                           95US-0369792.
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99US-0123675.
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                                                                                                                                                                     Rothbard J,
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                                                                                                                                                                                                         WPI; 1996-333937/33.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AA;
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                                                        04-JAN-1996;
                                                                                           06-JAN-1995;
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                   11-JUL-1996
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4 agfkg 8
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                                                                                                                                                                       Fugger LH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides peptides, therapeutic compositions, and methods for treatment of rheumatoid arthritis in mammals, specifically in humans. The peptides of the invention comprise fragments of type II collagen which bind specifically with human major histocompatibility complex proteins known to be genetically linked to susceptibility to rheumatoid arthritis. The therapeutic compositions of the invention comprise the peptides, alone or in combination with other collagen peptides. AMMO3105-107 are claimed peptides which can be used to treat rheumatoid arthritis by down-regulating the autoimmune response, esprendering I cells non-responsive to the rheumatoid arthritis-related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide fragments from human type II collagen - bind to specific major histocompatibility complex proteins and are useful, opt. with known collagen fragments, to treat rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                  Collagen; type II; Bovine; Human; rheumatoid arthritis; epitope;
human major histocompatibility complex; genetically linked.
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                                                                                                               Bovine type II collagen peptide (276-288).
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Pred. No.
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100.0%; Pred
0; M
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AAW03105 standard; peptide; 13 AA
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Best Local Similarity 100.0
Englished 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fugger LH, Rothbard J,
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AAW03106 RESULT

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02-OCT-1998;
12-NOV-1998;
09-MAR-1999;
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| agfkg 5
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                                                                                                                     Aharoni R,
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                                                                                           The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, the synthetic positively charged amino acids, negatively charged amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II protein associated with an autoimmune disease. The synthetic peptides have anti-inflammatory and anti-arthitic activities. They are used to treat inflammatory and anti-arthitic activities. They are used to treat inflammatory and anti-arthitical activities. They are used to treat inflammatory and demyelinating activities. The peptides have respecific for particular MHC class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random compliates; may include many repeats of the active sequence and/or contain amino acid analoques that improve stability (or other desired features). AAV8201 to AAV8201 to AAV82014 to AAV82014 or AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014 to AAV82014
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             New synthetic peptide, useful for treating autoimmune disease, e.g. rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen; antigen; autoimmune disease; multiple sclerosis; autoimmune haemolytic anaemia; autoimmune cophoritis; autoimmune haemolytic anaemia; autoimmune cophoritis; contact sensitivity disease; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; Hashimoto's disease; didlopathic myxedema; myasthenia gravis; psoriasis; pemphigus vulgaris; rheumatoid arthritis; systemic lupus erythematoid arthritis; antianaemic; antithyroid; antidiabetic; thyromimetic; antisonamatory; major histocompatibility complex; antifilammatory; therapy; major histocompatibility complex; MMC class II; human lymphocyte antigen; HLA-DR.
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                                                                Example 1; Page 19; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY58994 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type II collagen peptide 261-273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US16747.
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98US-0101825
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AA;
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| agfkg 5
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25-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                          New terpolymers, copeptides and copolymer I which contain three amino acids randomly joined in a linear array where one is aromatic, one is aliphatic and the other is charged, used to treat autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents type II collagen peptide 261-273. The peptide was used in the design of copeptides (see AAR58956-88) that show a high affinity for MHC class II proteins associated with an autoimmune disease, especially HLA-DR1, HLA-DR2 or HLA-DR4, bind to antigen presenting cells, and inhibit T cell responses. The copeptides are used to treat multiple sclerosis, autoimmune thyroiditis, autoimmune uveoretinitis, chronic immune thrombocytopenic purpura, coolitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all
                                                                                                                                                                                                                                   Sela M, Fridkis-Hareli M;
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100.0%; Pred. No. 38;
tive 0; Mismatches
                                                                                                                                                                                                                                   Arnon R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; Page 67; 147pp; English.
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                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD. (HARD ) HARVARD COLLEGE.
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98US-0102960.
98US-0108184.
99US-0123675.
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                                                                                                                                                                                                                               Teitelbaum D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.7
Best Local Similarity 100
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
                                                                                                                                                                                                                                                                 Strominger JL;
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The immunomodulatory peptide comprises a first peptide associated with autoimmune disease, allergy or asthma, or host-versus-graft rejection and which will bind to an antigen receptor on a set or subset of T cells, linked to a second immune modulating peptide which will cause a directed immune response by the set or subset of T cells to which the first peptide is attached. Alternatively, the second peptide will bind to a T cell receptor site on the surface of the T cell which will cause the set or subset of T cells to undergo anergy and apoptosis. The immunomodulatory peptides are useful for eliminating a set or subset of T cells involved in autoimmune response. They are useful for eliminating a set or subset of T cells involved in autoimmune response. They are useful for Novel immunomodulatory peptide construct useful for modulating an inappropriate immune response in an individual at risk for autoimmune disease, allergic reactions, asthma or host-graft or graft-host disease the treatment of autoimmune disease, allergic reactions, asthma or host-graft or graft-host rejections. The immunomodulatory peptides are also useful for interrupting an autoimmune disease associated pathway necessary to complete T cell activation. The present peptide is used to construct immunomodulatory peptides of the invention, and is representative of the first peptide. The specification describes an immunomodulatory peptide construct. Claim 2; Page 36; 55pp; English. 

13 AA; Sequence

Gaps .; 0 35.7%; Score 5; DB 22; Length 13; 100.0%; Pred. No. 38; tive 0; Mismatches 0; Indels Query Match 35.7 Best Local Similarity 100. Matches 5; Conservative

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064778 arian adeno 05392 streptomyce 09k14 streptomyce 046731 bos taurus 046719 bos taurus 04675 bos taurus 046756 bos taurus 046756 bos taurus 046756 bos taurus 046756 bos taurus 046756 bos taurus 029157 archaeoglob

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synechocyst

082701 medicago tr 031473 nerodia sip 068068 rhodobacter 09h6y4 homo sapien

streptomyce

Title: Perfect score:

Sequence:

OM protein

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Scoring table:

Word size :

Searched:

Database :

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ABDINE-9637999; PubMed-868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Butt C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: TO BACTERIÁL DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE.
EMBL; U67553; AAB99105.1; -.
TIGR; MJ102; -.
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SEQUENCE 161 AA; 18640 MW; 886357CB4A533CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN MJ1102.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A. 2661 / ATCC 43067;
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Q01737
Q39814
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P74069
Q64778
Q53952
Q9K3R4
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Q9FTT6
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Interpro; IPR001428; dUTPase.
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O68068
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046754
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150
151
161
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NCBI_TaxID=2190;
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O3O350 salmonella
Q51623 escherichia
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018958 bos taurus
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Q9jiw2 rattus norv
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Q9far2 streptomyce
Q9hzf4 pseudomonas
Q9a2e5 caulobacter
Q9p884 emericella
O18923 sus scrofa
                                                                                                                                     ; Search time 130.99 Seconds
(without alignments)
15.633 Million cell updates/sec
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09ae03 amycolatops
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                   473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                     January 31, 2002, 13:37:42
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                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                        OLIGO
Gapop 60.0 , Gapext 60.0
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Q69101
Q86610
Q9AE03
Q9FAR2
Q9FAR2
Q9HZF4
Q9AZE5
Q9P884
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Q51623
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sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
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sp_vertebrate:
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sp_bacteria:*
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Maximum DB seq
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Result No.  $\alpha$ 

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Indels

Length 259;

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259 AA; 28431 MW; 11C0DA5CD6FC6B58 CRC64;
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Pred. No. 46;
                                                                                                                                                                   Ouery Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 27; Matches 6; Conservative 0; Mismatches
EMBL; AL031155; CAA20072.1; -.
HSSP; P09030; 1AKO.
InterPro; IPR000097; AP_endonclse_family_l.
Pfam; PF01260; AP_endonucleas1; 1.
Exonuclease 259 AA; 28431 MW; 11C0DA5CD6FC
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                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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SEQUENCE FROM N.A.
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";

Mgl. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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O86610; OBLOWN-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 10, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 17, Last annotation update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
O1-JUN-1998 (TrEMBLrel. 17, Last annotation update)
SC3A7.09.
Streptomyces coelicolor.
Streptomyces coelicolor.
Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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MDELINE-9328441;
MDELINE-9328445.
MDELINE-9328445.
MOST R.;
Tanaka S., Liu Y., Mosti R.;
"Nuclectide sequence of the major DNA-binding protein gen
almplex virus type 2 and a comparison with the type 1.";
Arch. Virol. 129:183-196 (1993).
EMBL; D10658; BAA01507.1;
FMBL; D10658; BAA01507.1;
FMBL; D10658; Viral_DNA_bind.
FFAM; PRO0747; viral_LDNA_bb; N.
SEQUENCE 1197 AA; 128470 MW; AA3ADA75B8865BFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver K., Harris D.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    069101

01-NOV-1996 (TrEMBLEAL 01, Created)

01-NOV-1996 (TrEMBLEAL 01, Last sequence update)

01-JUN-2001 (TrEMBLEAL 17, Last annotation update)

DNA BINDING PROTEIN ICP8.

Herpes simplex virus (type 2).

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                      PRT; 1197 AA
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MEDLINE=97000351; PubMed-8843436;
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                                                110 SAVHDPGYEGRPEY 123
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429 PGYEGRP 435
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Amycolatopsis mediterranei.
Bacteria: Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=33910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S699;
MEDLINE=98165773; PubMed=9497318;
KRIM C.G., Yu T.W., Fryhle C.B., Handa S., Floss H.G.;
"3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the formation of the precursor of mC7N units in rifamycin and related antibiotics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Biosynthesis of the ansamycin antibiotic rifamycin: deductions the molecular analysis of the rif biosynthetic gene cluster of Amycolatopsis mediterranel $699."; chem. Biol. 5:69-79(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S699;
MEDLINE=98174059; PubMed=9512878;
August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Yu T.W.,
Taylor M., Hoffmann D., Kim C.G., Zhang X., Hutchinson C.R.,
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EMBL; AR040570; AR052988.1; --
SEQUENCE 473 AA; 53211 MW; 6DE809458209BF2C CRC64;
                                                                 Created)
Last sequence update)
Last annotation update)
473 AA
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Matches

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Q9BTG9

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RESULT

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MEDLINE-21173698; PubMed=11259647; MEDLINE-21173698; PubMed=11259647; Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta M., Maddock J.R., Potcoka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                       Stover C.K., Pham X.-O.T., Erwin A.L., Mizoquchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Madman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAOI, an Nature 406:959-964(2000).
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Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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Hypothetical protein; Complete proteome.
SEQUENCE 634 AA; 71197 MW; FE2043295E3770F9 CRC64;
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                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN PA3054.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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504 PGYEGR 509
539 DPGYEG 544
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1894;
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"Analysis of the chlortetracycline polyketide synthase genes from Streptomyces aureofaciens NRRL3203.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033379; BAB12569.1;
InterPro; IPR001962; Asn_synthase.
InterPro; IPR000583; GATase_2.
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004108; AAH04108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 1 1
SEQUENCE 487 AA; 51285 MW; EF643482D26BF14D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSO0443; GATASE_IYPE_II; UNKNOWN_1.
609 AA; 67138 MW; 9BFB791CD9586D65 CRC64;
                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3687782) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ASPARAGINE SYNTHASE HOMOLOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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100.0%; Pred. No. 58;
tive 0; Mismatches
                                                                                                                                                              487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6; DB 4; Pred. No. 47; 0; Mismatches
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 Mismatches
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100.0%; Pre/
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Pfam; PF00310; GATase_2; 1.
 0;
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 Conservative
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                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
Matches 6; Conservat
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Best Local Similarity
6, Conserva
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                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LYMPHOMA;
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| 261 AVHDPG 266
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246 PGYEGR 251
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                                   2 AVHDPG 7
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**09FAR2**;

909FAR22 909 DF 0110 909 DF 0110 909 DF 0110 909 DF 85 FR 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 SF 87 S

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
03-MATCHOSAULIA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
03-MATCHOSAULIA; Aves; Neognathae; Galliformes; Phasianinae;
03-MATCHOSAULIA; Neognathae; Galliformes; Phasianinae;
03-MATCHOSAULIA; Neognathae; Galliformes; Phasianinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miskeivich F., Zhu Y., Ranscht B., Sanes J.R.;
"Expression of Multiple Cadherins and Catenins in the Chick Optic
Tectum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 40;
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EMBL; AF098469; AAD16259.1; -1 NON_TER 40 40 40 SEQUENCE 40 AA; 4373 MW; B554B44C802BDAFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BONE MORPHOGENETIC PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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SEQUENCE FROM N.A.
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Q9PWN0
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ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THERACT WITH THEMSELVES IN A HOMOPHILIC
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CADHERIN-11 (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4) (FRAGMENT).
Sus scrofa (Pig).
Bukasyota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
NCBI_TAXID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
Andrade A.C., Van Nistelrooy J.G.M., Haas H., De Waard M.A.;
"ABC transporters and resistance to açole fungicides in the ima
mutants of Aspergillus nidulans.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ276241; CAB76823.1;
InterPro; IPR001393; AAA.
InterPro; IPR001393; AAA.
InterPro; IPR001647; HTH_LVSR.
InterPro; IPR001663; HTH_LVSR.
InterPro; IPR001063; Ribosomal_L22.
Pfam: PF00005; ABC_tran; 2.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2001 (TrEMBLrel. 17, Last annotation update)
ABC TRANSPORTER PROTEIN.
Emericella nidulans (Aspergillus nidulans).
Euraryota; Fungl: Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
42.9%; Score 6; DB 3; Length 1499;
Best Local Similarity 100.0%; pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                       Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00011; ABC_TRANSPORTER; UNKNOWN_1.
PROSITE; PS00044; HTH_LYER_FAMILY; UNKNOWN_1.
PROSITE; PS000464; HTH_LYER_FAMILY; UNKNOWN_1.
SEQUENCE 1498 AA; 167705 MW; AABDEA3FFDIABFEB CRC64;
                                                                                                        0; Indels
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                                   Query Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 61; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1498 AA.
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TISSUB-RETINA,
Lutz D.A., Zheng J.J.;
Submitted (NOV-1997) to c.
-! FUNCTION: CADHERINS A.
THEY PREFERENTLY A.
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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392 PGYEGR 397
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                                                                                                                                                              6 PGYEGR 11
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Q9P884;
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STRAIN=FISCHER344; TISSUE-TESTIS;
MEDLINE-20114371; PubMed-10650949;
Johnson K.J., Patel S.R., Boekelheide K.;
"Multiple cadherin superfamily members with unique expression profiles
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=95251649; PubMed=7733921;
Iwai N., Shimoike H., Kinoshita M.;
"Genes up-regulated in hypertrophied ventricle.";
Biochem. Biophys. Res. Commun. 209:527-534(1995).
HSSP; P00488; IF13.
SEQUENCE 101 AA; 11214 MW; DIEDCD4548E11469 CRC64;
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                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 15, Last annotation update)
TISSUE TYPE II TRANSCLUTAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CADHERIN-11 (FRAGMENT).
          101 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are produced in rat testis.";
Endocrinology 141:675-683(2000).
EMBL, PR177677, AAF87052.1.
InterPro; IPR000233; Cadherin_C_term.
Pfam; PF01049; Cadherin_C_term.
          PRT;
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Matches 5; Conservative
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mes 5; Conservative
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                                                                                                                                                                                          NCBI_TaxID=10118;
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|4 PGYEG 18
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72 GYEGR 76
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR0001651; EGF-like.
InterPro; IPR0001881; EGF-ca.
Pfam; PF000008; EGF: 1.
SMART; SM00179; EGF_CA; 1.
SMART; SR001196; EGF_Z; 1.
PROSITE; PS001186; EGF_Z; 1.
PROSITE; PS01187; EGF_CA; 1.
Calcium-binding; EGF_like domain; Glycoprotein; Hydroxylation; Repeat.
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Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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STRAIN-B73 INBRED LINE;
MEDLINE-97248483; PubMed-9094711;
MEDLINE-97248483; PubMed-9094711;
MEDLINE-97248483; PubMed-9094711;
"A novel suppressor of cell death in plants encoded by the LLS1 gene of maize.";
cell 89:25-31(1997).
Mendel; U77346; AAC49677.1; -.
Mendel; U3799; Zeama; 2476; 23979.
InterPro; IPR001395; Aldo_ket_red.
Pfan; PF0048; aldo_ket_red; 1.
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42 AA; 4739 MW; 4E5967160BCF9B24 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 8.0 KDA PROTEIN (FRAGMENT).
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o. 70;
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Best Local Similarity 100.0%; Pred. No. 70;
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30 GRPEY 34
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Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model OM protein

January 31, 2002, 13:39:19 ; Search time 46.78 Seconds (without alignments) 10.973 Million cell updates/sec Run on:

SAVHDPGYEGRPEY 14 US-08-957-709-75 14 1 SAVHDPGYRCBDEV Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

100059 seqs, 36664827 residues Searched:

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Length 1196; 0; Indels

50.0%; Score 7; DB 1; 100.0%; Pred. No. 0.99; Live 0; Mismatches

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δ g (Rel. 29, Created) (Rel. 29, Last sequence update) (Rel. 40, Last annotation update)

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RESULT 2 DNBI_HSV2

DNBI_HSV2 P36384; 01-JUN-1994 ( 01-JUN-1994 ( 20-AUG-2001 (

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17	S	'n	341		Y422_TREPA		
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24	S	•	400		PRTZ_HUMAN		
25	S	ď.	408		BPHG_BURCE	P37337 burkholderi	
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28	S	S	410	П	TDG_HUMAN	Q13569 homo sapien	
29	5	35.7	415	7	PROA_MYCTU	P71921 mycobacteri	
30				~	CBP1_HUMAN	P15085 homo sapien	
31	S		$\vdash$	Н	CBPA_BOVIN	_	
32	S.	35.7	419		PROA_STRCO	Q9rdk1 streptomyce	
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888888844444 499788601784	4. U	- I	0 Z N O C	E > K Z	-s-	3001	1	, F Q	μaε	≣ 0 0	. <b>M</b> H F O N O N
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TO CALGAGEN ALPHA 1(1); CHAIN PRECURSOR.

COLLAGEN ALPHA 1(1); CALGAGEN CALGAGEN ALPHA 1(1);

RM MELTAID-10090;

RM MEDIA 1(1); COLLAGEN CAMPINER CAMPINER CAMPINER ALPHA 1(1);

RM METRIX 13:223-233(1993).

COLLAGEN CALGAGEN VI ACTS AS A CELL-BINDING PROTEIN.

RM MEDIAN COLLAGEN VI ACTS AS A CELL-BINDING PROTEIN.

COLLAGEN ALPHA 2(1); AND ALPHA 3 CHAINS COMPOSED OF PREEE DIFFERENT CHAINS: ALPHA 1(VI),

COLLAGEN ALPHA 2(1); AND ALPHA 3 CHAINS AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING

COLLAGEN ALPHA 2(VI); AND ALPHA 3 CHAINS AND ALPHA 3 CHAINS: ALPHA 1(VI);

COLLAGEN ALPHA 2(VI); AND ALPHA 3 CHAINS AND ALPHA 3 CHAINS: ALPHA 1(VI);

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SEQUENCE OF 442-1025 FROM N.A.

AMEDILINE-93256888; PubMed-8489506;

Zhang R.Z., Pan T.C., Timpl R., Chu M.L.;

"Cloning and sequence analysis of cDNAs encoding the alpha 1, alpha 2 and a sequence analysis of cDNAs encoding the alpha 1, alpha 2 and a sequence analysis of CDNAs encoding the alpha 1, alpha 2 and 1931:787-792(193).

-I FOURTION: COLLAGEN VI ACTS AS A CELL-BINDING PROTEIN.

-I SUBUNT: TRIMERS COMPOSED OF THREE DIFFERENT CHAINS: ALPHA 1(VI), ALPHA 2(VI), AND ALPHA 3(VI).

-I FOUR PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G.X-Y) ARE HYDROXILATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A48350, A48350.
InterPro: IPR000635; Viral_DNA_bind.
Pfam: PF00747; Viral_DNA_bp; 1.
DNA-binding; DNA replication; Zinc-finger; Nuclear protein.
ZNE-TRING 499 512
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SEQUENCE 1197 AA; 128412 MW; C1576BB5B8865BFB CRC64;
                                                                                                                                                                                                                                MEDIATE-932844; PubMed-8385914; MEDIATE-932844; PubMed-8385914; MEDIATE-9328441; PubMed-8385914; MEDIATE-9328441; MINOLEOTIAE-9328441; MINOLEOTIAE-9328441; MINOLEOTIAE SEQUENCE Of the major DNA-binding protein gene of herpes simplex virus type 2 and a comparison with the type 1."; Arch. Virol. 122:183-196 (1993).
-!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA REPLICATION: UNCLEAR (PROBABLE).
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN FAMILY.
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MAJOR DNA-BINDING PROTEIN (INFECTED CELL PROTEIN 8) (ICP 8 PROTEIN).
DBP OR UL29 OR ICP8.
Viruses, samplex virus (type 2).
Viruses; dabna viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBL_TaxID=10310;
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Pred. No. 1;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDIATE-8874327; PubMed=2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
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21-JUL-1986 (Rel. 01, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
IMMEDIATE-EARLY PROTEIN IE12 (IMMEDIATE-EARLY-5) (VMW12).
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Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10299;
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Pred. No. 12;
0; Mismatches
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EMBL; X66406; CAA47033.1; -
EMBL; 218271; CAA379152.1; -
FIRS, S34839; S34839.
MCD: MCI:84659; Colfa1.
InterPro; IPR000087; Collagen.
Fram; PP01391; Collagen.
Fram; PP01391; Collagen.
Fram; PP01391; Collagen.
Fram; PP00321; WWR3.
SMART; SM00327; WWA: 3.
FRANTE; PS00321; WWA: 3.
EXTRACEJULAR mARTIX; Connective
Glycoprotein; Collagen; Cell adhe
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263 DPGYEG 268
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AC 191370;

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20-AUG-2001 (Rel. 40, Last annotation update) 50S RIBOSOMAL PROTEIN L20.
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                                                                                                                             NCBI_TaxID=2371;
                                         RPLT OR XF0740.
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                                     MEDLINE-82150256; PubMed-6278443; Watson R.J., Vande Woude G.F.; "DNA sequence of an immediate-early gene (IEMRNA-5) of herpes simplex varius type I."; Nucleic Acids Res. 10:979-991(1982).
                                                                                                                                                                   SEQUENCE OF 1-55 FROM N.A.
MEDLINE-82059456; PubMed-6272198;
Watson R.J., Umene K., Enquist L.W.;
"Reliterated sequences within the intron of an immediate-early gene of herpes simplex virus type 1.";
Nucleic Acids Res. 9:4189-4199(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A 3' Co-terminal family or mknas rrum rue merges and short region: two overlapping reading frames encode unrelated polypeptide one of which has highly reiterated amino acid sequence."; Nucleic Acids Res. 12:2473-2487(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIINE-85160822: PubMed-2984429;
McGeoch D.J.: Dolan A., Donald S., Rixon F.J.;
Msequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1.";
J. Mol. Biol. 181:1-13(1985).
                                                                                                                                                                                                                                                                                                                                                          Murchie M.-J., McGeoch D.J.; "DNA sequence analysis of an immediate-early gene region of the herpes simplex virus type 1 genome (map coordinates 0.950 to
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C5D2F662C71C88E0 CRC64;
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Pred. No. 19;
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100.0%; Pre
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MEDLINE-84169548; Pubmed-6324121;
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88 AA; 9806 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
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ID RL20_XX
AC Q9PFD8
DT 20-AUG
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REDINERSON A.J.G. Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaernga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvaernga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Bueno M.R.P., Calombo C., Costa R.F., Costa M.C.R., Costa Neto C.M.,
Colauto D.L., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Radrada J.S., Franca S.C., Franco M.C., Frome M., Fulan L.R.,
Radarier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ariegar J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Lemos M.V., Martins E.B., Lopes S.A., Lopes C.R., Machado J.A.,
Marques M.V., Martins E.L., Martins E.M.F., Marchado J.A.,
Marques M.V., Martins E.L., Martins E.M.F., Marsukuma A.Y.,
Mand M.Y., Martins E.L., Martins E.M., Pesquero J.B.,
Noon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Namin A. Jr., Nobrega F.C., Nunes L.R., Oliveira M.A.,
A do Oliveira M.C., de Oliveira R.C., Palmieri D.A., Pesquero J.B.,
A da Silve R.B., Pereira G.A.G., Santelli R.V., Sawasaki H.E.,
A da Silve A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., Tatiff D., Tasi S.M., Tsuhako M.H.,
RA da Silva A.M., Weidanis J.V., Sawasaki H.E.,
RA da Silva A.M., Weidanis J., Settoer A.J.,
RA da Silva A.M., Weidanis J., Settoer A.J.,
RA da Silva A.M., Verjovski-Almaida S., Vettore A.L.,
RA da Silva A.M., Verjovski-Almaida S., Vettore A.L.,
RA da Silva A.C.R., Truffi D., Tasi S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tasi S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Silva W.A., Verjovski-Almaida M.J., de Souza A.J.,
RA da Silva A.C.R., da Silva A.M., da Silva M.A., Sava M.A., Sava M.A., Satz M. Weidanis J., Settoer M.J., Sava S.M. S., Settor M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A., Sava M.A
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Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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PROSTTE; PS00337; RIBOSOMAL_L20; 1.
Ribosomal protein; RRNA-binding; Complete proteome.
SEQUENCE 119 AA; 13499 WW; FC2C9C68D3C554BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 25;
0; Mismatches
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Pfam; PF00453; Ribosomal_L20; 1.
PRINTS; PR00062; RIBOSOMALL20.
                                                                                                                                                                                                                                                                                     MEDLINE=20365717; PubMed=10910347;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P01180; INPO.
InterPro: IPR000981; Neurhypophys_horm.
Pfam; PF00120; hormone4; 1.
Pfam; PF00184; hormone5; 1.
PRINTS; PR00184; Neurhypophys_horm; 1.
SMART; SM00003; NH; 1.
PROSTIE; PS00264; Neurhypophys_Horm; 1.
PROSTIE; PS00264; Neurhypophys_Horm; 1.
MULTigene family; Signal.
                                                                                                                                                                                                                                                                    MEDIATE-89315773; PubMed=2748582;
MEDIATE-89315773; PubMed=2748582;
Richter D.;
Norley S.D., Figueroa J., Krentler C., Lederis K.,
Richter D.;
Vasotocin and isotocin precursors from the white sucker, Catostomus
commerson: cloning and sequence analysis of the cpMAs.";
Proc. Natl. Acad. Sci. U. S.A. 86:5245246(1989).
-I. FUNCTION: ISOTOCIN CANGES CONTRACTION OF SMOOTH MUSCLES.
-I. PTW. SEVEN DISULFIDE BONDS ARE PRESENT IN NEUROPHYSIN.
-I. SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                         "Two isotocin genes are present in the white sucker Catostomus commerson both lacking introns in their protein coding regions."; EMBO J. 8:2873-2877(1989).
     Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi; Cypriniformes; Catostomidae; Catostomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-30 PROVIDE AMIDE GROUP). 16FCB11A9DFFC517 CRC64;
                                                                             SEDUBNCE FROM N.A.
MEDILINE=90059870; PubMed=2583084;
Figueroa J., Morley S.D., Heierhorst J., Krentler C., Lederis K.,
Richter D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.7%; Score 5; DB 1; Length 154; 100.0%; Pred. No. 32; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOTOCIN.
NEUROPHYSIN IT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL ALDOLASE CLASS II PROTEIN AQ_1979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ_1979.
Aquifex aeolicus.
Bacteria, Aquificales; Aquificaceae; Aquifex.
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16053 MW;
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21
29
154 AA;
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Best Local Similarity
Matches 5; Conserv
                               Cypriniformes; C
NCBI_TaxID=7971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GYEGR 11
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|94 GYEGR 98
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YJ79_AQUAE
ID 737786;
DT 30-MAY-2000
DT 30-MAY-2000
DT 20-AUG-2001
DE AUG-2001
DE AUG-2001
CS AQUIFEX acol
CS AQUIFEX acol
CS AQUIFEX acol
CC BACTERIA; AG
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Matches
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HSP; P01180; 1NPO
HSP; P01180; 1NPO
HSP; P01180; 1NPO
Pfam; PF00220; hormone4; 1.
PF00220; hormone5; 1.
PRINTS; PR00181; NEUROPHYSIN.
PRODOM; P000166; Neurhypophys_horm; 1.
SMART; SM00003; NH; 1.
PROSITE; P800264; NEUROHYPOPHYS_HORM; 1.
HORMONE; Hypothalamus; Amidation; Cleavage on pair of basic residues; Inlane family; signal.
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                                                                                                                                                                                                                                                                                                                                                                                                      Catostomus commersoni (White sucker).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cyptiniformes; Catostomidae; Catostomus.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
BEDELINE-90059870; PubMed-2583084;
Figueroa J., Morley S.D., Heierhorst J., Krentler C., Lederis K.,
Richter D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ISOTICIN-NEUROPHYSIN IT 1 PRECURSOR [CONTAINS: ISOTOCIN (IT);
NEUROPHYSIN IT 1].
Catostomus commerson; (White sucker).
Catostomus commerson; (White sucker).
Catostomus (Relazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
1SOTICIN-NEUROPHYSIN IT 2 PRECURSOR [CONTAINS: ISOTOCIN (IT);
NEUROPHYSIN IT 2]
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NEUROPHYSIN IT 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
5. 31;
                             148 AA.
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Pred. No. 31;
0; Mismatches
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100.0%; Pro
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32 148 NEI
21 26 NEI
29 29 29 AM
148 AA; 15581 MW;
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es 5; Conservative
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                             STANDARD;
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94 GYEGR 98
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P15210;
                             CATCO
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AC NEU2_CATCO
DT 01-APR:
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DT 01-APR:
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STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-FBE-1994 (Rel. 28, Last sequence update)
02-OMO-2001 (Rel. 40, Last annotation update)
RIBOSE S-PHOSPHATE ISOMERASE A (EC 5.3.1.6) (PHOSPHORIBOISOMERASE RAPIA OR B2914 OR 24252 OR ECS3785.
                                        Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.B., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                         Nature 392:353-358(1998).
-!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY.
                                                                                                                                                                                                                                                                                                                                     Length 208;
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Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                       INC (BY SIMILARITY).
INC (BY SIMILARITY).
INC (BY SIMILARITY).
3295652C5ED17344 CRC64;
                                                                                                                                                                                                                                                               SIMILARITY).
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100.0%; Pred. No. 42;
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Pfam; PF00596; Aldolase_II; 1.
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                             MEDLINE=98196666; PubMed=9537320;
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101 ZI
174 ZI
23550 MW;
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5; Conservative
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101
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1208 AA;
         SEQUENCE FROM N.A.
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P27252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARDINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; Marsha T., Fanaka M., Tokeyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Fanaka M., Toke T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli oli7:H7 and genomic comparison with a laboratory strain K-12.";
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"Comparing the predicted and observed properties of proteins encoded to experichle of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
-:- CATALYTIC ACTIVITY: D-RIBOSE 5-PHOSPHATE = D-RIBULOSE 5-PHOSPHATE.
-:- PATHWAY: NONOXIDARIVE BRANCH OF THE PENTOSE PHOSPHATE PATHWAY.
-:- SUBJUNIT: HOWODIMER.
-:- SIMILARITY: BELONGS TO THE RIBOSE 5-PHOSPHATE ISOMERASE FAMILY.
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                                                                                                                                                                                                                                         STRAIM-OIS:H7 (EDL933 / ATCC 700927; STRAIM-OIS:H7 (EDL935) PubMed-11206551; Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.E., Evans P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Medoaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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J. Bacteriol. 173:5944-5953(1991).
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219 AA; 22860 MW; B53C49CC3DB188BC CRC64;
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EMBL; X66836; CAA47309.1; ALT_INIT.
EMBL; U28377; AAA69081.1; -.
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MEDLINE=97443975; PubMed=9298646;
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SWISS-2DPAGE; P27252; CC
EcoGene; EG11443; rpiA.
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$37500; $37500.
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Length 219;

35.7%; Score 5; DB 1;

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                                                                                                                                                                                                                          TRAIN—CSTBL/G.

STRAIN—CSTBL/G.

A MEDILINE—S08079105; Pubmed—9417125;

A MEDILINE—98079105; Pubmed—9417125;

A Danilov V. Blum M. Schweickert A. Campione M., Steinbeisser H.;

RT goosecold.";

T "Negative autoregulation of the organizer-specific homeobox gene
RT goosecold.";

G. I. Biol. Chem. 273:627-635(1998).

I. Biol. Chem. 273:627-635(1998).

C. I. BLOLL Chem. 273:627-635(1998).

INTO XENOPUS ENPRESSING REGIONS OF THE GASTRULATING
MOUSE EGG CYLINDER HAVE ORGANIZER-LIKE ACTIVITY WHEN TRANSPLANTED

C. I. SUBCELLULAR LOCATION: NUCLEAR.

C. I. TISSUE SPECIFICITY: IN PARK. GASTRULATION, EXPRESSED IN THE
DORSAL LIP. IN LATER STAGES OF DEVELOPMENT FOUND IN HEAD, LIMBS

C. I. TISSUE SPECIFICITY: OF THE PAIRED FAMILY OF HOMEOBOX PROTEINS.

C. I. INDICTION: BY ACTIVIN.

C. SIMILARITY: SELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.

C. SIMILARITY: SUBERAMILY.

C. "BIOLODE SUBFAMILY.

C. "BIOLODE SUBFAMILY.
Blum M., Gaunt S.J., Cho K.W.Y., Steinbeisser H., Blumberg B., Bittner D.A., de Robertis E.M.; "Gastrulation in the mouse: the role of the homeobox gene goosecoid."; Cell 69:1097-1106(1992).
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HSSP, P06601; HEJC.
HRANSFAC, 102047; --
MGD; MGI:95841; Gsc.
HOMEODOX; HOMEODOX:
Pfam; PF00146; HomeoDox; 1.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Bovelopmental protein; Nuclear protein; DNA-binding; Homeobox.
BOVALEND
DNA_BIND
160 219 HOMEOBOX.
BEQUENCE 256 AA; 27979 WW: 3639FB059AC3DB9E CRC64;
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SEQUENCE FROM N.A.
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CTISSUE-Leukocyte;

MEDLINE-94375063; PubMed-7916327;

MEDLINE-94375063; PubMed-7916327;

MEDLINE-94375063; PubMed-7916327;

Molecular cloning of the human homeobox gene goosecoid (GSC) and mapping of the gene to human chromosome 14q32.1.";

Genomics 21:388-393(1994).

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I Genomics 21:38
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Was musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bustrycus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MIM; J38890; -...
InterPro: J8890; -...
Fam; PF00046; homeobox; 1.

PROSITE; SMO0399; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

Develomental protein; Nuclear Protein; DNA-binding; Homeobox.

DNA_BIND 155 214

HOMEOBOX.

SEQUENCE 252 AA; 27853 MW; 6C0EEC48C084D323 CRC64;
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    Best Local Similarity 100.0%; Pred. No. 44; Matches 5; Conservative 0; Mismatches
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MEDLINE-92315328; Pubmed-1352187;
                                                                                                                                                                   152 GRPEY 156
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                                                                                                                      10 GRPEY 14
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TD GSC_MOUSE
AC 002591;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                               ;
0
 Length 256;
                               0; Indels
Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 50; Matches 5; Conservative 0; Mismatches
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Miller D.L.; "Elongation factor Ts of Chlamydia trachomatis: structure of the gene and properties of the protein."; Arch. Biochem. Biophys. 344:43-52(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
83D907C8C81D2C0E CRC64;
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STRAIN-MORN, V NIGG;
MEDLINE=20150255; Pubmed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K.,
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL) POTENTIAL.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_raxID=83560;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RPSB OR TCOOSI.
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SUSHI 2.
BY SIMILARITY.
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272
240
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N 30819 MW;
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M11061; AAA67527.1; U
M11062; AAA67527.1; U
M11063; AAA67527.1; U
M11064; AAA67527.1; U
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M15864; AAA59162.1;
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                             AAA67527
                                                                                                                                                                                                                EMBL; M15864; AAA59162
PIR; A01856; UHHU2.
PIR; A24113; A24113.
PDB; 11LM; 26-JAN-95.
PDB; 11LN; 26-JAN-95.
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Matches 5; Conserv
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                                                     M10322;
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SIGNAL
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P71145;
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TRANSMEM
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MEDLINE-86067183; PubMed-2999698;
IShlada N., Kanamori H., Noma T., Nikaido T., Sabe H., Suzuki N.,
Shlmizu A., Honjo T.;
"Molecular cloning and structure of the human interleukin 2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Regulation of the human interleukin-2 receptor alpha chain promoter activation of a nonfunctional promoter by the transactivator gene of
MEDLINE-85012734; PubMed-6090949;
Nikaido T., Shimizu A., Ishida N., Sabe H., Teshigawara K., Maeda M. Uchiyama T., Yodoi J., Honjo T.;
"Molecular cloning of cDNA encoding human interleukin-2 receptor.";
Nature 311:631-635(1984).
                                                                                                                                    MEDLINE-85012733; PubMed-6090948; Leonard W.J., Depper J.M., Crabtree G.R., Rudikoff S., Pumphrey J., Leonard W.J., Depper J.M., Crabtree G.R., Rudikoff S., Pumphrey J., Robb R.J., Kroenke M., Svetlik P.B., Peffer N.J., Waldmann T.A., Green W.C.; "Molecular cloning and expression of cDNAs for the human interleukin 2 receptor."; Nature 311:626-631(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-21 FROM N.A.
MEDLINE-87159546; PubMed=3030566;
Cross S.L., Feinberg M.B., Wolf J.B., Holbrook N.J., Wong-Stall F.,
Leonard W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=66018868; PubMed=2996141;
Leonard W.J., Depper J.M., Kanehla M., Kroenke M., Peffer N.J.,
Svetlik P.B., Sullivan M., Greene W.C.;
"Structure of the human interleukin-2 receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 13:7579-7589(1985)
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CAA26906.1;
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x03138; 0
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EMBL; EMBL; EMBL;

EMBL; EMBL; EMBL; EMBL;

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Gaps

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Length 272; Indels

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A Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
A Salzberg S.L., Eisen J., Fraser C.M.,
Salzberg S.L., Eisen J., Fraser C.M.,
The Salzberg S.L., Eisen J., Fraser C.M.,
The Salzberg S.L., Salzberg S.L., Schome sequences of Chlamydia trachomatis MoPn and Chlamydia

The meumoniae AR39.*;
The Salzberg S.B. 1397-1406(2000).

L Nucleic Acids Res. 28:1397-1406(2000).

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MEDLINE-99000809; Pubmed-9784136;
MEDLINE-99000809; Neahan S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.,
Bavis R.W.,
Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
Science 282:754-755(1998).
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29E4F309F45435F7 CRC64;
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30-MAY'2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
30S REDSORMAL PROTEIN S2.
RPSB OR RS2 OR CT680.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Pfam; PF00118; Ribosomal_S2: 1.
PROSTITE; PR00965; RIBOSOMAL_S2_1; 1.
PROSTITE; PS00965; RIBOSOMAL_S2_1; 1.
RIBOSOMAL_S2_1; 1.
RIBOSOMAL_S2_1; 1.
RIBOSOMAL_S2_2; 1.
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InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00318; Ribosomal_S2; 1.
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**HENDSE**
--- PATHWAY: PURINE SALVAGE.
--- SUBUNIT: HOMOTETRAMER:
--- SUBUNIT: HOMOTETRAMER:
--- STALLARITY: BELONGS TO THE IUNH FAMILY.
--- STALLARITY: BELONGS TO THE IUNH FAMILY.

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MEDIATRE-96244503; PubMed=864238;
Degano M., Gopaul D.N., Scapin G., Schramm V.L., Sacchettini J.C.;
"Three-dimensional structure of the inosine-uridine nucleoside N-
ribohydrolase from Crithidia fasciculata.";
Blochemistry 35:5971-5981(1996).
-!- FUNCTION: CATALYZES THE HYROLYZIS OF ALL OF THE COMMONY
COCUMRING PORINE AND PYRIMIDINE NUCLEOSIDES INTO RIBOSE AND THE
ASSOCIATED BASE, BUT HAS A PREFERENCE FOR INOSINE AND URIDINE AS
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MEDLINE-96214502; PubMed-8614237;
MEDLINE-96214502; Degano M., Sacchettini J.C., Schramm V.L.;
"Inosine-uridine nucleoside hydrolase from Crithidia fasciculata.
Genetic characterization, crystallization, and identification of histidine 21 as a catallytic site residue.";
Biochemistry 35:5963-5970(1996).
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-!- CATALYTIC ACTIVITY: A N-D-RIBOSYLPURINE + H(2)O = A PURINE + D-
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Eukaryota, Euglanozoa, Kinetoplastida, Trypanosomatidae, Crithidia.
NCBL_TaxID-5656,
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027546;
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 36, Last sequence update)
11-NOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (EC 3.2.2.1)
(IU-NUCLEOSIDE HYDROLASE) (PURINE NUCLEOSIDASE).
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PRINTS; PR00395; RIBOSOMALS2.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
RIBOSOMAI 1 protein; Complete proteome.
SEQUENCE 282 AA; 31146 MW; 63693C13CA6EA26B CRC64;
                                                                                                                                                                                                                                          Query Match 35.7%; Score 5; DB 1; Best Local Similarity 100.0%; Pred. No. 55; Matches 5; Conservative 0; Mismatches
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MUTAGEN 240 240 H->A: LOSS OF ACTIVITY. SEQUENCE 314 AA; 34194 MW; 21B51B3878A73FA1 CRC64; FT

0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels

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Sequence 11,
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-278-089A-25

US-08-278-089A-25

US-08-278-089A-25

US-08-278-089A-25

US-08-278-089A-25

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US-08-585-585A-12
US-08-685-808-11
US-08-505-860C-11
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TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)

TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)

TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins, TITLE OF INVENTION: and Methods for Purifying and Identifying Same NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS: 63

CORRESPONDENCE ADDRESS: 64

CORRESPONDENCE ADDRESS: 65

CORRESPONDENCE ADDRESS: 67

CORRESPONDENCE FORM: 67

CITY: Washington STATE: D.C.

ZIP: 20005

COMPUTER FRADABLE FORM: 67

COMPUTER FRADABLE FORM: 67

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: ISM PC compatible 67

COMPUTER: SYSTEM: PC COMPATIBLE FORM: 67

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 1486/43163
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-884
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 14; DB 4; I
llarity 100.0%; Pred. No. 2.3e-09;
Conservative 0; Mismatches 0;
                                        US-09-232-191-21
US-09-232-191-21
US-08-356-180-4
US-08-540-906-2
US-08-640-906-17
US-08-574-998-2
US-09-357-014-2
US-09-31-168-1
US-09-31-168-1
US-09-31-168-1
US-09-356-818A-2
US-09-356-818A-2
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                                                                                                                                                                                                                                                                                                                                                                                         US-09-033-153-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/08822774; Patent No. 6183997; GENERAL INFORMATION: APPLICANT: HOLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Best Local Similarity
Matches 14; Conserv
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GENERAL INFORMATION:
APPLICANT: HAYNES, CHARLES A., et al
APPLICANT: HAYNES, CHARLES A., et al
TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto.
STATE: California
COUNTRY: USA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: PATENTIN SYSTEM: PS. A -ULLY 1995
COMPUTER: PATENTIN RELEASE #3.750
FREING DATE: 24 -ULLY 1995
CITASSIFICATION NUMBER: CEDT.017.00US
FREING DATE: A -ULLY 1995
CLASSIFICATION NUMBER: CEDT.017.00US
TELECOMMUNICATION INFORMATION:
NAME: Rae-Venter, Barbara
NEGISTRATION NUMBER: CEDT.017.00US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION POR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,808
FILING DATE: 24-ULY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/505,860
FILING DATE: 24-ULY-1995
ATTOREY AGENT INFORMATION:
APPLICATION NUMBER: 32.750
FILING DATE: 24-ULY-1995
ATTOREY AGENT INFORMATION:
TELEPHONE: (650) 328-4400:
TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 20;
Mismatches
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US-08-505-860C-11
Sequence 11, Application US/08505860C
Patent No. 6174700
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; P.
Matches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 EGRPE 13
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5 EGRPE 9
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                                                                                                                                                                                                                                                             APPLICANT Alimonth Douglas G. APPLICANT Humphries, Keith R. APPLICANT Humphries, Keith R. APPLICANT Humphries, Keith R. APPLICANT Boheny. James G. APPLICANT Jervis, Enic APPLICANT Jervis, Enic APPLICANT Jervis, Enic APPLICANT Jervis, Enic APPLICANT Jervis, Enic APPLICANT Selection using growth factor-polysaccharide TITLE OF INVENTION: cell proliferation using growth factor-polysaccharide TITLE OF INVENTION: binding fusion proteins of the Companies of SeQuences: Law Group TITLE OF INVENTION: binding fusion proteins of the Companies of Sequence Applicants and Alone Sequences of Companies of Sequence Andro Companies of Companies of Sequence Readable Form: Law Group Sequence Readable Form: Law Group Companies Tight Occompanies of Companies 
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Parent No. 6048715
GENERAL INFORMATION
TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
TITLE OF INVENTION: 1 SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
ORNESSPONDENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSE: RAE-VENTER LAW GROUP
STREET 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 24;
                                                                                                     RESULT 2
US-08-585-585A-12
; Sequence 12, Application US/08585585A
? Datent No. 5874308
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%; Scallarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-585-585A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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US-08-685-808-11
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Indels
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APPLICANT: Suzuki, Shintaro
TITLE OF INFORTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.7%; Score 5; DB 1;
100.0%; Pred. No. 27;
Live 0; Mismatches
                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION UNBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION UNBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/188,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 31340 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: NO. 5597725and, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 31340 TELECOMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Sequence 24, Application US/08188228
: Patent No. 5597725
                                                                                                                                                                                               NAME: No. 5597725and, Greta E. REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                     TELEPANE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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6 GYEGR 10
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ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 GYEGR 11
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-188-228-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SUZUKI, Shintaro
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A. TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7%; Score 5; DB 6;
100.0%; Pred. No. 24;
Live 0; Mismatches
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMUNOGLOBULING

NUMBER OF SEQUENCES: 43

CURRENT APPLICATION DATA:

PELING DATE: 21-JAN-1994

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR DATE: 10-DEC-1992

APPLICATION NUMBER: 986,931

FILING DATE: 16-DEC-1991

PILING DATE: 12-NOV-1989

PILING DATE: 22-NOV-1989

PILING DATE: 23-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08188228 Patent No. 5597725
                      27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                           Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                          ; MOLECULE TYPE: protein; HYPOTHETICAL: no
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                       5514582-24
;Patent No. 5514582
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25 PGYEG 29
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                                                                                                                                                                                                                                                                                           5 EGRPE 9
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5514582-24
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US-08-188-228-18
                    LENGTH:
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GENERAL INFORMATION:

APPLICATION:
APPLICATION:
APPLICATION:
APPLICANT: SULUKI, SINITARO
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                     CUDNITY: 0.5A

CUDNITY: 0.5A

CUDNITY: 0.5A

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/332,643
FILING DATE:
APPLICATION NUMBER: 0S/07/872,643
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REFERENCE/DOCKET NUMBER: 35,302
REGISTATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,866/30795
TELECOMMUNICATION INFORMATION:
MET PRINCE/DOCKET NUMBER: 37,866/30795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.7%; Score 5; DB 18 Best Local Similarity 100.0%; Pred. No. 27, Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 and no acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08332643
Sequence 18, Application US/08332643
Patent No. 5639634
Patent No. 5639634
Patent No. 5639634
Patent No. 5639634
PAPLICANT: Suzuki, Shintaro
APPLICANT: Suzuki, Shintaro
APPLICANT: CADIERIN MATERIALS AND METHODS
NUMBER OF INVENTION: CADIERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Two First National Plaza, 20 South Clark
STREET: 1111nois
COUNTRY: USA
ZIP: 1111nois
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY AISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 GURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/332,643 FILING DATE:
                                                                                                                                                                                                                                                       Ouery Match 35.7%; Score 5; DB: Best Local Similarity 100.0%; Pred. No. 27, Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
TELEX: 25-3856
INPORMATION FOR ESQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acids
TYPE: 10POLOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: protein US-08-332-643-18
                                                                                                                                                 , MOLECULE TYPE: protein US-08-188-228-24
                                                                                                                                                                                                                                                                                                                                                     7 GYEGR 11
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6 GYEGR 10
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US-08-332-643-18
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0; Indels
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US-08-332-638-18
Sequence 18, Application US/08332638
Sequence 18, Application US/08332638
Sequence 18, Application US/08332638
TITLE INFORMATION: CAPHERIN MATERIALS AND METHODS
TITLE OF INVENTION: CAPHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STREET: 1111nos
COUNTRY: USA
LILIANDS
COUNTRY: USA
ZIP: 6060
COMPUTER READABLE FORM:
                                                                    ||||||
6 GYEGR 10
                                      7 GYEGR 11
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Length 40; 0; Indels

35.7%; Score 5; DB 100.0%; Pred. No. 27 tive 0; Mismatches

Query Match 35.7 Best Local Similarity 100. Matches 5; Conservative

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Length 40;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Breitman, Martin L.
APPLICANT: Rossant, Janet
APPLICANT: Wasnat, Janet
APPLICANT: Yamaguchi, Terry P.
TITLE OF INVENTION: No. 5681714el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFERALING SIJER: r. DOS/M9. DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,089A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                    35.7%; Score 5; DB 1; 100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.7%; Score 5; DB 1
100.0%; Pred. No. 30;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
                                (312) 474-63(
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.79
Best Local Similarity 100.(
Matches 5; Conservative
                                                                                                                                                      SEQUENCE CHARACTERISTICS: LENGTH: 40 amino acids
                            TELEPHONE: (312) 474-6
TELERAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-332-638-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 5681714ch
                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 568171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 GYEGR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GYEGR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-278-089A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25,
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FLING DATE: 01-NOV-1994
CLASSIFICATION: 435
PROCK APPLICATION: 435
PROCK APPLICATION NUMBER: US/08/049,460
APPLICATION NUMBER: US/08/049,460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: SUZUKI, SHINTARO
TITLE OF INVERTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%; Scc...
100.0%; Pred. No....
0; Mismatches
                                                                                                      SOFTWARE: PACENTIN RELEASE #1.0, VET CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,460
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE: ATGRATION:
AREFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08332638 Patent No. 5646250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITORNEY/AGENT INFORMATION:
NAME: NO. 564550and, Greta E.
REGERATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHRARETERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-332-638-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
60606
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RESULT 15

USC-08-083-590A-15

Sequence 15, Application US/08083590A

Patent No. 5786158

GENERAL INFORMATION:

TITLE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: Nucleic Acids

TITLE OF INVENTION: Nucleic Acids

TITLE OF INVENTION: Nucleic Acids

NUMBER OF SEQUENCES: 21

CORRESPONDENCE S: 21

CORRESPONDENCE S: 21

CORRESPONDENCE S: 21

COUNTY TOWN YORK

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTY IN NEW YORK

STATE: New YORK

STATE: New YORK

STATE: New YORK

COMPUTER READABLE FORM:

MEDION TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/08/083,590A

FILING DATE: 25-JUN-1993

FILING DATE: 25-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 78;
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/264,534
FILING DATE:
FILING DATE: US/08/264,534
FILING DATE: US/08/264,534
FILING DATE: US/08/264,534
FILING DATE: US/08/264,534
FILING DATE: US/08/264,534
FILING DATE: US/08/264,534
FILING PAPLICATION NUMBER: US/07/695,189
FILING DATE: US/08/MATION:
NAME: MISTOCK, S. Lealie
REGISTRATION NUMBER: 18,872
RECEPHONE: 212 790-9090
TELEPHONE: 212 780-9090
TELEPHONE: 212 780-9090
TELEPKX: 212 8698864/9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TVENCY AMINORALICATION
TO SECUENCE CHARACTERISTICS:
TVENCY AMINORALICATION
TO SEQUENCE CHARACTERISTICS:
TVENCY AMINORALICATION
TO SECUENCE CHARACTERISTICS
TVENCY AMINORALICATION
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TVENCY AMINORALICATION
TO SECUENCE CHARACTERISTICS
TVENCY AMINORALICATION
TO SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 5; DB 1;
Pred. No. 47;
0; Mismatches
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 7326-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; F
Matches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
WOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PGYEG 10
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70 PGYEG 74
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23. Application US/08264534
| Patent No. 5648464
| Patent No. 5648464 |
| Patent No. 5648464 |
| TILE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains CORRESPONDENCE 34
| TITLE OF INVENTION: Human No. 5648464ch And Methods Based Thereon CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: New York STATE: New York
                                                                                                                                                                                                                                                                                              APPLICANT: Breinan, Martin L.
APPLICANT: Breinan, Martin L.
APPLICANT: Rossant, Janet
APPLICANT: Manguchi, Terry p.
APPLICANT: Vamaguchi, Terry p.
TITLE OF INVENTION: No. 5998187el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: A.O. King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER RELABBLE FORMS

CONFUTER: IBM PC compatible

CONFOURER: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,957A

FILING DATE: 23-APR-1997

CLASSIFICATION NUMBER: 31-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KULGOYGY, Linda M.

REGISTRATON NUMBER: 34,971

REFERENCE/DOCKET NUMBER: 3153-212

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 24:

SEQUINCE CHARACTERISTICS: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.7%; Score 5; DB; Best Local Similarity 100.0%; Pred. No. 30, Best Local Si Conservative 0; Mismatches
                                                                                                                                                                                            Sequence 24, Application US/08838957A Patent No. 5998187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy A'
COMPUTER: IRM COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IMMEDIATE SOURCE:
CLONE: NO. 5998187ch
US-08-838-957A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 40 King
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GYEGR 11
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37 GYEGR 41
                                                                                                                                                               US-08-838-957A-24
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US-08-264-534-2
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Gaps .; 0

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; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-15

QUERY MAtch
35.7%; Score 5; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 6 PGYEG 10

| | | | | | |
| Db 70 PGYEG 74
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Search completed: January 31, 2002, 13:15:12 Job time: 93 sec

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; Search time 140.03 Seconds (without alignments) 7.406 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522463 seqs, 74073290 residues
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	Description	Methan	HSV-2	HSV-2	Partia	A huma	Partia	. Partia	Human	Human	Human	Human
SUMMARIES	ID	AAW72851	AAW72197	AAW72105	AAB81410	AAB08766	AAB81412	AAB81411	AAB15536	AAM24248	AAB90544	AAB90560
	DB	19	19	19	22	21	22	22	21	22	22	22
	ouery Match Length DB	14	623	1196	418	440	440	478	613	613	613	613
di	Query Match	100.0	50.0	50.0	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9
	Score	14	7	7	9	9	9	9	<b>.</b>	9	9	9
	Result No.	1	7	3	4	5	9	7	80	6	10	11

Junction sequence Peptide encoded by Amino acids encode prugAS expression Rat cadherin-1 cy Rat cadherin-1 cy Rat cadherin-1 cy Rat cadherin-1 cy Amino acid sequenc Tek receptor Notch Peptide #9170 enco Human colon cancer Human secreted pro C glutamicum prote HSV-1 ICPA7. Herp Wild type viral US Human secreted pro Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional inhib Bifunctional colon cancer Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia	se uridine-binding motif.  P deaminase; PCR;  n.  extracts and complexes - f nucleic acid polymerases, for replication
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Gaps

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Length 623;

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induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
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04-NOV-1996;
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Esser KM,
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                            This is the uridine-binding motif of the dCTP deaminase of methanococcus jannaschii. Sequences are provided (see AAW72849-57) of the uridine-binding motifs of dCTPases and dCTP deaminases of pyrococcus furiosus (see AAW72847), Methanococcus jannaschii, con the uridine-binding motifs of dCTPases and dCTP deaminaschii, con the consensus (see AAW72848) is also provided. A claimed herpesvirus; a consensus (see AAW72848) is also provided. A claimed herpesvirus; a consensus (see AAW72848) is also provided. A claimed performing the reaction in the presence of one or more of the following: a polymerase enhancing factor (PEF), a dCTPase, a collowing: a polymerase enhancing factor (PEF), a dCTPase, a criminal that turns-over dCTP and a protein having one or more of sequences provided in AAW72848-57. A claimed protein having PEF activity comprises one or more of sequences given in AAW72848-57. Contact of the sequences of the contact of the contact of sequences of the contact of the contact of sequences of the contact of the contact of sequences of the contact of sequences of the contact of sequences of the contact of the contact of sequences of the contact of sequences of the contact of the contact of sequences of the contact of the contact of sequences of the contact of the contact of sequences of the contact of sequences of the contact of sequences of the contact of the contact of sequences of the contact of the contact of the contact of sequences of the contact of the contact of sequences of the contact of the contact of the contact of sequences of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
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  Claim 71; Page 47; 161pp; English
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96US-0030279
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N-PSDB; AAV62176.
                                                                                                                                                                                                                                                                                                                                      14 AA;
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04-NOV-1996;
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Esser KM,
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SO.0%; Score 7; DB 19; Length 1196;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels
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AAW72105 standard; Protein; 1196 AA.
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Leary JJ;
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96US-0030279.
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Gaps

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Length 418; Indels

22;

AAB81410;

AAB81410

RESULT

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Domain Region Domain

Key

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Domain

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with Alzheimer's disease and Huntingdon's chorea, and inhibit growth and infection of agents such as bacteria, fungi, viruses and other parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferative disorder; actinic keratosis; atherosclerosis; bursitis; cirrhosis; hepatitis; mixed connective tissue disease; MCTD; myelofibrosis; paroxysmal nocturnal hemoglobinuria; cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; autoimmune disorder; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; Addison's disease; adult respiratory distress syndrome; AIDS; Addison's disease; amyloidosis; anaemia; asthma; autoimmune haemolytic anaemia; infection; Werner syndrome; haemodialysis; extracorporeal circulation; trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; leukocyte and blood related protein; LBAP; arteriosclerosis;
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353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human leukocyte and blood related protein (LBAP).
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/note= "immunoglobulin domain"
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                                                                                                                        DB 22
. 25;
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                                                                                                                        Score 6; 1
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                AAB08766 standard; Protein; 440 AA.
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Best Local Similarity
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                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            superfamily (195F). 195F polyperides and polynucleotides encoding them can be used for the prevention and treatment of disorders involving aberrant protein expression or biological activity. Members of the immunoglobulin superfamily are involved in cell shape, cell migration, recognition, cell growth and replication, cell shape, cell migration, immunological responses, molecular transport, shape recognition, toxin neutralisation, regulation of gene transcription and cell death marking. The 195F polypeptides can be used for the treatment of immune deficiencies, autoimmune disorders include multiple sclerosis, rheumatoid arthritis, cancer and insulin dependent diabetes mellitus. They can also be used to regulate haematopoiesis, treat osteoporosis and periodontal diseases, promote wound healing, treat including lesions associated arthritis, treat nervous system disorders including lesions associated
                                                                                                                                                                                                                                                           Human; IgSF; immunoglobulin superfamily; immunostimulant; immunosuppressive; cytostatic; antirheumatic; antiarthritic; nootropic; antidiabetic; osteopathic; vulnerary; antidiflammatory; neuroprotective; anticonvulsant; antimicrobial; gene therapy; immune disorder; autoimune disorder; infection; haematopolesis; osteoporosis; periodontal disease; inflammation; nervous system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide sequence encodes a novel member of the Immunoglobulin superfamily which can be used in treatment of immune deficiencies and disorders, promotion of wound healing and prevention of microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a novel member of the Immunoglobulin (Ig)
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/note= "forms loop region"
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/note= "forms loop region"
                                                                                                                                                                                                                       Partial human IgSF protein, SEQ ID NO: 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                 AAB81410 standard; Protein; 418 AA.
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|abel= Domain_2
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267..340
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N-PSDB; AAF82525.
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429 pgyegrp 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                                                                                                                                                                               18-JUN-2001
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Ford J,

us-08-957-709-75.rag

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The present sequence presents a human leukocyte and blood related protein, designated LBAP. LBAP polynucleotides and polypeptides are useful for treating or preventing a disorder associated with decreased expression or activity of LBAP including a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), cirrhosis, hepatitis, mixed connective tissue disease (MCTD), cirrhosis, hepatitis, mixed connective tissue disease (MCTD), cirrhosis, hepatitis, mixed connective tissue disease (MCTD), cancers in myelofibrosis, paroxysmal nocturnal hemoglobinuria, etc., cancers in actiona, teratocarcinoma and in particular cancers of the adrenal sarcoma, teratocarcinoma and in particular cancers of the adrenal and an autoimmune/inflammatory disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, andlicated immunodeficiency allergies, ankylosing spondylitis, anyloidosis, anemia, asthma, complications of cancer, haemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitlo, protozoan, and helminthic infections,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte and blood associated proteins and polynucleotides encoding
them, useful for diagnosis, treatment and prevention of
autoimmune/inflammatory disorders and cell proliferative disorders
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42.9%; Score 6; DB 21; Length 440;
Best Local Similarity 100.0%; Predc. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels
                            /note= "potential phosphorylation site" 410..434
                                                                                                      "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial human IgSF protein, SEQ ID NO: 7.
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N-PSDB; AAA64686.
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|199 pgyegr 204
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Modified-site
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The present sequence is a novel member of the Immunoglobulin (Ig)

superfamily (IgSP). IgSP polypeptides and polynucleotides encoding

them can be used for the prevention and treatment of disorders involving

aberrant protein expression or biological activity. Members of the

immunoglobulin superfamily are involved in cell attachment, cell-cell

recognition, cell growth and replication, cell shape, cell migration,

immunological responses, molecular transport, shape recognition, toxin

neutralisation, regulation of gene transcription and cell death marking.

The IgSP polypeptides can be used for the treatment of immune

celficiencies, autoimmune disorders and disorders caused by viral or

tungal infections. Such disorders include multiple sclerosis, rheumatoid

arthritis, cancer and insulin dependent diabetes mellitus. They can also

be used to regulate haematopoiesis, treat inflammatory disorders such as

diseases, promote wound healing, treat inflammatory disorders such as

carthritis, treat nervous system disorders including lesions associated

with Alzheimer's disease and Huntingdon's chorea, and inhibit growth and

infection of agents such as bacteria, fungi, viruses and other parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide sequence encodes a novel member of the Immunoglobulin superfamily which can be used in treatment of immune deficiencies and disorders, promotion of wound healing and prevention of microbial infections -
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1larity 100.0%; Pred. No. 26;
Conservative 0; Mismatches 0; Indels
                                                                1..99
/labbl= Domain_1
1..97
/note= "cysteine-bonded loop region"
                                                                                                                                                                                                                      289..371
/note= "forms loop region"
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                                        Location/Qualifiers
1..99
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AAB81411
ID AAB81411 standard; Protein; 478 AA.
XX
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/note= "forms loop
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/label- Domain_2
153..233
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N-PSDB; AAF82527.
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Best Local Similarity
Matches 6; Conserv
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                 Homo sapiens.
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28;

Pred. No.

100.0%;

Best Local Similarity

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immunosuppressive; cytostatic; antirheumatic; antiarthritic; nootropic; antidiabetic; osteopathic; vulnerary; antiinflammatory; neuroprotective; antidicorrobial; gene therapy; immune disorder; autoimmune disorder; infection, hemantopolesis; osteoporosis; perlodontal disease; inflammation; nervous system disorder.
                                                Human; IgSF; immunoglobulin superfamily; immunostimulant;
                                                                                                                                                       "cysteine-bonded loop region"
                                                                                                                                                                                                      /label= Domain_3
327..409
/note= "forms loop region"
                                                                                                                                                                            ..271
te= "forms loop region"
                                Partial human IgSF protein, SEQ ID NO: 5.
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                                                                                                                       Location/Qualifiers
                                                                                                                                                               /label= Domain_2
191..271
                                                                                                                                      /label= Domain_1
                                                                                                                                                                                                                                                                       16-OCT-2000; 2000WO-US28661
                                                                                                                                                                                                                                                                                       99US-0417791
                (first entry)
                                                                                                                                                             ...273
                                                                                                                                                                                              320..411
                                                                                                                                                       /note=
184..27
                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-273774/28.
N-PSDB; AAF82526.
                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                       Yeung G;
                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                      WO200127278-A2
                                                                                                                                                                                                                                                                                       14-OCT-1999;
                                                                                                        Homo sapiens
               18-JUN-2001
                                                                                                                                                                                                                                                      19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                       infections
AAB81411;
                                                                                                                                                                                                                                                                                                                      Ford J,
                                                                                                                               Doma in
                                                                                                                                               Region
                                                                                                                                                               Domain
                                                                                                                                                                                              Domain
                                                                                                                        Key
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The present sequence is a novel member of the Immunoglobulin (Ig) superfamily (IgSF). IgSF polypeptides and polynucleotides encoding them can be used for the prevention and treatment of disorders involving aberrant protein expression or biological activity. Members of the immunoglobulin superfamily are involved in cell attachment, cell-cell recognition, cell growth and replication, cell shape, cell migration, immunological responses, molecular transport, shape recognition, toxin neutralisation, regulation of gene transcription and cell death marking. The IgSF polypeptides can be used for the treatment of immune deficiencies, autoimmune disorders and disorders caused by viral or fungal infections. Such disorders include multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, promote wound healing, treat inflammatory disorders such as arthritis, treat nervous system disorders including lesions associated with Alzheimer's disease and Huntingdon's chorea, and inhibit growth and infection of agents such as bacteria, fungi, viruses and other parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis, cancer and insulin dependent diabetes mellitus. They can also be used to regulate haematopoiesis, treat osteoporosis and periodontal
Polynucleotide sequence encodes a novel member of the Immunoglobulin superfamily which can be used in treatment of immune deficiencies and disorders, promotion of wound healing and prevention of microbial
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This sequence represents a human immune system molecule (IMOL) encoded by the cDNA isolated as clone 2705028 from the Incyte PONSAZTO1 library. The human IMOLS (AAB1536-B1550) and their encoding polynucleotides (AAA95775-A95789), and compositions comprising them are useful for the diagnosis, treatment or prevention of immunological disorders, infections and cell proliferative disorders associated with decreased expression or activity of IMOL, such as immunological disorders and east to treat or prevent disorders associated with decreased expression or activity of IMOL, such as immunological disorders. (e.g. inflammation, actinic keratosis, AIDS, Addison's disease), haematopoietic cancer, infections caused by virus (e.g. adenovirus, parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus, Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. Bingella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. actinic keratosis, arteriosolerosis, bursitis), and cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also useful as immunogens for the development of antibodies that
                                                                                                                                                                                                                                                                                                                                               Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic: antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic; cancer; antigout; dermatological; antithyroid; virucide; hepatotropic; antibody; immunosuppressive; cytostafuc; fungicide; protozoacide; antibacterial; gene therapy; diagnostic; immunological disorder; viral infection; bacterial infection; fungal infection; parasitic infection; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray, to detect differences in gene sequences among normal, carrier and affected individuals, and for screening libraries of compounds in drug screening techniques. Antibodies which specifically bind to IMOL may be used for the diagnosis of disorders characterized
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to detect and quantify gene expression in biopsied tissues in which expression of IMOL may be correlated with the disease, as targets in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu DAM;
Indels
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  Mismatches
                                                                                                                                                                                 AAB15536 standard; Protein; 613 AA.
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99US-0132647.
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                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal P, Tang YT,
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-665005/64
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                                                                            237 pgyegr 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                      6 PGYEGR
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  9
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                                                                                                                                                                                                                         AAB15536;
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Matches
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Sequence

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Human; secreted protein; immunomodulatory; antisclerotic; defaratological; antinflammatory; anti-HV; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; noctropic; anti-angiogenic; ophthalmological; neuroprotectant; nottropic; anticonvulsant; antialzheimers; antiparkinsonian; protein coordinate data; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 32 human secreted polypeptides, useful for preventing diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    aker KP, Birse CE, Ebner R, Fiscella M, Komatsoulis
DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet
), Wei P, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 763-764; 890pp; English.
                                                                                                                                                                Human secreted protein, SEQ ID NO: 82.
                                                                                 AAB90544 standard; Protein; 613 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                         22-SEP-2000; 2000WO-US26013.
                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999; 99US-0155709.
                                                                                                                                      01-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-235311/24.
N-PSDB; AAF97884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baker KP,
                                                                                                                                                                                                                                                                                                                    WO200121658-A1.
                                                                                                                                                                                                                                                                                             Homo sapiens.
111111
372 pgyegr
                                                                                                                                                                                                                                                                                                                                              29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young PE,
                                                                                                           AAB90544;
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                                                     10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
by expression of IMOL, or in assays to monitor patients being treated with IMOL or agonists, antagonists, or inhibitors of IMOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                            Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
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                                                                                 21; Length 613;
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                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou P, Qian XB, Wang Z,
A, Zhang J, Werhman T;
                                                                                 DB 21
                                                                               Query Match 42.9%; Score 6; DB 3 Best Local Similarity 100.0%; Pred. No. 35; Best Local Similarity 100.0%; Mismatches 6; Conservative 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 1164-1165; 1275pp; English.
                                                                                                                                                                                                                                                                                                                    Human EST encoded protein SEQ ID NO: 1773.
                                                                                                                                                                                                                                   AAM24248 standard; Protein; 613 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476164/51.
N-PSDB; AAH98907.
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                                        613 AA
                                                                                                                                                      372 pgyegr 377
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200154477-A2.
                                                                                                                                     6 PGYEGR 11
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                          12-OCT-2001
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                                                                                                                                                                                                                                                              AAM24248;
                                        Sequence
                                                                                                                                                                                                         RESULT
AAM24248
SSXS
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The present sequence is one of 32 novel human secreted polypeptides. The nucleic acid molecules and polypeptides may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g. diagnosis, systematic luque erythematosus and human immunor deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher, Gaigase), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), anadyopentic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's diseases and parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid candences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of their expression and activity.
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches
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Gaps

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6 PGYEGR 11

372 pgyegr 377

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AAB90560 RESULT

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bifunctional inhibitor; platelet activation; thrombin; inhibit clot, formation; accretion; fibrin deposition; myocardial infarction; thrombosis; increasing reocclusion time; decreasing reperfusion; time; inhibiting metastatic cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See also AAR25142-54 AAR25382,3, AAQ25314,5 AAQ25884-90, AAQ31179,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the junction between the malE and applied portions of the malE-appilog fusion protein - produced as described in AAQ25890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bi:functional inhibitors of thrombin and platelet activation comprise glyco:protein IIB or IIIa and thrombin inhibitory moietles, for treating thrombotic diseases, atherosclerosis,
                                                                                                Junction sequence of malE-appilog fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.7%; Score 5; DB 13;
100.0%; Pred. No. 25;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer and neuro:degenerative conditions
                                                                                                                                                                                                                                                                                                                                                                                                                             Strauch KL,
                                                                                                                                                                                                                         Location/Qualifiers 7..8
             AAR25383 standard; Protein; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW15196 standard; Peptide; 24 AA.
                                                                                                                                                                                                                                            7..8 ·
/label= Factor Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 10; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide encoded by vector pTugAS.
                                                                                                                                                                                                                                                                                                                                            91WO-US09108
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                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 5; Conserv
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11 egrpe 15
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                                                                                                                                                                                                                                                                                                                                           05-DEC-1991;
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                                                                   04-JAN-1993
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                                                                                                                                                                                                 Synthetic
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                                         AAR25383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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AAR25383
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r DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR;
                                                                                                                                       Human; secreted protein; immunomodulatory; antisclerotic; dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant; vascular; anti-anglogenic; ophthalmological; neuroprotectant; nootropic; antionvulsant; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
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100.0%; Pred. No. 35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 784-786; 890pp; English.
                                                                                                             Human secreted protein, SEQ ID NO: 98.
                          AAB90560 standard; Protein; 613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wei P, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                             22-SEP-2000; 2000WO-US26013.
                                                                                                                                                                                                                                                                                                                                                         99US-0155709
                                                                                 (first entry)
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                           Homo sapiens
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                                                                                 01-JUN-2001
                                                                                                                                                                                                                                                                                                 29-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Young PE,
                                                     AAB90560;
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Thompson JS;

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Gaps

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Indels

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Oligosaccharide binding domain; cellulose binding domain;

372 pgyegr 377

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9

Length 17;

Kilburn DG;

920S-0865095. 900S-0603987. 940S-0249037. 950S-0505860.

96US-0685808.

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Two-phase partition affinity separation system useful for separating and purifying proteins comprises a phase-forming oligosaccharide polymer and a phase-separation agent -
                                                                                                                                                                                              Disclosure; Fig 3A; 46pp; English.
                                                                                           (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                               Tomme P,
                                                                                                                                  WPI; 2000-328038/28
                                        08-APR-1992;
25-OCT-1990;
24-MAY-1994;
24-JUL-1995;
           24 -JUL-1996;
                                                                                                                Haynes CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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ID AAB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acids encoded by 3' portion of prugAS vector SacI-HindIII region.
                                                                                                                                                                                                                                                                                                                Two peptides (AAW15195 and AAW15196) are respectively encoded by a nucleotide sequence located upstream of the SacI site (see AAT65087), and by the SacI-HindIII region (see AAT65088), of vector prugAS. This vector can be used for expression of cellulose-binding domain NI (AAW15193) of Cellulomonas fimi endoglucanase C (CenC) in Escherichia coli. NI can be produced for use in claimed methods of phase separation for large-scale protein purification and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                      Purifying a polypeptide containing a polysaccharide binding peptide - using a phase-forming oligosaccharide and separating the phases, useful for large scale purification of proteins and enrichment of
cellulase; endoglucanase C; CenC; purification; phase partition; two-phase system; affinity phase separation; extractive bloconversion; vector; prugAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prugAS vector; Cellulomonas fimi; endoglucanase C; CBD; cellulose binding domain; polysaccharide binding peptide; fusion protein; recombinant protein; cell separation; affinity phase separation.
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3A; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY81431 standard; peptide; 27 AA
                                                                                                                                                                                  (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                            96WO-US12282.
                                                                                                                                                               95US-0505860.
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/label= FXa
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                                                                                                                                                                                                      Haynes CA, Kilburn DG,
                                                                                                                                                                                                                          WPI; 1997-235878/21.
N-PSDB; AAT65088.
                                                                                                                                                                                                                                                                                                                                                                                                                       24 AA;
                                                           Key
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 EGRPE 13
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egrpe 6
                                                                                                                                            24-JUL-1996;
                                                                                                                                                               24-JUL-1995;
                                                                                                    WO9713841-A1
                                                                                                                       17-APR-1997.
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                                        Synthetic
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The invention relates to a novel two-phase partition system for affinity separation which comparises a phase-forming obligosaccharide polymer to which a polysaccharide binding peptide (PBP) binds, and a phase to which a polysaccharide binding peptide (PBP) binds, and a phase separation inducting agent. The system may be used for the separation and interest is expressed in the host cell as a fusion protein with a polysaccharide binding peptide, and the cell lustuces. The protein of polysaccharide binding peptide, and the cell lustuces in the protein of polysaccharide binding peptide, and the cell lustuces. The protein of comparing page of a solution with a low long strength, high pin or containing a classor of a solution with a low long strength, high pin or containing a classor protein by the use of chemical cleavage agents such as classor protein by the use of chemical cleavage agents such as classor protein by the use of chemical cleavage agents such as classor protein by the use of chemical cleavage agents such as classor protein by the use of chemical cleavage agents such as classor protein by the use of chemical cleavage agents such as classor classor by the fusion protein has been engineered such that the invention include a wide variety of medically and industrially continue and such be cleavaged from the PBP, which remains bound to the particular cell type; for example, a fusion protein comprising to a particular receptor can be useful for concentrating a lagrand of a particular receptor can be useful for concentrating a largand of a particular receptor can be useful for concentrating a component in a mixture, removing contaminants and for preparison of a vide state reagent for floations selective binding of PBP from the continuous purification. Selective binding of PBP from the continuous purification of selective binding of particular expense. Continuous suride polymer makes it suitable for prepare separate systems contaminants and continuous purification of selective binding of particular receptor of
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Best Local Similarity luv.
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The fusion protein SLF-CBD comprises the extracellular domain of murine steel factor (SLF) linked to the cellulose binding domain (CBD) of the cellulomonas fini exoglucanase Cex. The present sequence is a peptide ragment of prugAs expression vector. PrugAs can be used for high level expression of SLF-CBD fusion proteins in Escherichia coli. The present invention relates to the use of SLF-CBD as a component of a composition used for an annoing the rate of division and differentiation of growth factor chancing the rate of division and differentiation of growth factor a complex of viable cells, containing biologically active growth factor receptors and ligands of the receptors which are immobilised on a blocompatible solid phase via a polysaccharide binding domain i.e. SLF-CBD, (Which is diffused on the solid phase), so that cell surface localised growth factor receptor diffuses within the cell surface composition of the present invention may be used to enhance wound healing via a growth factor-CBD conjugate, which would stimulate local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for enhancing rate of division and differentiation of growth factor dependent cells, comprising a growth factor receptor complex and its immobilized ligand
                                                                                                                    SLF-CBD; murine; steel factor; pTugAS; cellulose binding domain; exoglucanase; Cex; cell division; differentiation; growth factor; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                             Doheny JG, Haynes CA;
                                                                                      prugas expression vector peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3A; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                  23-FEB-2000; 2000WO-CA00162.
                                                                                                                                                                                                                                                                                                                                     99US-0256499.
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Kilburn DG, Jervis E,
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                                                                                                                                                                                                                             WO200050570-A2
                                                                                                                                                                                            Unidentified.
                                                 10-JAN-2001
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                AAB26266;
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                                0; Gaps
    DB 21; Length 31;
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35.7%; Score 5; DB 2:
100.0%; Pred. No. 40;
tive 0; Mismatches
 Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
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Search completed: January 31, 2002, 13:18:10 Job time: 171 sec

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Q9vw98 drosophila

Perfect score:

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                Q9p8c9 piromyces s
Q9kgu2 thermoanaer
Q9lvx9 arabidopsis
Q9a4n9 caulobacter
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MEDLINE=9816572; PubMed=9497317;

MEDLINE=9816572; PubMed=9497317;

MEDLINE=9816572; PubMed=9497317;

MEDLINE=9816572; PubMed=9497317;

Prandishvlil D., Klenk H.P., Jakobs G., Schmiechen A., Hanselmann C., 10.2 I., 21111g W.;

"Biochemical and phylogenetic characterization of the duTpase from the archeal virus SIRV.";

J. Biol. Chem. 273:6024-6029(1998).

-I - CATALYTIC ACTIVITY: DUTP + H(2)O = DUMP + PYROPHOSPHATE.

EMBL; AF022221; AAC15873.1;

-InterPro; IPR001428; dUTPase.

InterPro; IPR003232; dCTP_deaminse.

Pfam; PF00692; dUTPase; I.
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Last annotation update)
PYROPHOSPHATASE) (DEOXYURIDINE-
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Pred. No. 2.3e-07;
Mismatches 0;
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Q9LVX9
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Q9KF64
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Viruses; unclassified viruses.
NCBI_TaxID=66287;
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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DUTPASE (EC 3.6.1.23) (DUTP
TRIPHOSPHATASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Q9RB12
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Q49668 mycobacteri
Q4844 bacteriopha
Q9957 leishmania
Q22723 caenorhabdi
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Q9y7z6 schizosacch
Q9agh6 chlorobium
Q9k105 vlbrio chol
069367 rhodococus
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09g084 bacteriopha
09lk94 arabidopsis
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Q9haq5 homo sapien
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                                                                                                      January 31, 2002, 13:37:43; Search time 130.99 Seconds
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09hp97
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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Score

Result Ş ö

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"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
TAC and BAC clones.":
DNA Res. 7.217-222(2000).
-!- CORCTOR: FAD (BY SIMILARITY).
-!- SIMILALITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
CLASS.II.
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

CYTOSOLIC MONODEHYDROASCORBATE REDICTASE.

Arabidopsis thaliana (Mouse-ear cress).

EURATYOCE, VITIAIPHATEA: Streptophyta: Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-970601201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Horsouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura &
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1960). EMBL: D90917: BANBS43.1; CHIPPOTE STRAINS COMPLETED TO THE SEQUENCE II NOTE STRAINS COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMPLETED PROTEIN: COMP
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Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata
Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 7; DB 10; Length 488; 100.0%; Pred. No. 11; 1:ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMEL, AP000371; BAB02528.1; -.
InterPro; IPR00137; FAD_pyr_redox.
InterPro; IPR001103; Pyridine_redox_2.
InterPro; IPR001100; Pyr_redox.
Pfam; PF00070; Pyr_redox; 1.
PRINTS; PR00410; PNDRDTASEI.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEI.
EAD; Flavoprotein; Oxidoreductase; Redox-active center.
EQUENCE 488 AA; 53526 MW; AC218119911780FA CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
BLT-TaxiD=1148;
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P74723; PO CTEMBLEG. 02, Created)
01-FEB-1997 (TEMBLEG. 02, Last sequence update)
01-FEB-1997 (TEMBLEG. 14, Last annotation update)
HYPOTHELICAL 11.8 KDA PROTEIN.
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Best Local Similarity 100.
Matches 7; Conservative
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PubMed=10907853;
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SCRII193;
MEDLINB-99392457; PubMed-10463161;
Vincent-Sealy L.V., Thomas J.D., Commander P., Salmond G.P.C.;
Vincent-Sealy L.V., Thomas J.D., Commander P., Salmond G.P.C.;
"Erwinia carrotovora DSDA mutants: evidence for a periplasmic-stress signal transduction system affecting transcription of genes encoding secreted proteins.";
Secreted proteins.";
Microbiology 145:1945-1958(1999).
EMBL: AF146615; AAD476815. -
SEQUENCE 89 AA: 10402 MW; 228FDDD71E865481 CRC64;
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                                                                                                                                                                                                                         Erwinia carotovora subsp. carotovora.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
NCBL_TaxID-555;
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Wichman H.A., Scott L.A., Yarber C.D., Bull J.J.;
"Experimental Evolution Recapitulates Natural Evolution.";
Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2000).
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Yarber C.D., Wichman H.A., Bull J.J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF214751; AAG29963.1; -.
SEQUENCE 328 AA; 34377 MW; EB942BA33DD2B4D9 CRC64;
                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last sequence update)
Last annotation update)
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Viruses; ssDNA viruses; Microviridae; Microvirus.
NCBI_TaxID=10844;
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Last sequence update)
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100.0%; Pred. No. 7.9;
tive 0; Mismatches
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Matches 7; Conservative 0;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
COMPLETE GENOME.
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091K94,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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36 AGFEGQL 42
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Q9LK94
ID Q91
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Wilson R., Ainscoun R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                  Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Oliver K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL390114; CAC01993.1; -.
Hypothetical protein.
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21440 MW; 890E3248C4410E5A CRC64;
                                                                                              09GY57;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 21.4 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ol-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
COSMID T24C12.
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                                                                        202 AA.
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100.0%; Pred. No. 57;
tive 0; Mismatches
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                                                                           PRELIMINARY;
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Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                        Leishmania major.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5664;
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SEQUENCE
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Alonso J.C., Luder G., Stiege A.C., Chai S., Weise F., Trautner T.A.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X97918; CAA66521.1; -.
                                                   Gaps
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Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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MEDIINE-96084954; PubMed-7489918;
Doukhan L., Predich M., Nair G., Dussurget O., Mandic-Mulec I.,
Cole S.T., Smith D.R., Smith I.;
"Genomic organization of the mycobacterial sigma gene cluster.";
Gene 165:67-70(1995).
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Length 110;
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                                                   0; Indels
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00012; AAA85934.1; -.
SEQUENCE 118 AA; 12963 MW; F99C9885EFA48FF8 CRC64;
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Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
COMPLETE NUCLEOTIDE SEQUENCE.
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100.0%; Pred. No. 35;
Live 0; Mismatches
DB 2;
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                        100.0%; Pred. No. 33; ive 0; Mismatches
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100.0%; Pred. No. 52;
tive 0; Mismatches
Score 6;
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42.98;
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Matches 6; Conservative
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NCBI_TaxID=10724;
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Matches 6; Conserv
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SEQUENCE FROM N.A.

MEDLINE-21173698; PubMed=11259647;

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Nielman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ernelaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. SGI. U.S.A. 98:4136-4141(2001).
                                                                        Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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SEQUENCE 260 AA; 27075 MW; 7DC145D069C89029 CRC64;
  01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 3-HYDROXYACYL-COA DEHYDROGENASE.
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                                                                                                                         Caulobacter.
NCBI_TaxID=69394;
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176 IVDAGF 181
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SEQUENCE TRAIN-6757BL/64; XA

STATAN-6757BL/64; XA

RAMANA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa J., Shinagawa A., Filbata K., Yoshino M., Itoh M., Ishii Y.,

A Arawawa T., Hara A., Fukunishi Y., Konno H., Adania J., Yamanaka I.

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.

A Atawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,

A Satto T., Ofazzaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

A Schriml L., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Bustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Toyo-oka K., Wang K., Wang K., Kawaji H., Kohtsuki S.,

A Wanshaw-Borits A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_raxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; wature 409:682-690(2001).
EMBL: AK007583; BAB2121.1, -
MGD: MG11.09201; Nat2.
InterPro; IPR001447; Acetyltransf2.
Prodom: PF00797; Acetyltransf2: 1.
Prodom: P0002783; Acetyltransf2: 1.
SEQUENCE 28 AA: 25378 MW; 1E3043003F4CFCCE CRC64;
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EMBL; U41037; AAA82390.1; -. SEQUENCE 218 AA; 24918 MW; 353C7801098301E7 CRC64;
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100.0%; Pred. No. 60;
Live 0; Mismatches
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01-JUN-2001 (TIEMBLIE). 17,
01-JUN-2001 (TIEMBLIE). 17,
NACETYL TRANSFERASE 2.
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Best Local Similarity 100.
Matches 6; Conservative
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50 IVDAGF 55
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Brucellaceae; Brucella.
NCBI_TaxID=235;
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Microbo. Comp. Genomics 3:21-29(1998).

EMBL, AF01921; AAC01567.1; -

Interpro: IPR001029; Flagellin_C.

Fram: PP00669; Flagellin_N.

Fram: PP00700; Flagellin_N.

Prom: PP00700; Flagellin_C; 1.

Prom: PP00700; Flagellin_C; 1.

Prom: PP00700; Flagellin_C; 1.

SEQUENCE 282 AA; 29099 MW; C3145All12BlDDC0 CRC64;
                                            01.JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
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42.9%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches
282 AA.
                                                                                                                                                                                                                                                                                                                     STRAIN=544;
MEDLINE=20468005; PubMed=11013709;
PRELIMINARY;
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Q9HAQ5
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Complete proteome.
SEQUENCE 349 AA;
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146 VDAGFE 151
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MEDLINE-20504483; PubMed=11016950;
MG W.V. Rennedy S.P., Mahairas G.G., Berquist B., Pan M.,
MG W.V., Rennedy S.P., Maliga W.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga W.S., Thorsson V., Sbrogna J.,
A Shukla H.D., Lasky S.R., Baliga W.S., Thorsson V., Sbrogna J.,
A shartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs W.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
T. Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
REMBL, AE005079; AAG19973.1; --.
REMBL, AE005079; AAG19973.1; --.
REMBL, RENOSTIE; PS01047; HMA: UNKNOWN_1.
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Cascorbi I., Roots I., Brockmoller J.;
"Homo sapiens NAT1 gene for arylamine N-acetyltransferase 1, NAT1*11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Archaea; Buryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF308866; AAG23842.1;
InterPro: IRF001447; Acetyltransf2.
Ffam, PF00797; Acetyltransf2; 1.
ProDom; PD002783; Acetyltransf2; 1.
Transferase; Acyltransferase.
SEQUENCE 290 AA; 33882 MW; 7FF417F3C24FDB11 CRC64;
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                                                                      01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARYLAMINE N-ACETYLTRANSFERASE 1 (EC 2.3.1.5).
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Last sequence update)
Last annotation update)
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290 AA.
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100.0%; Pred. No. 86;
iive 0; Mismatches
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
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Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
PRELIMINARY;
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SEOUENCE 325 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                               Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID=1299;
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                                          DB 2;
o. 91;
349 AA.
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100.0%; Pred. No.
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PRT;
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EMBL; AE001938; AAF10415.1;
TIGR; DR0836; -.
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Best Local Similarity 100.
Matches 6; Conservative
PRELIMINARY;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 31, 2002, 13:20:14; Search time 78.64 Seconds (without alignments) 13.561 Million cell updates/sec Run on:

US-08-957-709-76 14 1 PTIVDAGFEGQLTI 14 Perfect score: Sequence:

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219241 seqs, 76174552 residues Searched:

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Word size :

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES	Description	2 probable dCTP deam	probable dCTP	probable		restriction endon		hypothetical	hypothetical	arylamine N-a		arylamine	arylamine N-acety	arylamine	arylamine			hypotheti	pyruvate	pyruvate	pyruvate				hypothetical	maltose ABC t	hypothetical			י דב (וו (סה
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D96533	S59836	S63064	T02782	S51470	H69163	T14853	TDFFLK	F83727	A84039	B69984	A32055	T35283	E32716	B81031
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ALIGNMENTS

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probable dCTP deaminase (EC 3.5.4.13) [similarity] - Desulfurolobus ambivalens probable dCTP deaminase (EC 3.5.4.13) [similarity] - Desulfurolobus ambivalens (Species: Desulfurolobus ambivalens (Species: Desulfurolobus ambivalens (Species: Desulfurolobus ambivalens (Space) (Spa

ö Gaps .; 0 100.0%; Score 14; DB 2; Length 173; 100.0%; Pred. No. 4.4e-08; or Mismatches 0; Indels Best Local Similarity 100. Matches 14; Conservative Query Match

109 PTIVDAGFEGQLTI 122 1 PTIVDAGFEGQLTI 14 qq δ

probable dCTP deaminase (EC 3.5.4.13) APE0333 [similarity] - Aeropyrum pernix (strain

C; Species: Aeropyrum pernix.
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Accession: D7224
R; Kawarabayasi, Y:; Hino, Y:; Horikawa, H:; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H:; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83.101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID: 99310339

A, Accession: D72724
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-181
A, Cross-references: DDBJ:AP000059; NID:g5103911; PIDN:BAA79288.1; PID:g5103972
A, Experimental source: strain K1

C; Genetics:

A; Gene: APE0333

C; Superfamily: dCTP deaminase C; Keywords: hydrolase

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C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: JN0658
R;Dartois, V; De Backer, O.; Colson, C.
Gene 127, 105-110, 1993
A;Title: Sequence of the Salmonella typhimurium StyLT1 restriction-modification genes A;Title: Sequence of the Salmonella typhimurium StyLT1 restriction-modification genes A;Reference number: JN0657; MUID:9325265
A;Accession: JN0658
A;Holecule type: DNA
A;Residues: 1-984 < CDAR>
A;Comment: This enzyme belongs to the type-III restriction-modification system.
C;Comment: This enzyme belongs to the type-III restriction-modification system.
C;Comment: This enzyme is involved in DNA unwinding at the cleavage site.
C;Comment: This hydrolase; restriction modification system
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A;Accession: S76931
A;Accession: S76931
A;Molecule type: DNA
A;Residues: 1-110 <KANA
A;Residues: 1-110 <KANA
A;Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18843.1; PID:g165
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s1r0587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - phage SPP1
C;Species: phage SPP1
C;Species: phage SPP1
C;Date: Obace SPP1
C;Accession: T4234
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
A;Title: The complete nucleotide sequence and functional organization of Bacillus sub A;Reference number: 22137; MUID:98094274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-184 <ALO.
A;Cross-references: EMBL:X97918; PIDN:CAA66521.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Synechocystis sp.
A; Variety: PCC 1603
A; Variety: PCC 1603
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #sext_change 20-Jun-2000
C; Accession: S76931
C; Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yass A; Ille: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein slr0587 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 42.9%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 10; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.0%; Score 7; DB 2; Best Local Similarity 100.0%; Pred No. 6.1; Matches 7; Conservative 0; Mismatches
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315 VDAGFEG 321
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                                                                                                                                                                                                                                                                                    RESULT 3
70439
Probable dCTP deaminase (EC 3.5.4.13) dcd [similarity] - Aquifex aeolicus
Probable dCTP deaminase (EC 3.5.4.13) dcd [similarity] - Aquifex aeolicus
C.Species: Aquifex aeolicus
C.Species: Aquifex aeolicus
C.Species: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
C.SACCESSION: A70439
R.DecKert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Mostates: 1-180 cAOF>
A;Kosidues: 1-180 cAOF>
A;Cross-references: GB:AE000747; NID:g2983944; PIDN:AAC07499.1; PID:g2983951; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 392, 353-358, 1998
A'Itle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A'Reference number: A70300; MUID:98196666
A'Accession: A70439
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304045
gene H protein - phage S13
C:Species: phage S13
A; Note: Tescherichia coli
C:Species: phage S13
C:Species: phage S13
C:Species: phage S13
C:Species: phage S13
C:Species: phage S13
C:Species: phage S13
C:Species: phage S13
C:Species: J80459
C:Species: J80459
C:Species: J80459
C:Species: J80450; MUD:86165869
A; Title: Nucleoritde sequence and genome organization of bacteriophage S13 DNA.
A; Reference number: J80450; MUD:86165869
A; Molecule type: DNA
A; Residues: L328
A:MOlecule type: DNA
A; Residues: L328
C:Superfamily: phage phi-x174 gene H protein
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                                Length 181;
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JN0658
restriction endonuclease (EC 3.1....) - Salmonella typhimurium
c; Species: Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 180;
                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 328;
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                                    DB 2; L
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100.0%; Pred. No. 0.1
:ive 0; Mismatches
                                Query Match 78.6%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 7.3 Best Local Similarity 100.0%; Mismatches 11; Conservative 0; Mismatches
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A,Gene: dcd
C;Superfamily: dCTP deaminase
C,Keywords: hydrolase
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Best Local Similarity 100
Matches 8; Conservative
                                                                                                                                                                           117 VDAGFEGGLTI 127
                                                                                                                                                 4 VDAGFEGQLTI 14
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C;Accession: A28168; A28167
R;Obsako, S.; Ohtomi, M.; Sakamoto, Y.; Uyemura, K.; Deguchi, T.
J. Biol. Chem. 263, 7534-7538, 1988
A;Title: Arylamine N-acetyltransferase from chicken liver. II. Cloning of cDNA and ex
A;Reference number: A28168; MUID:88227946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nylternate names: arylamine actylase (Species: Oryctolagus cuniculus (domestic rabbit) (C.Species: Oryctolagus cuniculus (39970; S11559; S04138; A60882; A33181 (C.Sasaki, Y.: Obsako, S.: Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi, T. Deguchi
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Nucleic Acids Res. 18, 5295, 1990
A;Title: Nucleotide sequence of rabbit NAT2 encoding polymorphic liver arylamine N-ac
A;Reference number: S11559; MUID:90384846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Deguchi, T.; Sakamoto, Y.; Sasaki, Y.; Uyemura, K.
J. Biol. Chem. 263, 7528-7533, 1988
A;Title: Arylamine N.acetyltransferase from chicken liver. Monoclonal antibodies, imm
A;Reference number: A28167; MUID:88227945
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A; Residues: 1-290 CBL2>
A; Crosa-references: EMBL:X53767; NID:g1647; PIDN:CAA37786.1; PID:g1648
A; Crosa-references: EmBL:X53767; NID:g1647; PIDN:CAA37786.1; PID:g1648
B; Blum, M.; Grant, D.M.; Demierre, A.; Meyer, U.A.
Nucleic Acids Res. 17, 3589, 1989
A; Title: Nucleocitde sequence of a full-length cDNA for arylamine N-acetyltransferase
A; Reference number: S04138; MUID:89263801
A; Accession: S04138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Gallus gallus (chicken)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A28167
A;Molecule type: protein
A;Residues: 116-131;143-164;272-279 <DEG>
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A,Molecule type: mRNA
A,Residues: 1-290 cSA2>
A,Cross-references: GB:M90380
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A, Residues: 1-290 <SA1>
A, Cross-references: GB:M90378
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A; Residues: 1-287 <OHS>
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A; Molecule type: DNA
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3 IVDAGF 8
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C:Species: Mesocricetus auratus (golden hamster)
C:Species: Mesocricetus auratus (golden hamster)
C:Species: Mesocricetus auratus (golden hamster)
C:Accession: I78931: 148197
R:Magata, K.: Ozawa, S.: Miyata, M.: Shimada, M.: Yamazoe, Y.: Kato, R.
R:Magata, K.: Ozawa, S.: Miyata, M.: Shimada, M.: Yamazoe, Y.: Kato, R.
R:Magata, K.: Ozawa, S.: Miyata, M.: Shimada, M.: Yamazoe, Y.: Kato, R.
A:Title: Primary structure and molecular basis of polymorphic appearance of an acetyltra
A:Reference number: 158424; MUID:94362736
A:Reference: Tata cares
A:Reference: GB:S72007; NID:9565127; PIDN:AAB31918.1; PID:9565128
R:Rerguson, R.J.: Doll, M.A.: Baumstark, B.R.: Hein, D.W.
Gene 140, 247-249, 1994
A:Title: Polymorphic arylamine N-acetyltransferase encoding gene (NAT2) from homozygous A:Reference number: 148197; MUID:94193006
A:Reterence number: 148197; MUID:94193006
A:Reterence tumber: TATA cares
A:Reterence tumber: TATA cares
A:Reterence number: TATA cares
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134373
hypothetical protein T24C12.4 - Caenorhabditis elegans
hypothetical protein T24C12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34373
R;Miller, N; Stellylyes, L.
R;Miller, N; Stellylyes, L.
R;Miller, N; Stellylyes, L.
R;Miller, D; Stellylyes, L.
R;Miller, D; Stellylyes, L.
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                                          Length 184;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. ...
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches
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100.0%; Pred. No.
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C;Superfamily: arylamine acetyltransferase
C;Keywords: acyltransferase; coenzyme A
                                          Query Match 42.9
Best Local Similarity 100.
Matches 6; Conservative
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A;Introns: 49/1; 109/2; 168/3
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-218 <MIL>
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Eur. J. Biochem. 185, 253-261, 1989
A;Title: Two arrylamine N-acetyltransferases from chicken pineal gland as identified b A;Title: Two arrylamine N-acetyltransferases from chicken pineal gland as identified b A; Reference number: S06652; MUID:90060108
A;Accession: S06653
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-290 COHT>
A;Cross-references: BMBL:X16021; NID:962961; PIDN:CAA34153.1; PID:962962
C;Keywords: acylamine acetyltransferase
C;Keywords: acylamine acetyltransferase
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100.0%; Pred. No. 24;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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AXIAMATION N-acetyltransferase (EC 2.3.1.5), monomorphic - rabbit
C:Specias: Orycologues cuniculus (domestic rabbit)
C:Date: 30.5ep-1992 #sequence_revision 30-Sep-1992 #text_change 05-May-2000
R:Ssasut, Y:: Obasako, S:IDeguchi, T.
J. Biol. Chem. 266, 13243-13250, 1991
A;Title: Molecular and genetic analyses of arylamine N-acetyltransferase polymorphism of A;Accession: C39870
A;Molecule type: DNA
A;Reference number: A39870; MUD:91302353
A;Aocession: C39870
A;Molecule type: DNA
A;Residues: 1-290 < CSAS>
A;Aocession: C39870
A;Molecule type: DNA
A;Residues: 1-290 < CSAS>
A;Molecule type: DNA
A;Residues: 1-290 < CSAS>
A;Molecule type: DNA
A;Residues: 1-290 < CSAS>
A;Molecule type: DNA
A;Reference number: S11220; MUD:90384838
A;Accession: S11220
A;Molecule type: DNA
A;Residues: 1-284, YW, 286-290 < CSUD>
A;Molecule type: DNA
A;Residues: 1-284, YW, 286-290 < CSUD>
A;Molecule type: DNA
A;Cross_references: EMBL:X53765; NID:91644; PIDN:CAA37785.1; PID:91645
C;Genetics: acyltransferase; Coenzyme A
C;Superfamily: arylamine acetyltransferase
C;Reywords: acyltransferase; Coenzyme A
A; Residues: 1-290 <BLU>
A; Residues: 1-290 <BLU>
A; Across references: EMBL:X14673; NID:g1437; PIDN:CAA32803.1; PID:g1438
B; Arcross references: EMBL:X14673; NID:g1437; PIDN:CAA32803.1; PID:g1438
B; Andress, H.H.: Vogel, R.S.; Tarr, G.E.; Johnson, L.; Weber, W.W.
Mol. Pharmacol. 31, 446-456, 1987
Mol. Pharmacol. 31, 446-456, 1987
A; Atlerication, physicochemical, and kinetic properties of liver acetyl-CoA:aryla A; Reference number: A60882; MUD:87201456
A; Accession: A60882; MUD:87201456
A; Molecule type: Drotein
A; Residues: 10-13:19-33:118-125, K'; 128-151;154-158, C', 160-162, 'D', 164-165;167-178;189-18010; Properties: 10-13:19-33:118-125, K'; 128-151;154-158, C', 160-162, 'D', 164-165;167-178;189-18010; Properties: The last two fragments attributed to this enzyme is deleted in slow acetylator rabbits the rebbits: Polymorphism of the homologous enzyme is deleted in slow acetylator rabbits the rebbits: Polymorphism of the homologous enzyme in humans affects the rate of N-acetylatic C; Genetics: This protein contains no amino sugars and no cofactors. The amino end is bloc C; Genetics: #status absent
C; Superfamily: arylamine acetyltransferase
C; Superfamily: arylamine acetyltransferase
C; Superfamily: arylamine acetyltransferase
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RESULT 15
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arylamine N-acetyltransferase (EC 2.3.1.5) Nat2 - mouse (strain C57BL/6J)
Crylamine N-acetyltransferase (EC 2.3.1.5) Nat2 - mouse (strain C57BL/6J)
Crylamine N-acetyltransferase (EC 2.3.1.5) Nat2 - mouse (strain C57BL/6J)
Crylamicoll 12-May-1994 #sequence_revision 09-Sep-1994 #text_change 05-May-2000
Crylacesion: B01267
Crylacesion: B1267
Nol. Pharmacoll 40, 218-227, 1991
A; Reference number: A61267, MUID:91342604
A; Reference number: A61267; MUID:91342604
A; Reference number: A61267
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-290 cMAR>
A; Cross-references: GB:U35887; NID:g1008571; PIDN:AAA78944.1; PID:g1008572
C; Superfamily: arylamine acetyltransferase
C; Keywords: acyltransferase; coenzyme A
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A;Gene: GDB:AAC1; NAT1
A;Cross-references: GDB:125364; OMIM:108345
A;Map position: 8p23.1-8p21.3
C;Function:
A;Description: catalyzes the N-acetylation of arylamines by acetyl-CoA A;Pathway: detoxification
C;Superfamily: arylamine acetyltransferase
C;Keywords: acyltransferase; coenzyme A; detoxification; liver
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches
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100.0%; Pred. No. 24;
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Best Local Similarity 100.
Matches 6; Conservative
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120 IVDAGF 125

3 IVDAGF 8

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Perfect score:

Title:

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Sequence:

Scoring table:

Word size :

Searched:

Database :

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Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
Sequence 2, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 14, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
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TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
TITLE OF INVENTION: Bextracts, PEF Protein Complexes, Isolate
TITLE OF INVENTION: and Methods for Purifying and Identifyin
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADRRESS:
ADDRESSE: Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
ZIP: 2000S
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                         US-08-378-761A-7
US-08-378-286-7
US-09-097-767A-14
5248606-45
US-08-378-761A-5
US-08-38-761A-5
US-08-31-478-7
US-08-321-478-7
US-08-321-478-9
US-08-321-478-9
US-08-321-478-9
US-08-321-478-9
US-08-321-478-9
US-09-318-794A-2
US-09-318-793A-4
5248606-41
                                                                                                                                                                                                                                                                                                                                                                                             US-08-980-832-37
US-08-378-761A-2
US-08-485-286-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/08822774 Patent No. 6183997 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEC ID NO. 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTIVDAGFEGQLTI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE:
US-08-822-774-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH:
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Sequence 2, Appli
Patent No. 5514582
Sequence 21, Appl
Sequence 45, Appl
Sequence 17, Appli
Sequence 117, Appli
Sequence 117, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 60, Appli
Sequence 9, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 6, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Appl
Sequence 23, Appl
Sequence 60, Appl
Sequence 9, Appli
Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                                              ; Search time 65.13 Seconds
(without alignments)
4.837 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 117, P
Sequence 117, P
Sequence 117, P
Sequence 15, App
Patent No. 52486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-23-155A 45
US-08-23-916-2
US-08 464-531-117
US-08-32-137-117
US-08-32-137-117
US-08-32-389-15
524866-47
US-08-2389-10
US-08-238-2138-60
US-08-378-78-9
US-08-483-857-9
US-08-378-761A-11
US-08-378-761A-11
US-08-485-286-13
US-08-485-286-13
US-08-485-286-13
US-08-485-286-13
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US-08-485-286-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-822-774-57
US-09-154-874-8
US-08-360-606B-2
5514582-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212252 seqs, 22503292 residues
                                                                                                                                                                                 January 31, 2002, 13:15:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                         1 PTIVDAGFEGQLTI
                                                                                                                                                                                                                                                                             US-08-957-709-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.7%; Score 5; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
55145827
; Patent No. 5514582
; Patent No. 5514582
; Patent No. 5514582
; Patent No. 5514582
; Patent No. 5514582
; IMMUNOGLOWINS
; IMMUNOGLOWINS
; IMMUNOGLOWINS
; RECOMBINANT DNA ENCODING HYBRID
; IMMUNOGLOWINS
; REQUENCES: 43
; CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/185,670
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 806,331
; FILING DATE: 08-DEC-1992
; FILING DATE: 08-DEC-1991
; FILING DATE: 16-DEC-1991
; FILING DATE: 22 NOV-1989
; FILING DATE: 22 NOV-1989
; FILING DATE: 22 NOV-1989
; FILING DATE: 32 NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: Yes
FRACHENT TYPE: internal fragment
ORIGINAL SOURCE: accharomyces cerevisiae
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM FC compatible
COMPUTER: TIBM FC compatible
COMPUTER: TIBM FC compatible
COMPUTER: TIBM FC compatible
COMPUTER: TIBM FC COMPATIBLE
COMPUTER: TIBM FOR TIBM
COMPUTER: MS WORD 7.0
COMPATION OWNER: DCS/MS-DOS
FILING DATE: December 21, 1994
FILING DATE: December 21, 1994
CLASSIFICATION UNBER: US/08/360,606B
FILING DATE: December 21, 1994
CLASSIFICATION UNBER: 30,243
REFERENCE/DOCKET UNBER: 30,243
REFERENCE/DOCKET UNBER: 30,243
FELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
SEQUENCE: CHARACTERISTICS:
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Best Local Similarity 100.0%; P
Matches 5; Conservative 0;
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                                                                                      RESULT 2

US-09-154-874-8

Sequence B, Application US/09154874

Patent No. 6054636

GENERAL INFORMATION:
TITLE OF INVENTION: ISOFLAVONE BIOSYNTHETIC ENZYMES

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
DORRESPONDENCE ADDRESS:
COURTEY: WILMINGTON
STREET: 1007 WARKET STREET

COUNTRY: UNITED STATES OF AMERICA

IP 19898

COMPUTER READBALE FORM:
MEDIUM TYPE: DISKETTE; 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: SYSTEM: MICROSOFT WINDOWS 95

SOFTWARE: WICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

SAPLICATION NUMBER: US/09/154,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
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3
US-08-360-608-2
Sequence 2, Application US/08360606B
Sequence 2, Application US/08360606B
Sequence 2, Application US/08360606B
Sequence 2, Application US/08360606B
Sequence 3, Sigist 2, Sequence 3, Sequence 4, Septiment Richard C, Garrad APPLICANT: Richard C, Garrad APPLICANT: Robert P. Peery 7 ITLE OF INVENTION: Methods and Reagents for TITLE OF INVENTION: Detecting Fungal Pathogens in a TITLE OF INVENTION: Detecting Fungal Pathogens in NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSE: ADDORESSE: ADDRESSE: ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 6; DB 3
100.0%; Pred. No. 25;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLLASSIFCATION
PCLASSIFCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/931,668
FILING DATE: SEPTEMBER: 1, 1997
ATTORNEY AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1098-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERA: 302-73-016
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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1 PTIVDAGFEGQLTI 14
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300 VDAGFE 305
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APPLICANT: Ljubimova M.D., Julia Y.
TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH LIVER
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0: Mismatches
                                 SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-028
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 38,459
REFERENCE/DOCKET NUMBER: P07 34306
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/533,996A FILING DATE: 27-SEP-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: FUJIta ESG., Sharon M. REGISTRATION NUMBER: 38,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08533996A
Patent No. 5866329
                                                                                                                                                                                                                                                                                                                                         : 38 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7 Best Local Similarity 100. Matches 5; Conservative
                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECCREATE: 213-022
TELEPHONE: 213-022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 213-489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-253-155A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-533-996A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
COUNTRY: US
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GFEGQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GFEGQ 7
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-533-996A-2
                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                          APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: GELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: GELL DEATH AND DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR: 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W MULTAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 5718-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
ATITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 38; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Score 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-253-155A-45; Sequence 45, Application US/08253155A; Patent No. 5691147
                                                         Sequence 21, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INPORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Schas 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-810-009-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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9 TIVDA 13
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                      RESULT 5
US-08-810-009-21
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APPLICANT: BROALD: Jun
APPLICANT: MANFREDI, John
APPLICANT: MURFREDI, John
APPLICANT: MURPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: PAUL, Jeremy
APPLICANT: PROBLEMENT: Joshua
TITLE OF INVENTION: PERSONENES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROANT AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,598
FILING DATE: 05-JUN-1995
FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,137
FILING DATE: 20-58P-1994
APPLICATION NUMBER: US 08/309,313
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US 08/100,328
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US 08/14,431
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US 08/14,431
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: US 08/14,431
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, INFORMATION:
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: POLWKES-2F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMM
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches
Best Local Similarity 100.0%; P
Matches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202-737-3528
                                                                                                                                     3 IVDAG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOWLKES, Dana M.
APPLICANT: BRACK! Jim
APPLICANT: MANFRED! John
APPLICANT: MANFRED! John
APPLICANT: MANFRED! John
APPLICANT: MANFRED! John
APPLICANT: PAUL. Jeremy
APPLICANT: PAUL. Jeremy
APPLICANT: PRUEHERAT: Joshua
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR CORRESPONDENCE ADDRESS:
ADDRESSE: BROWNY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Weahington
STATE: D.C.
CONTRY: ONA
                                                                                     Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,531
FILING DATE: 05-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/32,137
FILING DATE: 13-CCT-1994
PRIOR APPLICATION NUMBER: US/08/309,313
FILING DATE: 31-AN-1994
PRIOR APPLICATION NUMBER: US/08/309,313
FILING DATE: 31-AN-1994
PRIOR APPLICATION NUMBER: US/08/190,328
FILING DATE: 31-AN-1994
PRIOR APPLICATION NUMBER: US/08/190,328
FILING DATE: 31-AN-1993
APPLICATION NUMBER: US/08/190,328
FILING DATE: 31-AN-1993
APPLICATION NUMBER: US/08/190,328
FILING DATE: US/08/190,328
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FILING DATE: US/08/190,328
FILING DATE: US/08/190,328
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
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FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,338
FILING DATE: US/08/190,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 117, Application US/08464531
; Patent No. 5789184
; GENERAL INFORMATION:
                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        os: single
linear
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STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: peptide
US-08-464-531-117
                                                                                                                                                                                                                                                                 10 GQLTI 14
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0; Indels

Length 62;

35.7%; Score 5; DB 1;

Query Match

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5248606-47
Patent No. 5248606
Patent No. 5248606
Patent No. 5248606
TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
NUMBER NO. SOUTHORES: 49
CURRENT APPLICATION DATA:
PAPPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
SEQ ID NO:47:
                                                                    APPLICANT: Freeman Jr., Robert M.
APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION TATA:
APPLICATION NUMBER: US/08/202,389
FILING APPLICATION TATA:
APPLICATION NUMBER: US 07/983,926
FILING APPLICATION NUMBER: US 07/983,926
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING APPLICATION NUMBER: US 07/829,141
FILING APPLICATION NUMBER: US 07/829,111
ATPONENTY/AGENT INFORMATION:
ATTAING DATE: 26-JUN-1991
ATTAING DATE: 26-JUN-1991
ATTAING DATE: 26-JUN-1991
ATTAING DATE: 26-JUN-1991
ATTAING DATE: 26-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BIH92-05MA
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 15, Application US/08202389 Patent No. 5536536 GENERALINFORMATION: GENERALING APPLICANT: Freeman Jr., Robert M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%; Sco.
100.0%; Pro
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 97 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                USA
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84 IVDAG 88
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                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                  APPLICANT: PAUL, Jeremy
APPLICANT: TRUBHEART, JOSHUA
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,137
FILING DATE: J3-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/309,313
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,431
FILING DATE: J1-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28 005
REGISTRATION NUMBER: 28 005
REGISTRATION NUMBER: 28 005
REGISTRATION NUMBER: 28 005
REGISTRATION NUMBER: 28 005
REGISTRATION NUMBER: 28 005
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%; Score 5, 100.0%; Pred. No. 63;
                                                                                                                                       Sequence 117, Application US/08322137
Patent No. 6100042
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 248633
INFORMATION FOR SEQ ID NO: 117:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                             MANFREDI, John
KLEIN, Christine
MURPHY, Andrew J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.7
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-322-137-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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21 IVDAG 25
                        21 IVDAG 25
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                                                                                           RESULT 10
US-08-322-137-117
                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Indels

RESULT

Length 97;

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APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERENCE: 4-30562A
CURRENT APPLICATION WUNBER: US/09/335,409
CURRENT APPLICATION WUNBER: US/09/335,409
CURRENT APPLICATION WUNBER: US/09/335,409
SOFTWARE: PALENTIN Ver: 2.0
SSO ID NO 23
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60, Application US/08928213B
Patent No. 6238905
GENERAL INFORMATION:
APPLICANT: MCHenry, Charles S.
Seville, Mark
Cull, Millard G.
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 35.7%; Score 5; DB 3; Length 135; Best Local Similarity 100.0%; Pred. No. 1.2e+0; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: USA
COMPUTE: 94104
COMPUTE: READABLE FORM:
COMPUTER: IS PER FIDEPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILIANTON NUMBER: US/08/928,213B
FILIANTON DATE: 12-Sep-1997
CLASSIFICATION: CURNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS: 205
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: ENZYCO-02550
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-705-8410
TELEFAX: 415-397-8338
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
                                                                                     Sequence 23, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 219 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Sorangium cellulosum US-09-335-409-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AGFEG 10
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                                                                                          ore 5; DB 6; Length 113;
red. No. 1.1e+02;
Mismatches 0; Indels
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1.1.2e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: LAC
STATE: WA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/20,389
FILING DATE: 28-FEB-1994
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
FILING DATE: 01-DEC-1992
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN.1991
FILING DATE: 31-JAN.1991
APPLICATION NUMBER: US 07/721,112
FILING DATE: 36-JUN.1991
ATORNEY/AGENT INFORMATION:
AREFERENCE/COCKET NUMBER: B1992-05MA
FELERANICATION INFORMATION:
ATELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
FNGTH: 126 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Preeman Jr., Robert M.
APPLICANT: Plutzky, Jorge
APPLICANT: Plutzky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%; Score 5; DB Best Local Similarity 100.0%; Pred. No. 1., Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08202389; Patent No. 5536636; GENERAL INFORMATION:
                                                                                        Query Match
Best Local Similarity 100.0%; P
Matches 5; Conservative 0;
                                                                                                                                                                                                          11111
30 VDAGF 34
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5248606-47
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| 84 IVDAG 88
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0; Gaps
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-08-928-213B-60
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| | | | | |
| Db 132 FEGOL 136
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Search completed: January 31, 2002, 13:15:13 Job time: 94 sec

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